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(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN BONE MARROW

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene expression in a sample derived from human bone marrow is described. Also described are single exon nucleic acid probes expressed in the bone marrow and their use in methods for detecting gene expression.

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HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
FOR ANALYSIS OF GENE EXPRESSION IN HUMAN BONE MARROW

CROSS REFERENCE TO RELATED APPLICATIONS

5

The present application is a continuation-in-part of U.S.
patent application serial nos. 09/632,366, filed August 3,
2000 and 09/608,408, filed June 30, 2000; claims the
benefit under 35 U.S.C. s 119(e) of U.S. provisional patent
10 application serial nos. 60/236,359, filed September 27,
2000, 60/234,687, filed September 21, 2000, 60/207,456,
filed May 26, 2000, and 60/180,312, filed February 4, 2000;
and further claims the benefit under 35 U.S.C. s 119(a) of
UK patent application no. 0024263.6, filed October 4, 2000,
15 the disclosures of which are incorporated herein by
reference in their entireties.

REFERENCE TO SEQUENCE LISTING AND INCORPORATION BY
REFERENCE THEREOF

20

The present application includes a Sequence Listing in
electronic format, filed pursuant to PCT Administrative
Instructions 801 - 806 on a single CD-R disc, in
triplicate, containing a file named pto_BONE_MARROW.txt,
25 created 24 January 2001, having 26,421,347 bytes. The
Sequence Listing contained in said file on said disc is
incorporated herein by reference in its entirety.

Field of the Invention

30

The present invention relates to genome-derived
single exon microarrays useful for verifying the expression
of regions of genomic DNA predicted to encode protein. In
particular, the present invention relates to unique genome-
35 derived single exon nucleic acid probes expressed in human

bone marrow and single exon nucleic acid microarrays that include such probes.

Background of the Invention

5 For almost two decades following the invention of general techniques for nucleic acid sequencing, Sanger et al., *Proc. Natl. Acad. Sci. USA* 70(4):1209-13 (1973); Gilbert et al., *Proc. Natl. Acad. Sci. USA* 70(12):3581-4 (1973), these techniques were used principally as tools to
10 further the understanding of proteins -- known or suspected -- about which a basic foundation of biological knowledge had already been built. In many cases, the cloning effort that preceded sequence identification had been both informed and directed by that antecedent
15 biological understanding.

 For example, the cloning of the T cell receptor for antigen was predicated upon its known or suspected cell type-specific expression, by its suspected membrane association, and by the predicted assembly of its gene via
20 T cell-specific somatic recombination. Subsequent sequencing efforts at once confirmed and extended understanding of this family of proteins. Hedrick et al., *Nature* 308(5955):153-8 (1984).

 More recently, however, the development of high
25 throughput sequencing methods and devices, in concert with large public and private undertakings to sequence the human and other genomes, has altered this investigational paradigm: today, sequence information often precedes understanding of the basic biology of the encoded protein
30 product.

 One of the approaches to large-scale sequencing is predicated upon the proposition that expressed sequences -- that is, those accessible through isolation of mRNA -- are of greatest initial interest. This "expressed
35 sequence tag" ("EST") approach has already yielded vast

amounts of sequence data (see for example Adams et al.,
Science 252:1651 (1991); Williamson, *Drug Discov. Today*
4:115 (1999)). For nucleic acids sequenced by this
approach, often the only biological information that is
5 known *a priori* with any certainty is the likelihood of
biologic expression itself. By virtue of the species and
tissue from which the mRNA had originally been obtained,
most such sequences are also annotated with the identity of
the species and at least one tissue in which expression
10 appears likely.

More recently, the pace of genomic sequencing has
accelerated dramatically. When genomic DNA serves as the
initial substrate for sequencing efforts, expression cannot
be presumed; often the only *a priori* biological information
15 about the sequence includes the species and chromosome (and
perhaps chromosomal map location) of origin.

With the ever-accelerating pace of sequence
accumulation by directed, EST, and genomic sequencing
approaches — and in particular, with the accumulation of
20 sequence information from multiple genera, from multiple
species within genera, and from multiple individuals within
a species — there is an increasing need for methods that
rapidly and effectively permit the functions of nucleic
sequences to be elucidated. And as such functional
25 information accumulates, there is a further need for
methods of storing such functional information in
meaningful and useful relationship to the sequence itself;
that is, there is an increasing need for means and
apparatus for annotating raw sequence data with known or
30 predicted functional information.

Although the increase in the pace of genomic
sequencing is due in large part to technological changes in
sequencing strategies and instrumentation, Service, *Science*
280:995 (1998); Pennisi, *Science* 283: 1822-1823 (1999),
35 there is an important functional motivation as well.

While it was understood that the EST approach would rarely be able to yield sequence information about the noncoding portions of the genome, it now also appears the EST approach is capable of capturing only a fraction of
5 a genome's actual expression complexity.

For example, when the *C. elegans* genome was fully sequenced, gene prediction algorithms identified over 19,000 potential genes, of which only 7,000 had been found by EST sequencing. *C. elegans* Sequencing Consortium,
10 *Science* 282:2012 (1998). Analogously, the recently completed sequence of chromosome 2 of *Arabidopsis* predicts over 4000 genes, Lin et al., *Nature*, 402:761 (1999), of which only about 6% had previously been identified via EST sequencing efforts. Although the human genome has the
15 greatest depth of EST coverage, it is still woefully short of surrendering all of its genes. One recent estimate suggests that the human genome contains more than 146,000 genes, which would at this point leave greater than half of the genes undiscovered. It is now predicted that many
20 genes, perhaps 20 to 50%, will only be found by genomic sequencing.

There is, therefore, a need for methods that permit the functional regions of genomic sequence – and most importantly, but not exclusively, regions that
25 function to encode genes – to be identified.

Much of the coding sequence of the human genome is not homologous to known genes, making detection of open reading frames ("ORFs") and predictions of gene function difficult. Computational methods exist for predicting
30 coding regions in eukaryotic genomes. Gene prediction programs such as GRAIL and GRAIL II, Uberbacher et al., *Proc. Natl. Acad. Sci. USA* 88(24):11261-5 (1991); Xu et al., *Genet. Eng.* 16:241-53 (1994); Uberbacher et al., *Methods Enzymol.* 266:259-81 (1996); GENEFINDER, Solovyev et
35 al., *Nucl. Acids. Res.* 22:5156-63 (1994); Solovyev et al.,

Ismb 5:294-302 (1997); and GENESCAN, Burge *et al.*, *J. Mol. Biol.* 268:78-94 (1997), predict many putative genes without known homology or function. Such programs are known, however, to give high false positive rates. Burset *et al.*,
5 *Genomics* 34:353-367 (1996). Using a consensus obtained by a plurality of such programs is known to increase the reliability of calling exons from genomic sequence. Ansari-Lari *et al.*, *Genome Res.* 8(1):29-40 (1998)

Identification of functional genes from genomic
10 data remains, however, an imperfect art. For example, in reporting the full sequence of human chromosome 21, the Chromosome 21 Mapping and Sequencing Consortium reports that prior bioinformatic estimates of human gene number may need to be revised substantially downwards. *Nature*
15 405:311-199 (2000); Reeves, *Nature* 405:283-284 (2000).

Thus, there is a need for methods and apparatus that permit the functions of the regions identified bioinformatically – and specifically, that permit the expression of regions predicted to encode protein – readily
20 to be confirmed experimentally.

Recently, the development of nucleic acid microarrays has made possible the automated and highly parallel measurement of gene expression. Reviewed in Schena (ed.), DNA Microarrays : A Practical Approach
25 (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 – 60 (1999); Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

30 It is common for microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, such as those from the I.M.A.G.E. consortium, Lennon *et al.*, *Genomics* 33(1):151-2 (1996), or from the construction of "problem specific" libraries
35 targeted at a particular biological question, R.S. Thomas

et al., *Cancer Res.* (in press). Such microarrays by definition can measure expression only of those genes found in EST libraries, and thus have not been useful as probes for genes discovered solely by genomic sequencing.

5 The utility of using whole genome nucleic acid microarrays to answer certain biological questions has been demonstrated for the yeast *Saccharomyces cerevisiae*. De Risi et al., *Science* 278:680 (1997). The vast majority of yeast nuclear genes, approximately 95% however, are single
10 exon genes, i.e., lack introns, Lopez et al., *RNA* 5:1135-1137 (1999); Goffeau et al., *Science* 274:563-67 (1996), permitting coding regions more readily to be identified. Whole genome nucleic acid microarrays have not generally been used to probe gene expression from more complex
15 eukaryotic genomes, and in particular from those averaging more than one intron per gene.

 Because bone marrow is the tissue in which blood cells originate, diseases of the bone marrow are a significant cause of human morbidity and mortality.
20 Increasingly, genetic factors are being found that contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these diseases. Although mutations in single genes have in some cases been identified as causal - notably in the thalassemias and sickle cell anemia
25 - disorders of the bone marrow are, for the most part, believed to have polygenic etiologies. There is a need for methods and apparatus that permit prediction, diagnosis and prognosis of diseases of the bone marrow, particularly those diseases with polygenic etiology.

30

Summary of the Invention

 The present invention solves these and other problems in the art by providing methods and apparatus for
35 predicting, confirming, and displaying functional

information derived from genomic sequence. The present invention also provides apparatus for verifying the expression of putative genes identified within genomic sequence.

5 In particular, the invention provides novel genome-derived single exon nucleic acid microarrays useful for verifying the expression of putative genes identified within genomic sequence.

The present invention also provides compositions
10 and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

Accordingly, in a first aspect of the invention,
15 there is provided a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human bone marrow, comprising a plurality of single exon nucleic acid probes according to any one of the nucleotide sequences set out in SEQ ID NOs:
20 1 - 13,114 or a complementary sequence, or a portion of such a sequence.

By plurality is meant at least two, suitably at least 20, most suitably at least 100, preferably at least 1000 and, most preferably, upto 5000.

25 In one embodiment of the first aspect, each of said plurality of probes is separately and addressably amplifiable.

In an alternative embodiment, each of said plurality of probes is separately and addressably
30 isolatable from said plurality.

In a preferred embodiment, each of said plurality of probes is amplifiable using at least one common primer. Preferably, each of said plurality of probes is amplifiable using a first and a second common primer.

35 In yet another embodiment, said set of single

exon nucleic acid probes comprises between 50 - 20,000 probes, for example, 50 - 5000.

Suitably, said set of single exon nucleic acid probes comprises at least 50 - 1000 discrete single exon nucleic acid probes having a sequence as set out in any of SEQ ID NOS.: 1 - 26,012 or a complimentary sequence, or a portion of such a sequence.

Preferably, the average length of the single exon nucleic acid probes is between 200 and 500 bp. It is preferred that the average length should be at least 200bp, suitably at least 250bp, most suitably at least 300bp, preferably at least 400bp and, most preferably, 500 bp.

In another embodiment, the single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

In another preferred embodiment, said single exon nucleic acid lack homopolymeric stretches of A or T. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

Preferably, a spatially-addressable set of single exon nucleic acid probes in accordance with the first aspect of the invention is addressably disposed upon a substrate.

Suitable substrates include a filter membrane which may, preferably, be nitrocellulose or nylon. The nylon may preferably, be positively-charged. Other suitable substrates include glass, amorphous silicon, crystalline silicon, and plastic. Further suitable materials include

polymethylacrylic, polyethylene, polypropylene,
polyacrylate, polymethylmethacrylate, polyvinylchloride,
polytetrafluoroethylene, polystyrene, polycarbonate,
polyacetal, polysulfone, celluloseacetate,
5 cellulosenitrate, nitrocellulose, and mixtures thereof.

In a second aspect of the invention, there is
provided a microarray comprising a spatially addressable
set of single exon nucleic acid probes in accordance with
the first aspect of the invention.

10 In one embodiment, a genome-derived single-exon
microarray is packaged together with such an ordered set of
amplifiable probes corresponding to the probes, or one or
more subsets of probes, thereon. In alternative
embodiments, the ordered set of amplifiable probes is
15 packaged separately from the genome-derived single exon
microarray.

In another aspect, the invention provides genome-
derived single exon nucleic acid probes useful for gene
expression analysis, and particularly for gene expression
20 analysis by microarray. In particular embodiments of this
aspect, the present invention provides human single-exon
probes that include specifically-hybridizable fragments of
SEQ ID Nos. 13,115 - 26,012, wherein the fragment
hybridizes at high stringency to an expressed human gene.
25 In particular embodiments, the invention provides single
exon probes comprising SEQ ID Nos. 1 - 13,114.

Accordingly, in a third aspect of the invention,
there is provided a single exon nucleic acid probe for
measuring human gene expression in a sample derived from
30 human bone marrow which is a nucleic acid molecule
comprising a nucleotide sequence as set out in any of SEQ
ID NOs.: 1 - 13,114 or a complementary sequence or a
fragment thereof wherein said probe hybridizes at high
stringency to a nucleic acid expressed in the human bone
35 marrow.

In one embodiment, a single exon nucleic acid probe in accordance with the third aspect comprises a nucleotide sequence as set out in any of SEQ ID NOs.: 13,115 - 26,012 or a complementary sequence or a fragment thereof.

In a fourth aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human bone marrow which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOs.: 26,013 - 38,628 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human bone marrow.

Preferably, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention comprises between at least 15 and 50 contiguous nucleotides of said SEQ ID NO:. It is preferred that the single exon nucleic acid probe comprises at least 15, suitably at least 20, more suitably at least 25 or preferably at least 50 contiguous nucleotides of said SEQ ID NO:.

In another preferred embodiment, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention is between 3kb and 25kb in length. It is preferred that said probe is no more than 3kb, suitably no more than 5kb, more suitably no more than 10kb, preferably 15kb, more preferably 20kb or, most preferably, no more than 20kb in length.

Preferably, a single exon nucleic acid probe in accordance with either the fifth or sixth aspect of the invention is DNA, preferably single-stranded DNA, RNA or PNA.

In another embodiment of either the third or fourth aspect of the invention, a single exon nucleic acid

probe is detectably labeled. Suitable detectable labels include a radionuclide, a fluorescent label or a first member of a specific binding pair. Suitable fluorescent labels include dyes such as cyanine dyes, preferably Cy3 and Cy5 although other suitable dyes will be known to those skilled in the art.

In a particularly preferred embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks prokaryotic and bacteriophage vector sequence. In yet another embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks homopolymeric stretches of A or T.

In a fifth aspect of the invention, there is provided an amplifiable nucleic acid composition, comprising:

the single exon nucleic acid probe in accordance with either of the third or fourth aspects of the invention; and at least one nucleic acid primer; wherein said at least one primer is sufficient to prime enzymatic amplification of said probe.

In an sixth aspect of the invention, there is provided a method of measuring gene expression in a sample derived from human bone marrow, comprising:

contacting the single exon microarray in accordance with the second aspect of the invention, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human bone marrow; and then measuring the label detectably bound to each probe of said microarray.

In a seventh aspect of the invention, there is provided a method of identifying exons in a eukaryotic genome, comprising:

algorithmically predicting at least one exon from

genomic sequence of said eukaryote; and then

detecting specific hybridization of detectably
labeled nucleic acids to a single exon probe,

wherein said detectably labeled nucleic acids are
5 derived from mRNA from the bone marrow of said eukaryote,
said probe is a single exon probe having a fragment
identical in sequence to, or complementary in sequence to,
said predicted exon, said probe is included within a single
exon microarray in accordance with the first aspect of the
10 invention, and said fragment is selectively hybridizable at
high stringency.

In a eighth aspect of the invention, there is
provided a method of assigning exons to a single gene,
comprising:

15 identifying a plurality of exons from genomic
sequence in accordance with the seventh aspect of the
invention; and then

measuring the expression of each of said exons in
a plurality of tissues and/or cell types using
20 hybridization to single exon microarrays having a probe
with said exon,

wherein a common pattern of expression of said
exons in said plurality of tissues and/or cell types
indicates that the exons should be assigned to a single
25 gene.

In an ninth aspect of the invention, there is
provided a nucleic acid sequence as set out in any of SEQ
ID NOS: 1 - 26,012 wherein said sequence encodes a peptide.

In a tenth aspect of the invention, there is
30 provided a peptide encoded by a sequence comprising a
sequence as set out in any of SEQ ID NOS: 13,115 - 26,012,
or a complementary sequence or coding portion thereof.

In a preferred embodiment, a peptide may be
encoded by a sequence comprising a sequence set out in any
35 of SEQ ID NOS.: 1 - 13,114.

In a further aspect, the invention provides peptides comprising an amino acid sequence translated from the DNA fragments, said amino acid sequences comprising SEQ ID NOS.: 26,013 - 38,628.

5 Accordingly in a eleventh aspect of the invention there is provided a peptide comprising a sequence as set out in any of SEQ ID NOs: 26,013 - 38,628, or fragment thereof.

 In another aspect, the invention provides means
10 for displaying annotated sequence, and in particular, for displaying sequence annotated according to the methods and apparatus of the present invention. Further, such display can be used as a preferred graphical user interface for electronic search, query, and analysis of such annotated
15 sequence.

Detailed Description of the Invention

20 Definitions

 As used herein, the term "microarray" and phrase "nucleic acid microarray" refer to a substrate-bound collection of plural nucleic acids, hybridization to each of the plurality of bound nucleic acids being separately
25 detectable. The substrate can be solid or porous, planar or non-planar, unitary or distributed.

 As so defined, the term "microarray" and phrase "nucleic acid microarray" include all the devices so called in Schena (ed.), DNA Microarrays: A Practical Approach
30 (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); Nature Genet. 21(1)(suppl):1 - 60 (1999); and Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376). As so defined, the
35 term "microarray" and phrase "nucleic acid microarray"

further include substrate-bound collections of plural nucleic acids in which the nucleic acids are distributably disposed on a plurality of beads, rather than on a unitary planar substrate, as is described, *inter alia*, in Brenner et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); in such case, the term "microarray" and phrase "nucleic acid microarray" refer to the plurality of beads in aggregate.

As used herein with respect to a nucleic acid microarray, the term "probe" refers to the nucleic acid that is, or is intended to be, bound to the substrate; in such context, the term "target" thus refers to nucleic acid intended to be bound thereto by Watson-Crick complementarity. As used herein with respect to solution phase hybridization, the term "probe" refers to the nucleic acid of known sequence that is detectably labeled.

As used herein, the expression "probe comprising SEQ ID NO.", and variants thereof, intends a nucleic acid probe, at least a portion of which probe has either (i) the sequence directly as given in the referenced SEQ ID NO., or (ii) a sequence complementary to the sequence as given in the referenced SEQ ID NO., the choice as between sequence directly as given and complement thereof dictated by the requirement that the probe hybridize to mRNA.

As used herein, the term "open reading frame" and the equivalent acronym "ORF" refer to that portion of an exon that can be translated in its entirety into a sequence of contiguous amino acids i.e. a nucleic acid sequence that, in at least one reading frame, does not possess stop codons; the term does not require that the ORF encode the entirety of a natural protein.

As used herein, the term "amplicon" refers to a PCR product amplified from human genomic DNA, containing the predicted exon.

As used herein the term "exon" refers to the

consensus prediction of the various exon and gene predicting algorithms i.e. a nucleic acid sequence bioinformatically predicted to encode a portion of a natural protein.

5 As used herein, the term "peptide" refers to a sequence of amino acids. The sequences referred to as PEPTIDE SEQ ID NOS.: are the predicted peptide sequences that would be translated from one of the exons, or a portion thereof set out in exon SEQ ID NOS.: The codons
10 encoding the peptide are wholly contained within the exon.

 As used herein, a "portions" of a defined nucleotide sequence or sequences can be and, preferably, are fragments unique to that sequence or to one or a combination of those sequences. A fragment unique to a
15 nucleic acid molecule is one that is a signature for the larger nucleic acid molecule.

 As used herein, the phrase "expression of a probe" and its linguistic variants means that the ORF present within the probe, or its complement, is present
20 within a target mRNA.

 As used herein, "stringent conditions" refers to parameters well known to those skilled in the art. When a nucleic acid molecule is said to be hybridisable to another of a given sequence under "stringent conditions" it is
25 meant that it is homologous to the given sequence.

 As used herein, the phrase "specific binding pair" intends a pair of molecules that bind to one another with high specificity. Binding pairs are said to exhibit specific binding when they exhibit avidity of at least 10^7 ,
30 preferably at least 10^8 , more preferably at least 10^9 liters/mole. Nonlimiting examples of specific binding pairs are: antibody and antigen; biotin and avidin; and biotin and streptavidin.

 As used herein with respect to the visual display
35 of annotated genomic sequence, the term "rectangle" means

any geometric shape that has at least a first and a second border, wherein the first and second borders each are capable of mapping uniquely to a point of another visual object of the display.

5 As used herein, a "Mondrian" means a visual display in which a single genomic sequence is annotated with predicted and experimentally confirmed functional information.

10

Brief Description of the Drawings

The present invention is further illustrated with reference to the following non-limiting figures and
15 examples in which:

FIG. 1 illustrates a process for predicting functional regions from genomic sequence, confirming the functional activity of such regions experimentally, and associating and displaying the data so obtained in
20 meaningful and useful relationship to the original sequence data;

FIG. 2 further elaborates that portion of the process schematized in FIG. 1 for predicting functional regions from genomic sequence;

25 FIG. 3 illustrates a Mondrian visual display;

FIG. 4 presents a Mondrian showing a hypothetical annotated genomic sequence;

FIG. 5 is a histogram showing the distribution of ORF length and PCR products as obtained, with ORF length
30 shown in black and PCR product length shown in dotted lines;

FIG. 6 is a histogram showing the distribution, among exons predicted according to the methods described, of expression as measured using simultaneous two color
35 hybridization to a genome-derived single exon microarray.

The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), or expressed in all tissues tested ("10");

5 FIG. 7 is a pictorial representation of the expression of verified sequences that showed expression with signal intensity greater than 3 in at least one tissue, with: FIG. 7A showing the expression as measured by microarray hybridization in each of the 10 measured
10 tissues, and the expression as measured "bioinformatically" by query of EST, NR and SwissProt databases; with FIG. 7B showing the legend for display of physical expression (ratio) in FIG. 7A; and with FIG. 7C showing the legend for scoring EST hits as depicted in FIG. 7A;

15 FIG. 8 shows a comparison of normalized CY3 signal intensity for arrayed sequences that were identical to sequences in existing EST, NR and SwissProt databases or that were dissimilar (unknown), where black denotes the signal intensity for all sequence-verified products with a
20 BLAST Expect ("E") value of greater than $1e-30$ (1×10^{-30}) ("unknown") and a dotted line denotes sequence-verified spots with a BLAST expect ("E") value of less than $1e-30$ (1×10^{-30}) ("known");

FIG. 9 presents a Mondrian of BAC AC008172 (bases
25 25,000 to 130,000), containing the carbamyl phosphate synthetase gene (AF154830.1); and

FIG. 10 is a Mondrian of BAC A049839.

30 Methods and Apparatus for Predicting, Confirming,
Annotating, and Displaying Functional Regions From Genomic
Sequence Data

FIG. 1 is a flow chart illustrating in broad
35 outline a process for predicting functional regions from

genomic sequence, confirming and characterizing the functional activity of such regions experimentally, and then associating and displaying the information so obtained in meaningful and useful relationship to the original
5 sequence data.

The initial input into process 10 of the present invention is drawn from one or more databases 100 containing genomic sequence data. Because genomic sequence is usually obtained from subgenomic fragments, the sequence
10 data typically will be stored in a series of records corresponding to these subgenomic sequenced fragments. Some fragments will have been catenated to form larger contiguous sequences ("contigs"); others will not. A finite percentage of sequence data in the database will
15 typically be erroneous, consisting *inter alia* of vector sequence, sequence created from aberrant cloning events, sequence of artificial polylinkers, and sequence that was erroneously read.

Each sequence record in database 100 will
20 minimally contain as annotation a unique sequence identifier (accession number), and will typically be annotated further to identify the date of accession, species of origin, and depositor. Because database 100 can contain nongenomic sequence, each sequence will typically
25 be annotated further to permit query for genomic sequence. Chromosomal origin, optionally with map location, can also be present. Data can be, and over time increasingly will be, further annotated with additional information, in part through use of the present invention, as described below.
30 Annotation can be present within the data records, in information external to database 100 and linked to the records thereto, or through a combination of the two.

Databases useful as genomic sequence database 100 in the present invention include GenBank, and particularly
35 include several divisions thereof, including the

- htgs(draft), NT (nucleotide, command line), and NR (nonredundant) divisions. GenBank is produced by the National Institutes of Health and is maintained by the National Center for Biotechnology Information (NCBI).
- 5 Databases of genomic sequence from species other than human, such as mouse, rat, Arabidopsis, *C. elegans*, *C. brigssii*, *Drosophila*, zebra fish, and other higher eukaryotic organisms will also prove useful as genomic sequence database 100.
- 10 Genomic sequence obtained by query of genomic sequence database 100 is then input into one or more processes 200 for identification of regions therein that are predicted to have a biological function as specified by the user. Such functions include, but are not limited to,
- 15 encoding protein, regulating transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription into mRNA, of regulating message degradation after transcription into mRNA, and the like. Other functions include directing
- 20 somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, and the like.
- The particular genomic sequence to be input into process 200 will depend upon the function for which
- 25 relevant sequence is to be identified as well as upon the approach chosen for such identification. Process step 200 can be iterated to identify different functions within a given genomic region. In such case, the input often will be different for the several iterations.
- 30 Sequences predicted to have the requisite function by process 200 are then input into process 300, where a subset of the input sequences suitable for experimental confirmation is identified. Experimental confirmation can involve physical and/or bioinformatic
- 35 assay. Where the subsequent experimental assay is

bioinformatic, rather than physical, there are fewer constraints on the sequences that can be tested, and in this latter case therefore process 300 can output the entirety of the input sequence.

5 The subset of sequences output from process 300 is then used in process 400 for experimental verification and characterization of the function predicted in process 200, which experimental verification can, and often will, include both physical and bioinformatic assay.

10 Process 500 annotates the sequence data with the functional information obtained in the physical and/or bioinformatic assays of process 400. Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by
15 incorporating the functional data into the sequence data record itself, by linking records in a hierarchical or relational database, by linking to external databases, by a combination thereof, or by other means well known within the database arts. The data can even be submitted for
20 incorporation into databases maintained by others, such as GenBank, which is maintained by NCBI.

As further noted in FIG. 1, additional annotation can be input into process 500 from external sources 600.

The annotated data is then displayed in process
25 800, either before, concomitantly with, or after optional storage 700 on nontransient media, such as magnetic disk, optical disc, magnetooptical disk, flash memory, or the like.

FIG. 1 shows that the experimental data output
30 from process 400 can be used in each preceding step of process 10: e.g., facilitating identification of functional sequences in process 200, facilitating identification of an experimentally suitable subset thereof in process 300, and facilitating creation of physical and/or informational
35 substrates for, and performance of subsequent assay, of

functional sequences in process 400.

Information from each step can be passed directly to the succeeding process, or stored in permanent or interim form prior to passage to the succeeding process.

5 Often, data will be stored after each, or at least a plurality, of such process steps. Any or all process steps can be automated.

FIG. 2 further elaborates the prediction of functional sequence within genomic sequence according to
10 process 200.

Genomic sequence database 100 is first queried 20 for genomic sequence.

The sequence required to be returned by query 20 will depend, in the first instance, upon the function to be
15 identified.

For example, genomic sequences that function to encode protein can be identified *inter alia* using gene prediction approaches, comparative sequence analysis approaches, or combinations of the two. In gene prediction
20 analysis, sequence from one genome is input into process 200 where at least one, preferably a plurality, of algorithmic methods are applied to identify putative coding regions. In comparative sequence analysis, by contrast, corresponding, e.g., syntenic, sequence from a plurality of
25 sources, typically a plurality of species, is input into process 200, where at least one, possibly a plurality, of algorithmic methods are applied to compare the sequences and identify regions of least variability.

The exact content of query 20 will also depend
30 upon the database queried. For example, if the database contains both genomic and nongenomic sequence, perhaps derived from multiple species, and the function to be determined is protein coding regions in human genomic sequence, the query will accordingly require that the
35 sequence returned be genomic and derived from humans.

Query 20 can also incorporate criteria that compel return of sequence that meets operative requirements of the subsequent analytical method. Alternatively, or in addition, such operative criteria can be enforced in
5 subsequent preprocess step 24.

For example, if the function sought to be identified is protein coding, query 20 can incorporate criteria that return from genomic sequence database 100 only those sequences present within contigs sufficiently
10 long as to have obviated substantial fragmentation of any given exon among a plurality of separate sequence fragments.

Such criteria can, for example, consist of a required minimal individual genomic sequence fragment
15 length, such as 10 kb, more typically 20 kb, 30 kb, 40kb, and preferably 50 kb or more, as well as an optional further or alternative requirement that sequence from any given clone, such as a bacterial artificial chromosome ("BAC"), be presented in no more than a finite maximal
20 number of fragments, such as no more than 20 separate pieces, more typically no more than 15 fragments, even more typically no more than about 10 - 12 fragments.

Results using the present invention have shown that genomic sequence from bacterial artificial chromosomes
25 (BACs) is sufficient for gene prediction analysis according to the present invention if the sequence is at least 50 kb in length, and if additionally the sequence from any given BAC is presented in fewer than 15, and preferably fewer than 10, fragments. Accordingly, query 20 can incorporate
30 a requirement that data accessioned from BAC sequencing be in fewer than 15, preferably fewer than 10, fragments.

An additional criterion that can be incorporated into the query can be the date, or range of dates, of sequence accession. Although the process has been
35 described above as if genomic sequence database 100 were

static, it is of course understood that the genomic
sequence databases need not be static, and indeed are
typically updated on a frequent, even hourly, basis. Thus,
as further described in Examples 1 and 2, *infra*, it is
5 possible to query the database for newly added sequence,
either newly added after an absolute date, or newly added
relative to a prior analysis performed using the methods
and apparatus of the present invention. In this way, the
process herein described can incorporate a dynamic,
10 temporal component.

One utility of such temporal limitation is to
identify, from newly accessioned genomic sequence, the
presence of novel genes, particularly those not previously
identified by EST sequencing (or other sequencing efforts
15 that are similarly based upon gene expression). As further
described in Example 1, such an approach has shown that
newly accessioned human genomic sequence, when analyzed for
sequences that function to encode protein, readily
identifies genes that are novel over those in existing EST
20 and other expression databases. This makes the methods of
the present invention extremely powerful gene discovery
tools. And as would be appreciated, such gene discovery
can be performed using genomic sequence from species other
than human.

25 If query 20 incorporates multiple criteria, such
as above-described, the multiple criteria can be performed
as a series of separate queries or as a single query,
depending in part upon the query language, the complexity
of the query, and other considerations well known in the
30 database arts.

If query 20 returns no genomic sequence meeting
the query criteria, the negative result can be reported by
process 22, and process 200 (and indeed, entire process 10)
ended 23, as shown. Alternatively, or in addition to
35 report and termination of the initial inquiry, a new query

20 can be generated that takes into account the initial negative result.

When query 20 returns sequence meeting the query criteria, the returned sequence is then passed to optional preprocessing 24, suitable and specific for the desired analytical approach and the particular analytical methods thereof to be used in process 25.

Preprocessing 24 can include processes suitable for many approaches and methods thereof, as well as processes specifically suited for the intended subsequent analysis.

Preprocessing 24 suitable for most approaches and methods will include elimination of sequence irrelevant to, or that would interfere with, the subsequent analysis. Such sequence includes repetitive sequence, such as Alu repeats and LINE elements, vector sequence, artificial sequence, such as artificial polylinkers, and the like. Such removal can readily be performed by identification and subsequent masking of the undesired sequence.

Identification can be effected by comparing the genomic sequence returned by query 20 with public or private databases containing known repetitive sequence, vector sequence, artificial sequence, and other artifactual sequence. Such comparison can readily be done using programs well known in the art, such as CROSS_MATCH, or by proprietary sequence comparison programs the engineering of which is well within the skill in the art.

Alternatively, or in addition, undesirable, including artifactual, sequence can be identified algorithmically without comparison to external databases and thereafter removed. For example, synthetic polylinker sequence can be identified by an algorithm that identifies a significantly higher than average density of known restriction sites. As another example, vector sequence can be identified by algorithms that identify nucleotide or

codon usage at variance with that of the bulk of the genomic sequence.

Once identified, undesired sequence can be removed. Removal can usefully be done by masking the undesired sequence as, for example, by converting the specific nucleotide references to one that is unrecognized by the subsequent bioinformatic algorithms, such as "X". Alternatively, but at present less preferred, the undesired sequence can be excised from the returned genomic sequence, leaving gaps.

Preprocessing 24 can further include selection from among duplicative sequences of that one sequence of highest quality. Higher quality can be measured as a lower percentage of, fewest number of, or least densely clustered occurrence of ambiguous nucleotides, defined as those nucleotides that are identified in the genomic sequence using symbols indicating ambiguity. Higher quality can also or alternatively be valued by presence in the longest contig.

Preprocessing 24 can, and often will, also include formatting of the data as specifically appropriate for passage to the analytical algorithms of process 25. Such formatting can and typically will include, *inter alia*, addition of a unique sequence identifier, either derived from the original accession number in genomic sequence database 100, or newly applied, and can further include additional annotation. Formatting can include conversion from one to another sequence listing standard, such as conversion to or from FASTA or the like, depending upon the input expected by the subsequent process.

Preprocessing, which can be optional depending upon the function desired to be identified and the informational requirements of the methods for effecting such identification, is followed by sequence processing 25, where sequences with the desired function are identified

within the genomic sequence.

As mentioned above, such functions can include, but are not limited to, encoding protein, regulating transcription, regulating message transport after
5 transcription into mRNA, regulating message splicing after transcription, of regulating message degradation, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X
10 chromosome inactivation, or the like.

The methods of the present invention are particularly useful for gene discovery, that is, for identifying, from genomic sequence, regions that function to encode genes, and in a particularly useful embodiment,
15 for identifying regions that function to encode genes not hitherto identified by expression-based or directed cloning and sequencing. In conjunction with verification using the novel single exon microarrays of the present invention, as further described below, the methods herein described
20 become powerful gene discovery tools.

Accordingly, in a preferred embodiment of the present invention, process 25 is used to identify putative coding regions. Two preferred approaches in process 25 for identifying sequence that encodes putative genes are gene
25 prediction and comparative sequence analysis.

Gene prediction can be performed using any of a number of algorithmic methods, embodied in one or more software programs, that identify open reading frames (ORFs) using a variety of heuristics, such as GRAIL, DICTION, and
30 GENEFINDER. Comparative sequence analysis similarly can be performed using any of a variety of known programs that identify regions with lower sequence variability.

As further described in Example 1, below, gene finding software programs yield a range of results. For
35 the newly accessioned human genomic sequence input in

Example 1, for example, GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed; GENEFINDER was second, calling 1%; and DICTION yielded the least putative coding region, with
5 0.8% of genomic sequence called as coding region.

Increased reliability can be obtained when consensus is required among several such methods. Although discussed herein particularly with respect to exon calling, consensus among methods will in general increase
10 reliability of predicting other functions as well.

Thus, as indicated by query 26, sequence processing 25, optionally with preprocessing 24, can be repeated with a different method, with consensus among such iterations determined and reported in process 27.

15 Process 27 compares the several outputs for a given input genomic sequence and identifies consensus among the separately reported results. The consensus itself, as well as the sequence meeting that consensus, is then stored in process 29a, displayed in process 29b, and/or output to
20 process 300 for subsequent identification of a subset thereof suitable for assay.

Multiple levels of consensus can be calculated and reported by process 27. For example, as further described in Example 1, *infra*, process 27 can report
25 consensus as between all specific pairs of methods of gene prediction, as consensus among any one or more of the pairs of methods of gene prediction, or as among all of the gene prediction algorithms used. Thus, in Example 1, process 27 reported that GRAIL and GENEFINDER programs agreed on 0.7%
30 of genomic sequence, that GRAIL and DICTION agreed on 0.5% of genomic sequence, and that the three programs together agreed on 0.25% of the data analyzed. Put another way, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

35 Furthermore, consensus can be required among

different approaches to identifying a chosen function.

For example, if the function desired to be identified is coding of protein sequence, and a first used approach to exon calling is gene prediction, the process
5 can be repeated on the same input sequence, or subset thereof, with another approach, such as comparative sequence analysis. In such a case, where comparative sequence analysis follows gene prediction, the comparison can be performed not only on genomic nucleic acid sequence,
10 but additionally or alternatively can be performed on the predicted amino acid sequence translated from the ORFs prior identified by the gene prediction approach.

Although shown as an iterative process, the multiple analyses required to achieve consensus can be done
15 in series, in parallel, or some combination thereof.

Predicted functional sequence, optionally representing a consensus among a plurality of methods and approaches for determination thereof, is passed to process
20 300 for identification of a subset thereof for functional assay.

In the preferred embodiment of the methods of the present invention, wherein the function sought to be identified is protein coding, process 300 is used to identify a subset thereof suitable for experimental
25 verification by physical and/or bioinformatic approaches.

For example, putative ORFs identified in process 200 can be classified, or binned, bioinformatically into putative genes. This binning can be based *inter alia* upon consideration of the average number of exons/gene in the
30 species chosen for analysis, upon density of exons that have been called on the genomic sequence, and other empirical rules. Thereafter, one or more among the gene-specific ORFs can be chosen for subsequent use in gene expression assay.

35 Where such subsequent gene expression assay uses

amplified nucleic acid, considerations such as desired amplicon length, primer synthesis requirements, putative exon length, sequence GC content, existence of possible secondary structure, and the like can be used to identify
5 and select those ORFs that appear most likely successfully to amplify. Where subsequent gene expression assay relies upon nucleic acid hybridization, whether or not using amplified product, further considerations involving hybridization stringency can be applied to identify that
10 subset of sequences that will most readily permit sequence-specific discrimination at a chosen hybridization and wash stringency. One particular such consideration is avoidance of putative exons that span repetitive sequence; such sequence can hybridize spuriously to nonspecific message,
15 reducing specific signal in the hybridization.

For bioinformatic assay, there are fewer constraints on the sequences that can be tested experimentally, and in this latter case therefore process
300 can output the entirety of the input sequence.

20 The subset of sequences identified by process 300 as suitable for use in assay is then used in process 400 to create the physical and/or informational substrate for experimental verification of the predictions made in process 200, and thereafter to assay those substrates.

25 As mentioned, the methods of the present invention are particularly useful for identifying potential coding regions within genomic sequence. In a preferred embodiment of process 400, therefore, the expression of the sequences predicted to encode protein is verified. The
30 combination of the predictive and experimental methods provides a powerful gene discovery engine.

Thus, in another aspect, the present invention provides methods and apparatus for verifying the expression of putative genes identified within genomic sequence. In
35 particular, the invention provides a novel method of

verifying gene expression in which expression of predicted ORFs is measured and confirmed using a novel type of nucleic acid microarray, the genome-derived single exon nucleic acid microarrays of the present invention.

5 Putative ORFs as predicted by a consensus of gene calling, particularly gene prediction, algorithms in process 200, and as further identified as suitable by process 300, are amplified from genomic DNA using the polymerase chain reaction (PCR). Although PCR is
10 conveniently used, other amplification approaches can also be used.

Amplification schemes can be designed to capture the entirety of each predicted ORF in an amplicon with minimal additional (that is, intronic or intergenic)
15 sequence. Because ORFs predicted from human genomic sequence using the methods of the present invention differ in length, such an approach results in amplicons of varying length.

However, most predicted ORFs are shorter than 500
20 bp in length, and although amplicons of at least about 100 or 200 base pairs can be immobilized as probes on nucleic acid microarrays, early experimental results using the methods of the present invention have suggested that longer amplicons, at least about 400 or 500 base pairs, are more
25 effective. Furthermore, certain advantages derive from application to the microarray of amplicons of defined size.

Therefore, amplification schemes can alternatively, and preferably, be designed to amplify regions of defined size, preferably at least about 300, 400
30 or 500 bp, centered about each predicted ORF. Such an approach results in a population of amplicons of limited size diversity, but that typically contain intronic and/or intergenic nucleic acid in addition to putative ORF.

Conversely, somewhat fewer than 10% of ORFs
35 predicted from human genomic sequence according to the

methods of the present invention exceed 500 bp in length. Portions of such extended ORFs, preferably at least about 300, 400 or 500 bp in length, can be amplified. However, it has been discovered that the percentage success at
5 amplifying pieces of such ORFs is low, and that such putative exons are more effectively amplified when larger fragments, at least about 1000 or 1500 bp, and even as large as 2000 bp are amplified.

The putative ORFs selected in process 300 are
10 thus input into one or more primer design programs, such as PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>), with a goal of amplifying at least about 500 base pairs of genomic sequence centered within or about ORFs predicted to be no
15 more than about 500 bp, or at least about 1000 - 1500 bp of genomic sequence for ORFs predicted to exceed 500 bp in length, and the primers synthesized by standard techniques. Primers with the requisite sequences can be purchased commercially or synthesized by standard techniques.

20 Conveniently, a first predetermined sequence can be added commonly to the ORF-specific 5' primer and a second, typically different, predetermined sequence commonly added to each 3' ORF-unique primer. This serves to immortalize the amplicon, that is, serves to permit
25 further amplification of any amplicon using a single set of primers complementary respectively to the common 5' and common 3' sequence elements. The presence of these "universal" priming sequences further facilitates later sequence verification, providing a sequence common to all
30 amplicons at which to prime sequencing reactions. The common 5' and 3' sequences further serve to add a cloning site should any of the ORFs warrant further study.

Such predetermined sequence is usefully at least about 10, 12 or 15 nt in length, and usually does not
35 exceed about 25 nt in length. The "universal" priming

sequences used in the examples presented *infra* were each 16 nt long.

The genomic DNA to be used as substrate for amplification will come from the eukaryotic species from which the genomic sequence data had originally been obtained, or a closely related species, and can conveniently be prepared by well known techniques from somatic or germline tissue or cultured cells of the organism. See, e.g., Short Protocols in Molecular Biology : A Compendium of Methods from Current Protocols in Molecular Biology, Ausubel et al. (eds.), 4th edition (April 1999), John Wiley & Sons (ISBN: 047132938X) and Maniatis et al., Molecular Cloning : A Laboratory Manual, 2nd edition (December 1989), Cold Spring Harbor Laboratory Press (ISBN: 0879693096). Many such prepared genomic DNAs are available commercially, with the human genomic DNAs additionally having certification of donor informed consent.

Although the intronic and intergenic material flanking putative coding regions in the amplicons could potentially interfere with hybridizations during microarray experiments, we have found, surprisingly, that differential expression ratios are not significantly affected. Rather, the predominant effect of exon size is to alter the absolute signal intensity, rather than its ratio. Equally surprising, the art had suggested that single exon probes would not provide sufficient signal intensity for high stringency hybridization analyses; we find that such probes not only provide adequate signal, but have substantial advantages, as herein described.

After partial purification, as by size exclusion spin column, with or without confirmation as to amplicon quality as by gel electrophoresis, each amplicon (single exon probe) is disposed in an array upon a support substrate.

Methods for creating microarrays by deposition and fixation of nucleic acids onto support substrates are well known in the art (Reviewed by Schena et al., see above).

5 Typically, the support substrate will be glass, although other materials, such as amorphous or crystalline silicon or plastics. Such plastics include polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride, 10 polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, or mixtures thereof, can also be used. Typically, the support will be rectangular, although other shapes, particularly circular disks and even 15 spheres, present certain advantages. Particularly advantageous alternatives to glass slides as support substrates for array of nucleic acids are optical discs, as described in WO 98/12559.

 The amplified nucleic acids can be attached 20 covalently to a surface of the support substrate or, more typically, applied to a derivatized surface in a chaotropic agent that facilitates denaturation and adherence by presumed noncovalent interactions, or some combination thereof.

25 Robotic spotting devices useful for arraying nucleic acids on support substrates can be constructed using public domain specifications (The MGuide, version 2.0, <http://cmgm.stanford.edu/pbrown/mguide/index.html>), or can conveniently be purchased from commercial sources 30 (MicroArray GenII Spotter and MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Spotting can also be effected by printing methods, including those using ink jet technology.

 As is well known in the art, microarrays 35 typically also contain immobilized control nucleic acids.

For controls useful in providing measurements of background signal for the genome-derived single exon microarrays of the present invention, a plurality of *E. coli* genes can readily be used. As further described in Example 1, 16 or
5 32 *E. coli* genes suffice to provide a robust measure of background noise in such microarrays.

As is well known in the art, the amplified product disposed in arrays on a support substrate to create a nucleic acid microarray can consist entirely of natural
10 nucleotides linked by phosphodiester bonds, or alternatively can include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained in the hybridization. If enzymatic amplification is used to produce the
15 immobilized probes, the amplifying enzyme will impose certain further constraints upon the types of nucleic acid analogs that can be generated.

Although particularly described herein as using high density microarrays constructed on planar substrates,
20 the methods of the present invention for confirming the expression of ORFs predicted from genomic sequence can use any of the known types of microarrays, as herein defined, including lower density planar arrays, and microarrays on nonplanar, nonunitary, distributed substrates.

25 For example, gene expression can be confirmed using hybridization to lower density arrays, such as those constructed on membranes, such as nitrocellulose, nylon, and positively-charged derivatized nylon membranes. Further, gene expression can also be confirmed using
30 nonplanar, bead-based microarrays such as are described in Brenner et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); U.S. Patent No. 6,057,107; and U.S. Patent No. 5,736,330. In theory, a packed collection of such beads provides in aggregate a higher density of nucleic acid
35 probe than can be achieved with spotting or lithography

techniques on a single planar substrate.

Planar microarrays on solid substrates, however, provide certain useful advantages, including high throughput and compatibility with existing readers. For example, each standard microscope slide can include at least 1000, typically at least 2000, preferably 5000 and upto 10,000 - 50,000 or more nucleic acid probes of discrete sequence. The number of sequences deposited will depend on their required application.

Each putative gene can be represented in the array by a single predicted ORF. Alternatively, genes can be represented by more than one predicted ORF. For purposes of measuring differential splicing, more than one predicted ORF will be provided for a putative gene. And as is well known in the art, each probe of defined sequence, representing a single predicted ORF, can be deposited in a plurality of locations on a single microarray to provide redundancy of signal.

The genome-derived single exon microarrays described above differ in several fundamental and advantageous ways from microarrays presently used in the gene expression art, including (1) those created by deposition of mRNA-derived nucleic acids, (2) those created by *in situ* synthesis of oligonucleotide probes, and (3) those constructed from yeast genomic DNA.

Most nucleic acid microarrays that are in use for study of eukaryotic gene expression have as immobilized probes nucleic acids that are derived - either directly or indirectly - from expressed message. As discussed above, it is common, for example, for such microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, see Lennon et al., or from the *de novo* construction of "problem specific" libraries targeted at a particular biological question, R.S. Thomas et al., *Cancer Res.* (in press). Such

microarrays are herein collectively denominated "EST microarrays".

Such EST microarrays by definition can measure expression only of those genes found in EST libraries, shown herein to represent only a fraction of expressed genes. Furthermore, such libraries - and thus microarrays based thereupon - are biased by the tissue or cell type of message origin, by the expression levels of the respective genes within the tissues, and by the ability of the message successfully to have been reverse-transcribed and cloned.

Thus, as further discussed in Example 1, the methods of the present invention enable sequences that do not appear in EST or other expression databases to be determined - subsequently arrayed for expression measurements could not, therefore, have been represented as probes on an EST microarray. And as further demonstrated in the examples, *infra*, the remaining population of genes identified from genomic sequence by the methods of the present invention - that is, the one third of sequences that had previously been accessioned in EST or other expression databases - are biased toward genes with higher expression levels.

Representation of a message in an EST and/or cDNA library depends upon the successful reverse transcription, optionally but typically with subsequent successful cloning, of the message. This introduces substantial bias into the population of probes available for arraying in EST microarrays.

In contrast, neither reverse transcription nor cloning is required to produce the probes arrayed on the genome-derived single exon microarrays of the present invention. And although the ultimate deposition of a probe on the genome-derived single exon microarray of the present invention depends upon a successful amplification from genomic material, *a priori* knowledge of the sequence of the

desired amplicon affords greater opportunity to recover any given probe sequence recalcitrant to amplification than is afforded by the requirement for successful reverse transcription and cloning of unknown message in EST
5 approaches.

Thus, the genome-derived single exon microarrays of the present invention present a far greater diversity of probes for measuring gene expression, with far less bias, than do EST microarrays presently used in the art.

10 As a further consequence of their ultimate origin from expressed message, the probes in EST microarrays often contain poly-A (or complementary poly-T) stretches derived from the poly-A tail of mature mRNA. These homopolymeric stretches contribute to cross-hybridization, that is, to a
15 spurious signal occasioned by hybridization to the homopolymeric tail of a labeled cDNA that lacks sequence homology to the gene-specific portion of the probe.

In contrast, the probes arrayed in the genome-derived single exon microarrays of the present invention
20 lack homopolymeric stretches derived from message polyadenylation, and thus can provide more specific signal. Typically, at least about 50, 60 or 75% of the probes on the genome-derived single exon microarrays of the present invention lack homopolymeric regions consisting of A or T,
25 where a homopolymeric region is defined for purposes herein as stretches of 25 or more, typically 30 or more, identical nucleotides.

A further distinction, which also affects the specificity of hybridization, is occasioned by the typical
30 derivation of EST microarray probes from cloned material. Because much of the probe material disposed as probes on EST microarrays is excised or amplified from plasmid, phage, or phagemid vectors, EST microarrays typically include a fair amount of vector sequence, more so when the
35 probes are amplified, rather than excised, from the vector.

In contrast, the vast majority of probes in the genome-derived single exon microarrays of the present invention contain no prokaryotic or bacteriophage vector sequence, having been amplified directly or indirectly from genomic DNA. Typically, therefore, at least about 50, 60, 70 or 80% or more of individual exon-including probes disposed on a genome-derived single exon microarray of the present invention lack vector sequence, and particularly lack sequences drawn from plasmids and bacteriophage. Preferably, at least about 85, 90 or more than 90% of exon-including probes in the genome-derived single exon microarray of the present invention lack vector sequence. With attention to removal of vector sequences through preprocessing 24, percentages of vector-free exon-including probes can be as high as 95 - 99%. The substantial absence of vector sequence from the genome-derived single exon microarrays of the present invention results in greater specificity during hybridization, since spurious cross-hybridization to a probe vector sequence is reduced.

As a further consequence of excision or amplification of probes from vectors in construction of EST microarrays, the probes arrayed thereon often contain artificial sequence, derived from vector polylinker multiple cloning sites, at both 5' and 3' ends. The probes disposed upon the genome-derived single exon microarrays need have no such artificial sequence appended thereto.

As mentioned above, however, the ORF-specific primers used to amplify putative ORFs can include artificial sequences, typically 5' to the ORF-specific primer sequence, useful for "universal" (that is, independent of ORF sequence) priming of subsequent amplification or sequencing reactions. When such "universal" 5' and/or 3' priming sequences are appended to the amplification primers, the probes disposed upon the genome-derived single exon microarray will include

artificial sequence similar to that found in EST
microarrays. However, the genome-derived single exon
microarray of the present invention can be made without
such sequences, and if so constructed, presents an even
5 smaller amount of nonspecific sequence that would
contribute to nonspecific hybridization.

Yet another consequence of typical use of cloned
material as probes in EST microarrays is that such
microarrays contain probes that result from cloning
10 artifacts, such as chimeric molecules containing coding
region of two separate genes. Derived from genomic
material, typically not thereafter cloned, the probes of
the genome-derived single exon microarrays of the present
invention lack such cloning artifacts, and thus provide
15 greater specificity of signal in gene expression
measurements.

A further consequence of the cloned origin of
probes on many EST microarrays is that the individual
probes often have disparate sizes, which can cause the
20 optimal hybridization stringency to vary among probes on a
single microarray. In contrast, as discussed above, the
probes arrayed on the genome-derived single exon
microarrays of the present invention can readily be
designed to have a narrow distribution in sizes, with the
25 range of probe sizes no greater than about 10% of the
average size, typically no greater than about 5% of the
average probe size.

Because of their origin from fully- or partially-
spliced message, probes disposed upon EST arrays will often
30 include multiple exons. The percentage of such exon-
spanning probes in an EST microarray can be calculated, on
average, based upon the predicted number of exons/gene for
the given species and the average length of the immobilized
probes. For human genes, the near-complete sequence of
35 human chromosome 22, Dunham *et al.*, *Nature* 402(6761):489-95

(1999), predicts that human genes average 5.5 exons/gene. Even with probes of 200 - 500 bp, the vast majority of human EST microarray probes include more than one exon.

In contrast, by virtue of their origin from
5 algorithmically identified ORFs in genomic sequence, the probes in the genome-derived single exon microarrays of the present invention can consist of individual exons. Thus, in contrast to EST microarrays, at least about 50, 60, 70, 75, 80, 85, 95 or 99% of probes deposited in the genome-
10 derived microarray of the present invention consist of, or include, no more than one predicted ORF.

This provides the ability, not readily achieved using EST microarrays, to use the genome-derived single exon microarrays of the present invention to measure
15 tissue-specific expression of individual exons, which in turn allows differential splicing events to be detected and characterized, and in particular, allows the correlation of differential splicing to tissue-specific expression patterns.

20 Furthermore, the exons that are represented in EST microarrays are often biased toward the 3' or 5' end of their respective genes, since sequencing strategies used for EST identification are so biased. In contrast, no such 3' or 5' bias necessarily inheres in the selection of exons
25 for disposition on the genome-derived single exon microarrays of the present invention.

Conversely, the probes provided on the genome-derived single exon microarrays of the present invention typically, but need not necessarily, include intronic
30 and/or intergenic sequence that is absent from EST microarrays, which are derived from mature mRNA. Typically, at least about 50, 60, 70, 80 or 90% of the exon-including probes on the genome-derived single exon microarrays of the present invention include sequence drawn
35 from noncoding regions. As discussed above, the additional

presence of noncoding region does not significantly interfere with measurement of gene expression, and provides the additional opportunity to assay prespliced RNA, and thus measure such phenomena such as nuclear export control.

5 The genome-derived single exon microarrays of the present invention are also quite different from *in situ* synthesis microarrays, where probe size is severely constrained by inadequacies in the photolithographic synthesis process.

10 Typically, probes arrayed on *in situ* synthesis microarrays are limited to a maximum of about 25 bp. As a well known consequence, hybridization to such chips must be performed at low stringency. In order, therefore, to achieve unambiguous sequence-specific hybridization
15 results, the *in situ* synthesis microarray requires substantial redundancy, with concomitant programmed arraying for each probe of probe analogues with altered (*i.e.*, mismatched) sequence.

 In contrast, the longer probe length of the
20 genome-derived single exon microarrays of the present invention allows much higher stringency hybridization and wash. Typically, therefore, exon-including probes on the genome-derived single exon microarrays of the present invention average at least about 100, 200, 300, 400 or
25 500 bp in length. By obviating the need for substantial probe redundancy, this approach permits a higher density of probes for discrete exons or genes to be arrayed on the microarrays of the present invention than can be achieved for *in situ* synthesis microarrays.

30 A further distinction is that the probes in *in situ* synthesis microarrays typically are covalently linked to the substrate surface. In contrast, the probes disposed on the genome-derived microarray of the present invention typically are, but need not necessarily be, bound
35 noncovalently to the substrate.

Furthermore, the short probe size on *in situ* microarrays causes large percentage differences in the melting temperature of probes hybridized to their complementary target sequence, and thus causes large
5 percentage differences in the theoretically optimum stringency across the array as a whole.

In contrast, the larger probe size in the microarrays of the present invention create lower percentage differences in melting temperature across the
10 range of arrayed probes.

A further significant advantage of the microarrays of the present invention over *in situ* synthesized arrays is that the quality of each individual probe can be confirmed before deposition. In contrast, the
15 quality of probes cannot be assessed on a probe-by-probe basis for the *in situ* synthesized microarrays presently being used.

The genome-derived single exon microarrays of the present invention are also distinguished over, and present
20 substantial benefits over, the genome-derived microarrays from lower eukaryotes such as yeast. Lashkari *et al.*, *Proc. Natl. Acad. Sci. USA* 94:13057-13062 (1997).

Only about 220 - 250 of the 6100 or so nuclear genes in *Saccharomyces cerevisiae* - that is, only about 4
25 - 5% - have standard, spliceosomal, introns, Lopez *et al.*, *Nucl. Acids Res.* 28:85-86 (2000); Spingola *et al.*, *RNA* 5(2):221-34 (1999). Furthermore, the entire yeast genome has already been sequenced. These two facts permit the ready amplification and disposition of single-ORF amplicons
30 on such microarray without the requirement for antecedent use of gene prediction and/or comparative sequence analyses.

Thus, a significant aspect of the present invention is the ability to identify and to confirm
35 expression of predicted coding regions in genomic sequence

drawn from eukaryotic organisms that have a higher percentage of genes having introns than do yeast such as *Saccharomyces cerevisiae*, particularly in genomic sequence drawn from eukaryotes in which at least about 10, 20 or 50% of protein-encoding genes have introns. In preferred embodiments, the methods and apparatus of the present invention are used to identify and confirm expression of novel genes from genomic sequence of eukaryotes in which the average number of introns per gene is at least about one, two or three or more.

After the physical substrate is prepared, experimental verification of predicted function is performed.

In a preferred embodiment of the present invention, where the function sought to be identified in genomic sequence is protein coding, experimental verification is performed by measuring expression of the putative ORFs, typically through nucleic acid hybridization experiments, and in particularly preferred embodiments, through hybridization to genome-derived single exon microarrays prepared as above-described.

Expression is conveniently measured and expressed for each probe in the microarray as a ratio of the expression measured concurrently in a plurality of mRNA sources, according to techniques well known in the microarray art, Reviewed in Schena et al., and as further described in Example 2, below. The mRNA source for the reference against which specific expression is measured can be drawn from a homogeneous mRNA source, such as a single cultured cell-type, or alternatively can be heterogeneous, as from a pool of mRNA derived from multiple tissues and/or cell types, as further described in Example 2, *infra*.

mRNA can be prepared by standard techniques, see Ausubel et al. and Maniatis et al., or purchased commercially. The mRNA is then typically reverse-

transcribed in the presence of labeled nucleotides: the index source (that in which expression is desired to be measured) is reverse transcribed in the presence of nucleotides labeled with a first label, typically a fluorophore (fluorochrome; fluor; fluorescent dye); the reference source is reverse transcribed in the presence of a second label, typically a fluorophore, typically fluorometrically-distinguishable from the first label. As further described in Example 2, *infra*, Cy3 and Cy5 dyes prove particularly useful in these methods. After partial purification of the index and reference targets, hybridization to the probe array is conducted according to standard techniques, typically under a coverslip.

After wash, microarrays are conveniently scanned using a commercial microarray scanning device, such as a Gen3 Scanner (Molecular Dynamics, Sunnyvale, CA). Data on expression is then passed, with or without interim storage, to process 500, where the results for each probe are related to the original sequence.

Often, hybridization of target material to the genome-derived single exon microarray will identify certain of the probes thereon as of particular interest. Thus, it is often desirable that the user be able readily to obtain sufficient quantities of an individual probe, either for subsequent arrayed deposition upon an additional support substrate, often as part of a microarray having a plurality of probes so identified, or alternatively or additionally as a solitary solid-phase or solution-phase probe, for further use.

Thus, in another aspect, the present invention provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

In this aspect, a small quantity of each probe is

disposed, typically without attachment to substrate, in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is obtained using higher density arrays, such as are provided by microtiter plates having 384, 864, 1536, 3456, 6144, or 9600 wells, and although microtiter plates having physical depressions (wells) are conveniently used, any device that permits addressable withdrawal of reagent from fluidly-noncommunicating areas can be used.

In this aspect of the invention, therefore, a fluidly noncommunicating addressable ordered set of individual probes, corresponding to those on a genome-derived single exon microarray, is provided, with each probe in sufficient quantity to permit amplification, such as by PCR. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this preferred embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes from the amplifiable ordered set.

Each discrete amplifiable probe can also be packaged with amplification primers, solutes, buffers, etc., and can be provided in dry (e.g., lyophilized) form or wet, in the latter case typically with addition of agents that retard evaporation.

In another aspect of the present invention, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In some embodiments, the microarray and/or ordered probe set are further packaged with recordable media that provide probe identification and addressing information, and that can additionally contain annotation
5 information, such as gene expression data. Such recordable media can be packaged with the microarray, with the ordered probe set, or with both.

If the microarray is constructed on a substrate that incorporates recordable media, such as is described in
10 international patent application no. WO 98/12559, then separate packaging of the genome-derived single exon microarray and the bioinformatic information is not required.

The amount of amplifiable probe material should
15 be sufficient to permit at least one amplification sufficient for subsequent hybridization assay.

Although the use of high density genome-derived microarrays on solid planar substrates is presently a preferred approach for the physical confirmation and
20 characterization of the expression of sequences predicted to encode protein, other types of microarrays (as herein defined) can also be used.

Furthermore, as earlier mentioned, experimental verification of the function predicted from genomic
25 sequence in process 200 can be bioinformatic, rather than, or additional to, physical verification.

For example, where the function desired to be identified is protein coding, the predicted ORFs can be compared bioinformatically to sequences known or suspected
30 of being expressed.

Thus, the sequences output from process 300 (or process 200), can be used to query expression databases, such as EST databases, SNP ("single nucleotide polymorphism") databases, known cDNA and mRNA sequences,
35 SAGE ("serial analysis of gene expression") databases, and

more generalized sequence databases that allow query for expressed sequences. Such query can be done by any sequence query algorithm, such as BLAST ("basic local alignment search tool"). The results of such query -
5 including information on identical sequences and information on nonidentical sequences that have diffuse or focal regions of sequence homology to the query sequence - can then be passed directly to process 500, or used to inform analyses subsequently undertaken in process 200,
10 process 300, or process 400.

Experimental data, whether obtained by physical or bioinformatic assay in process 400, is passed to process 500 where it is usefully related to the sequence data itself, a process colloquially termed "annotation". Such
15 annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the record itself, by linking records in a hierarchical or relational database, by linking to external databases, or
20 by a combination thereof. Such database techniques are well within the skill in the art.

The annotated sequence data can be stored locally, uploaded to genomic sequence database 100, and/or displayed 800.

25 The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Coupled with the escalating pace at which sequence now accumulates, the rapid pace of sequence annotation produces a need for methods of displaying the
30 information in meaningful ways.

FIG. 3 shows visual display 80 presenting a single genomic sequence annotated according to the present invention. Because of its nominal resemblance to artistic works of Piet Mondrian, visual display 80 is alternatively
35 described herein as a "Mondrian".

Each of the visual elements of display 80 is aligned with respect to the genomic sequence being annotated (hereinafter, the "annotated sequence"). Given the number of nucleotides typically represented in an annotated sequence, representation of individual nucleotides would rarely be readable in hard copy output of display 80. Typically, therefore, the annotated sequence is schematized as rectangle 89, extending from the left border of display 80 to its right border. By convention herein, the left border of rectangle 89 represents the first nucleotide of the sequence and the right border of rectangle 89 represents the last nucleotide of the sequence.

As further discussed below, however, the Mondrian visual display of annotated sequence can serve as a convenient graphical user interface for computerized representation, analysis, and query of information stored electronically. For such use, the individual nucleotides can conveniently be linked to the X axis coordinate of rectangle 89. This permits the annotated sequence at any point within rectangle 89 readily to be viewed, either automatically - for example, by time-delayed appearance of a small overlaid window upon movement of a cursor or other pointer over rectangle 89 - or through user intervention, as by clicking a mouse or other pointing device at a point in rectangle 89.

Visual display 80 is generated after user specification of the genomic sequence to be displayed. Such specification can consist of or include an accession number for a single clone (e.g., a single BAC accessioned into GenBank), wherein the starting and stopping nucleotides are thus absolutely identified, or alternatively can consist of or include an anchor or fulcrum point about which a chosen range of sequence is anchored, thus providing relative endpoints for the

sequence to be displayed. For example, the user can anchor such a range about a given chromosomal map location, gene name, or even a sequence returned by query for similarity or identity to an input query sequence. When visual display 80 is used as a graphical user interface to computerized data, additional control over the first and last displayed nucleotide will typically be dynamically selectable, as by use of standard zooming and/or selection tools.

Field 81 of visual display 80 is used to present the output from process 200, that is, to present the bioinformatic prediction of those sequences having the desired function within the genomic sequence. Functional sequences are typically indicated by at least one rectangle 83 (83a, 83b, 83c), the left and right borders of which respectively indicate, by their X-axis coordinates, the starting and ending nucleotides of the region predicted to have function.

Where a single bioinformatic method or approach identifies a plurality of regions having the desired function, a plurality of rectangles 83 is disposed horizontally in field 81. Where multiple methods and/or approaches are used to identify function, each such method and/or approach can be represented by its own series of horizontally disposed rectangles 83, each such horizontally disposed series of rectangles offset vertically from those representing the results of the other methods and approaches.

Thus, rectangles 83a in FIG. 3 represent the functional predictions of a first method of a first approach for predicting function, rectangles 83b represent the functional predictions of a second method and/or second approach for predicting that function, and rectangles 83c represent the predictions of a third method and/or approach.

Where the function desired to be identified is protein coding, field 81 is used to present the bioinformatic prediction of sequences encoding protein. For example, rectangles 83a can represent the results from
5 GRAIL or GRAIL II, rectangles 83b can represent the results from GENEFINDER, and rectangles 83c can represent the results from DICTION.

Optionally, and preferably, rectangles 83 collectively representing predictions of a single method
10 and/or approach are identically colored and/or textured, and are distinguishable from the color and/or texture used for a different method and/or approach.

Alternatively, or in addition, the color, hue, density, or texture of rectangles 83 can be used further to
15 report a measure of the bioinformatic reliability of the prediction. For example, many gene prediction programs will report a measure of the reliability of prediction. Thus, increasing degrees of such reliability can be indicated, e.g., by increasing density of shading. Where
20 display 80 is used as a graphical user interface, such measures of reliability, and indeed all other results output by the program, can additionally or alternatively be made accessible through linkage from individual rectangles 83, as by time-delayed window ("tool tip" window), or by
25 pointer (e.g., mouse)-activated link.

As earlier described, increased predictive reliability can be achieved by requiring consensus among methods and/or approaches to determining function. Thus, field 81 can include a horizontal series of rectangles 83
30 that indicate one or more degrees of consensus in predictions of function.

Although FIG. 3 shows three series of horizontally disposed rectangles in field 81, display 80 can include as few as one such series of rectangles and as
35 many as can discriminably be displayed, depending upon the

number of methods and/or approaches used to predict a given function.

Furthermore, field 81 can be used to show predictions of a plurality of different functions.

5 However, the increased visual complexity occasioned by such display makes more useful the ability of the user to select a single function for display. When display 80 is used as a graphical user interface for computer query and analysis, such function can usefully be indicated and user-
10 selectable, as by a series of graphical buttons or tabs (not shown in FIG. 3).

Rectangle 89 is shown in FIG. 3 as including interposed rectangle 84. Rectangle 84 represents the portion of annotated sequence for which predicted
15 functional information has been assayed physically, with the starting and ending nucleotides of the assayed material indicated by the X axis coordinates of the left and right borders of rectangle 84. Rectangle 85, with optional inclusive circles 86 (86a, 86b, and 86c) displays the
20 results of such physical assay.

Although a single rectangle 84 is shown in FIG. 3, physical assay is not limited to just one region of annotated genomic sequence. It is expected that an increasing percentage of regions predicted to have function
25 by process 200 will be assayed physically, and that display 80 will accordingly, for any given genomic sequence, have an increasing number of rectangles 84 and 85, representing an increased density of sequence annotation.

Where the function desired to be identified is
30 protein coding, rectangle 84 identifies the sequence of the probe used to measure expression. In embodiments of the present invention where expression is measured using genome-derived single exon microarrays, rectangle 84 identifies the sequence included within the probe
35 immobilized on the support surface of the microarray. As

noted *supra*, such probe will often include a small amount of additional, synthetic, material incorporated during amplification and designed to permit reamplification of the probe, which sequence is typically not shown in display 80.

5 Rectangle 87 is used to present the results of bioinformatic assay of the genomic sequence. For example, where the function desired to be identified is protein coding, process 400 can include bioinformatic query of expression databases with the sequences predicted in
10 process 200 to encode exons. And as earlier discussed, because bioinformatic assay presents fewer constraints than does physical assay, often the entire output of process 200 can be used for such assay, without further subsetting thereof by process 300. Therefore, rectangle 87 typically
15 need not have separate indicators therein of regions submitted for bioinformatic assay; that is, rectangle 87 typically need not have regions therein analogous to rectangles 84 within rectangle 89.

 Rectangle 87 as shown in FIG. 3 includes smaller
20 rectangles 880 and 88. Rectangles 880 indicate regions that returned a positive result in the bioinformatic assay, with rectangles 88 representing regions that did not return such positive results. Where the function desired to be predicted and displayed is protein coding, rectangles 880
25 indicate regions of the predicted exons that identify sequence with significant similarity in expression databases, such as EST, SNP, SAGE databases, with rectangles 88 indicating genes novel over those identified in existing expression data bases.

30 Rectangles 880 can further indicate, through color, shading, texture, or the like, additional information obtained from bioinformatic assay.

 For example, where the function assayed and displayed is protein coding, the degree of shading of
35 rectangles 880 can be used to represent the degree of

sequence similarity found upon query of expression databases. The number of levels of discrimination can be as few as two (identity, and similarity, where similarity has a user-selectable lower threshold). Alternatively, as
5 many different levels of discrimination can be indicated as can visually be discriminated.

Where display 80 is used as a graphical user interface, rectangles 880 can additionally provide links directly to the sequences identified by the query of
10 expression databases, and/or statistical summaries thereof. As with each of the precedingly-discussed uses of display 80 as a graphical user interface, it should be understood that the information accessed via display 80 need not be resident on the computer presenting such display, which
15 often will be serving as a client, with the linked information resident on one or more remotely located servers.

Rectangle 85 displays the results of physical assay of the sequence delimited by its left and right
20 borders.

Rectangle 85 can consist of a single rectangle, thus indicating a single assay, or alternatively, and increasingly typically, will consist of a series of rectangles (85a, 85b, 85c) indicating separate physical
25 assays of the same sequence.

Where the function assayed is gene expression, and where gene expression is assayed as herein described using simultaneous two-color fluorescent detection of hybridization to genome-derived single exon microarrays,
30 individual rectangles 85 can be colored to indicate the degree of expression relative to control. Conveniently, shades of green can be used to depict expression in the sample over control values, and shades of red used to depict expression less than control, corresponding to the
35 spectra of the Cy3 and Cy5 dyes conventionally used for

respective labeling thereof. Additional functional information can be provided in the form of circles 86 (86a, 86b, 86c), where the diameter of the circle can be used to indicate expression intensity. As discussed *infra*, such
5 relative expression (expression ratios) and absolute expression (signal intensity) can be expressed using normalized values.

Where display 80 is used as a graphical user interface, rectangle 85 can be used as a link to further
10 information about the assay. For example, where the assay is one for gene expression, each rectangle 85 can be used to link to information about the source of the hybridized mRNA, the identity of the control, raw or processed data from the microarray scan, or the like.

15 FIG. 4 is rendition of display 80 representing gene prediction and gene expression for a hypothetical BAC, showing conventions used in the Examples presented *infra*. BAC sequence ("Chip seq.") 89 is presented, with the physically assayed region thereof (corresponding to
20 rectangle 84 in FIG. 3) shown in white. Algorithmic gene predictions are shown in field 81, with predictions by GRAIL shown, predictions by GENEFINDER, and predictions by DICTION shown. Within rectangle 87, regions of sequence that, when used to query expression databases, return
25 identical or similar sequences ("EST hit") are shown as white rectangles (corresponding to rectangles 880 in FIG. 3), gray indicates low homology, and black indicates unknowns (where black and gray would correspond to rectangles 88 in FIG. 3).

30 Although FIGS. 3 and 4 show a single stretch of sequence, uninterrupted from left to right, longer sequences are usefully represented by vertical stacking of such individual Mondrians, as shown in FIGS. 9 and 10.

35 Single Exon Probes Useful For Measuring Gene Expression

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Where the function to be identified is protein coding, the methods and apparatus of the present invention rapidly identify and confirm the expression of portions of genomic sequence that function to encode protein. As a direct result, the methods and apparatus of the present invention rapidly yield large numbers of single-exon nucleic acid probes, the majority from previously unknown genes, each of which is useful for measuring and/or surveying expression of a specific gene in one or more tissues or cell types.

It is, therefore, another aspect of the present invention to provide genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray.

Using the methods and genome-derived single-exon microarrays of the present invention, we have for example readily identified a large number of unique ORFs from human genomic sequence. Using single exon probes that encompass these ORFs, we have demonstrated, through microarray hybridization analysis, the expression of 13,114 of these ORFs in bone marrow.

As would immediately be appreciated by one of skill in the art, each single exon probe having demonstrable expression in bone marrow is currently available for use in measuring the level of its ORF's expression in bone marrow.

Because bone marrow is the tissue in which blood cells originate, diseases of the bone marrow are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these diseases. Although mutations

in single genes have in some cases been identified as causal - notably in the thalassemias and sickle cell anemia - disorders of the bone marrow are, for the most part, believed to have polygenic etiologies.

5 For example, cancers that originate in the bone marrow and lymphatic tissues such as the lymphomas, leukemias, and myeloma have been recognized as a major health concern. An estimated 632,000 Americans are presently living with lymphoma, leukemia or myeloma, and
10 over 110,000 new cases are anticipated each year. The new cases alone account for 11% of all cancer cases reported in the United States.

 Lymphoma is a general term for a group of cancers of lymphocytes that manifest in the tissues of the
15 lymphatic system. Eventually, monoclonal proliferation crowds out healthy cells and creates tumors which enlarge lymph nodes. Approximately 450,000 members of the U.S. population are living with lymphoma: 160,000 with Hodgkin disease (HD) and 290,000 with non-Hodgkin lymphoma.

20 Hodgkin disease (HD) is a specialized form of lymphoma, and represent about 8% of all lymphomas. HD can be distinguish in tissues by the presence of an abnormal cell called the Reed-Sternberg cell. Incidence rates of HD are higher in adolescents and young adults, but HD is
25 considered to be one of the most curable forms of cancer. Symptoms of HD include painless swelling of lymph glands, fatigue, recurrent high fever, sweating at night, skin irritations and loss of weight.

 Although an infectious etiology has been proposed
30 to account for the disproportionate incidence of HD among siblings reared together - particularly an association with Epstein Barr Virus (EBV) - multiple genetic contributions have also been suggested.

 As early as 1986, linkage to HLA was suggested,
35 with Klitz et al., Am. J. Hum. Genet. 54: 497-505 (1994)

reporting an overall association of the nodular sclerosing (NSHD) group with the HLA class II region. Results of the study suggested that susceptibility to NSHD is influenced by more than 1 locus within the class II region. Through a literature search, Shugart and Collins (2000), *Europ. J. Hum. Genet.* 8: 460-463 (2000), performed a combined segregation and linkage analysis on 59 nuclear families with HD and concluded that HD is most likely determined by both an HLA-associated major gene and other non-HLA genetic factors, in conjunction with environmental effects.

Non-Hodgkin lymphoma (NHL) is a malignant monoclonal proliferation of the lymphoid cells in the immune system, including bone marrow, spleen, liver and GI tract. The pathologic classification of NHL continues to evolve, reflecting new insights into the cells of origin and the biologic bases of these heterogeneous diseases. The course of NHL varies from indolent and initially well tolerated to rapidly fatal. Furthermore, common clinical symptoms of NHL, but rare in HD, are congestion and edema of the face and neck and ureteral compression.

Non-Hodgkin lymphoma (NHL) has been linked to a variety of specific genetic defects, including 26 mutated genes and at least 9 identified chromosomal translocations. Among the mutated genes are: ALK (2p23); API2 (MIHC, cIAP2) (11q22-q23); API4 (survivin, SVV) (17q25(?)); ATM (ATA, ATC) (11q22.3); BCL1 (11q13.3); BCL10 (CLAP, CIPER) (1p22); BCL2 (18q21.3); BCL6 (LAZ3, ZNF51) (3q27); BLYM (1p32); BMI1 (10p13); CCND1 (D11S287E, Cyclin D, PRAD1) (11q13); CD44 (MDU3, HA, MDU2) (11pter-p13); FRAT1 (10q23-q24(?)); FRAT2 (GBP) (10(?)); IL6 (IFNB2) (7p21); IRF4 (MUM1, LSIRF) (6p25-p23); LCP1 (PLS2) (13q14.1-q14.3); MALT1 (MLT) (18q21); MUC1 (PUM, PEM) (1q21); MYBL1 (AMYB, A-MYB) (8q22); MYC (CMYC, C-MYC) (8q24.12-q24.13); NBS1 (8q21); NPM1 (B23) (5q35); PCNA (20p12); TIAM1 (21q22.1); and TP53 (p53, P53) (17q13.1).

Among the chromosomal abnormalities are: t(1;14)

(p22;q32); t(14;18)(q32;q21); t(3;14)(q27;q32);
t(6;14)(p25;q32); t(11;18)(q21;q21); t(1;14)(q21;q32);
t(2;5)(p23;q35); add(14q32) / dup(14p32); and
t(11;14)(q13;q32).

5 Additional genetic loci, as yet undiscovered, are believed to account for other occurrences of NHL.

As another example, acute leukemia is a malignant disease of blood-forming tissues such as the bone marrow. It is characterized by the uncontrolled growth of white
10 blood cells. As a result, immature myeloid cells (in acute myelogenous leukemia (AML)) or lymphoid cells (in acute lymphocytic leukemia (ALL)) rapidly accumulate and progressively replace the bone marrow; diminished
production of normal red cells, white cells, and platelets
15 ensues. This loss of normal marrow function in turn gives rise to the typical clinical complications of leukemia: anemia, infection, and bleeding.

If untreated, ALL is rapidly fatal; most patients die within several months of diagnosis. With appropriate
20 therapy, many patients can be cured. The survival rate for patients diagnosed with AML or ALL is 14% and 58% respectively. However, the incidences of AML is expected to be greater than ALL: an estimated 10,000 new cases of AML, predominantly in older adults, is anticipated in the
25 U.S. alone, whereas 3,100 new cases of ALL are expected, with 1,500 of these new cases occurring among children.

The etiology of acute leukemia is not known. Although human T-cell lymphotropic virus type I (HTLV-I), a causative agent of adult T-cell leukemia, and HTLV-II,
30 obtained from several patients with a syndrome resembling hairy cell leukemia, have been isolated, the etiologic link between HTLV and malignancy is uncertain. There is, however, evidence which suggests a genetic predisposition to incidences of acute leukemia.

35 For example, genetic disorders such as Fanconi

anemia and Down syndrome appear to increase risk of acute leukemia, specifically, AML. Evidence supporting a chromosome 21 locus for acute myelogenous leukemia (AML) includes the finding of linkage to 21q22.1-q22.2 in a family with a platelet disorder and propensity to develop AML (Ho et al., Blood 87: 5218-5224 (1996), an increased incidence of leukemia in Down syndrome, and frequent somatic translocation in leukemia involving the CBFA gene on 21q22.3. In addition, Horwitz et al., Am. J. Hum. Genet. 61:873-881 (1997), suggest that a gene on 16q22 may be a second cause of acute myelogenous leukemia. Nonparametric linkage analysis gave a P-value of 0.00098 for the conditional probability of linkage. Mutational analysis excluded expansion of the AT-rich minisatellite repeat FRA16B fragile site and the CAG trinucleotide repeat in the E2F-4 transcription factor. Large CAG repeat expansion was excluded as a cause of leukemia in this family.

Similarly, acute lymphoblastic leukemia (ALL) has been suggested to have a genetic predisposition. In particular, linkage to chromosome 9p has been reported by a number of groups. Chilcote et al., New Eng. J. Med. 313: 286-291 (1985), found that 6 of 8 patients with clinical features of lymphomatous ALL (LALL), a distinct category of ALL of T-cell lineage, had karyotypic abnormalities leading to loss of bands 9p22-p21. The mechanisms varied and included deletions, unbalanced translocations, and loss of the entire chromosome; only 1 of 57 patients without LALL had an abnormality of chromosome 9 at diagnosis. Kowalczyk et al., Cancer Genet. Cytogenet. 9:383-385 (1981), had earlier found changes in 9p in a subgroup of ALL cases. Chilcote et al. (1985) pointed out that there is a fragile site at 9p21 and raised the question of familial predisposition on this basis. This fragile site is the breakpoint in the translocation t(9;11)(p21-22;q23), which

is associated with acute nonlymphocytic leukemia with monocytic features, ANLL-AMoL-M5a. In a large series, Murphy et al., New Eng. J. Med. 313:1611 (1985), confirmed an abnormality of 9p in 10 to 11% of cases (33 out of more than 300) of acute lymphoblastic leukemia. The breakpoints in 9p clustered in the p22-p21 region. They could not, however, corroborate the specific association with T-cell origin or so-called lymphomatous clinical features. In addition, Taki et al., Proc. Natl. Acad. Sci. USA 96:14535 (1999), recently identified AF5q31, a new AF4-related gene, fused to MLL in infant ALL with ins(5;11)(q31;q13q23), and suspects that AF5q31 and AF4 might define a new family particularly involved in the pathogenesis of 11q23-associated-ALL.

As yet a further example of a disease affecting bone marrow with likely polygenic etiology is multiple myeloma (MM).

MM is a cancer of plasma cells, the final differentiated stage of B lymphocyte maturation. The malignant clone proliferates in the bone marrow and frequently invades the adjacent bone, producing extensive skeletal destruction that results in bone pain and fractures. Anemia, hypercalcemia, and renal failure are some clinical manifestations associated with MM.

MM causes 1% of all cancer deaths in Western countries. A genetic component to its etiology is suggested by disparate incidence among various groups in the country. Its incidence is higher in men than in women, in people of African descent relative to the U.S. population at large, and in older adults as compared to the young. It has been estimated that 14,000 new cases of myeloma will be diagnosed in the U.S., and over 11,000 persons will die from MM within the year.

Although, Kaposi's sarcoma-associated herpes virus has been associated with MM (Retig et al., Science

276:1851 (1997)), there is evidence that chromosomal abnormalities, such as the deletion of 13q14 and rearrangements of 14q increase the proliferation of myeloma cells.

5 Up to 30% of patients who suffer with MM have a balanced translocation, t(4;14)(p16.3;q32), that places the fibroblast growth factor receptor 3 (FGFR3) gene under the control of IgH promoter elements (Chesi et al., Nat. Genet. 16:260 (1997)). This results in increased expression of
10 FGFR3, a member of a family of tyrosine kinase receptors implicated in control of cellular proliferation.

According to Zoger et al., Blood 95:1925 (2000), monoallelic deletions of the retinoblastoma-1 (rb-1) gene and the D13S319 locus were observed in 48 of 104 patients
15 (46.2%) and in 28 of 72 (38.9%) patients, respectively, with newly diagnosed MM. Fluorescence in situ hybridization (FISH) studies found that 13q14 was deleted in all 17 patients with karyotypic evidence of monosomy 13 or deletion of 13q but also in 9 of 19 patients with
20 apparently normal karyotypes. Patients with a 13q14 deletion were more likely to have higher serum levels of beta(2)-microglobulin ($P=0.059$) and a higher percentage of bone marrow plasma cells ($P=0.085$) than patients with a normal 13q14 status on FISH analysis. In patients with a
25 deletion of 13q14, myeloma cell proliferation was markedly increased. The presence of a 13q14 deletion on FISH analysis was associated with a significantly lower rate of response to conventional-dose chemotherapy (40.8% compared with 78.6%; $P=.009$) and a shorter overall
30 survival (24.2 months compared with > 60 months; $P<.005$) than in patients without the deletion.

There are numerous other mutated genes and chromosomal abnormalities that may predispose to MM. Examples of such genes are: B2M (15q21-q22); CCND1
35 (D11S287E, Cyclin D, PRAD1)(11q13); CD19 (16p11.2); HGF

(HPTA) (7q21.1); IL6 (IFNB2) (7p21); IRF4 (MUM1, LSIRF) (6p25-p23); LTA (TNFB, LT) (6p21.3); SDC1 (2p24.1); and TNF (TNFA, TNFSF2, DIF) (6p21.3). Examples of chromosomal abnormalities include: t(6;14)(p25;q32) and
5 t(11;14)(q13;q32).

Other significant diseases or disorders of the bone marrow are also believed, or likely to have, a genetic, typically polygenic, etiologic component. These diseases include, for example, chronic myeloid leukemia,
10 chronic lymphoid leukemia, polycythemia vera, myelofibrosis, primary thrombocythemia, myelodysplastic syndromes, Wiskott-Aldrich, lymphoproliferative syndrome, aplastic anemia, Fanconi anemia, Down syndrome, sickle cell disease, thalassemia, granulocyte disorders, Kostmann
15 syndrome, chronic granulomatous disease, Chediak-Higashi syndrome, platelet disorders, Glanzmann thrombasthenia, Bernard-Soulier syndrome, metabolic storage diseases, osteoporosis, congenital hemophagocytic syndrome.

The human genome-derived single exon nucleic acid
20 probes and microarrays of the present invention are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of human bone marrow, particularly those diseases with polygenic etiology. With each of the single exon probes described herein shown to be expressed
25 at detectable levels in human bone marrow, and with about 2/3 of the probes identifying novel genes, the single exon microarrays of the present invention provide exceptionally high informational content for such studies.

For example, diagnosis, grading, and/or staging
30 of a disease can be based upon the quantitative relatedness of a patient gene expression profile to one or more reference expression profiles known to be characteristic of a given bone marrow disease, or to specific grades or stages thereof.

35 In one embodiment, the patient gene expression

profile is generated by hybridizing nucleic acids obtained directly or indirectly from transcripts expressed in the patient's bone marrow (or cells cultured therefrom) to the genome-derived single exon microarray of the present invention. Reference profiles are obtained similarly by hybridizing nucleic acids obtained directly or indirectly from transcripts expressed in the bone marrow of individuals with known disease. Methods for quantitatively relating gene expression profiles, without regard to the function of the protein encoded by the gene, are disclosed in WO 99/58720, incorporated herein by reference in its entirety.

In another approach, the genome-derived single exon probes and microarrays of the present invention can be used to interrogate genomic DNA, rather than pools of expressed message; this latter approach permits predisposition to and/or prognosis of diseases of bone marrow to be assessed through the massively parallel determination of altered copy number, deletion, or mutation in the patient's genome of exons known to be expressed in human bone marrow. The algorithms set forth in WO 99/58720 can be applied to such genomic profiles without regard to the function of the protein encoded by the interrogated gene.

The utility is specific to the probe; at sufficiently high hybridization stringency, which stringencies are well known in the art - see Ausubel et al. and Maniatis et al. - each probe reports the level of expression of message specifically containing that ORF.

It should be appreciated, however, that the probes of the present invention, for which expression in the bone marrow has been demonstrated are useful for both measurement in the bone marrow and for survey of expression in other tissues.

Significant among such advantages is the presence

of probes for novel genes.

As mentioned above and further detailed in Examples 1 and 2, the methods described enable ORFs which are not present in existing expression databases to be identified. And the fewer the number of tissues in which the ORF can be shown to be expressed, the more likely the ORF will prove to be part of a novel gene: as further discussed in Example 2, ORFs whose expression was measurable in only a single of the tested tissues were represented in existing expression databases at a rate of only 11%, whereas 36% of ORFs whose expression was measurable in 9 tissues were present in existing expression databases, and fully 45% of those ORFs expressed in all ten tested tissues were present in existing expressed sequence databases.

Either as tools for measuring gene expression or tools for surveying gene expression, the genome-derived single exon probes of the present invention have significant advantages over the cDNA or EST-based probes that are currently available for achieving these utilities.

The genome-derived single exon probes of the present invention are useful in constructing genome-derived single exon microarrays; the genome-derived single exon microarrays, in turn, are useful devices for measuring and for surveying gene expression in the human.

Gene expression analysis using microarrays - conventionally using microarrays having probes derived from expressed message - is well-established as useful in the biological research arts (see Lockhart et al. Nature 405, 827-836).

Microarrays have been used to determine gene expression profiles in cells in response to drug treatment (see, for example, Kaminski et al., "Global Analysis of Gene Expression in Pulmonary Fibrosis Reveals Distinct Programs Regulating Lung Inflammation and Fibrosis," *Proc.*

Natl. Acad. Sci. USA 97(4):1778-83 (2000); Bartosiewicz et al., "Development of a Toxicological Gene Array and Quantitative Assessment of This Technology," Arch. Biochem. Biophys. 376(1):66-73 (2000)), viral infection (see for
5 example, Geiss et al., "Large-scale Monitoring of Host Cell Gene Expression During HIV-1 Infection Using cDNA Microarrays," Virology 266(1):8-16 (2000)) and during cell processes such as differentiation, senescence and apoptosis (see, for example, Shelton et al., "Microarray Analysis of
10 Replicative Senescence," Curr. Biol. 9(17):939-45 (1999); Voehringer et al., "Gene Microarray Identification of Redox and Mitochondrial Elements That Control Resistance or Sensitivity to Apoptosis," Proc. Natl. Acad. Sci. USA 97(6):2680-5 (2000)).

15 Microarrays have also been used to determine abnormal gene expression in diseased tissues (see, for example, Alon et al., "Broad Patterns of Gene Expression Revealed by Clustering Analysis of Tumor and Normal Colon Tissues Probed by Oligonucleotide Arrays," Proc. Natl.
20 Acad. Sci. USA 96(12):6745-50 (1999); Perou et al., "Distinctive Gene Expression Patterns in Human Mammary Epithelial Cells and Breast Cancers, Proc. Natl. Acad. Sci. USA 96(16):9212-7 (1999); Wang et al., "Identification of Genes Differentially Over-expressed in Lung Squamous Cell
25 Carcinoma Using Combination of cDNA Subtraction and Microarray Analysis," Oncogene 19(12):1519-28 (2000); Whitney et al., "Analysis of Gene Expression in Multiple Sclerosis Lesions Using cDNA Microarrays," Ann. Neurol. 46(3):425-8 (1999)), in drug discovery screens (see, for
30 example, Scherf et al., "A Gene Expression Database for the Molecular Pharmacology of Cancer," Nat. Genet. 24(3):236-44 (2000)) and in diagnosis to determine appropriate treatment strategies (see, for example, Sgroi et al., "In vivo Gene Expression Profile Analysis of Human Breast Cancer

Progression," *Cancer Res.* 59(22):5656-61 (1999)).

In microarray-based gene expression screens of pharmacological drug candidates upon cells, each probe provides specific useful data. In particular, it should be appreciated that even those probes that show no change in expression are as informative as those that do change, serving, in essence, as negative controls.

For example, where gene expression analysis is used to assess toxicity of chemical agents on cells, the failure of the agent to change a gene's expression level is evidence that the drug likely does not affect the pathway of which the gene's expressed protein is a part.

Analogously, where gene expression analysis is used to assess side effects of pharmacological agents — whether in lead compound discovery or in subsequent screening of lead compound derivatives — the inability of the agent to alter a gene's expression level is evidence that the drug does not affect the pathway of which the gene's expressed protein is a part.

WO 99/58720 provides methods for quantifying the relatedness of a first and second gene expression profile and for ordering the relatedness of a plurality of gene expression profiles. The methods so described permit useful information to be extracted from a greater percentage of the individual gene expression measurements from a microarray than methods previously used in the art.

Other uses of microarrays are described in Gerhold et al., *Trends Biochem. Sci.* 24(5):168-173 (1999) and Zweiger, *Trends Biotechnol.* 17(11):429-436 (1999); Schena et al.

The invention particularly provides genome-derived single-exon probes known to be expressed in bone marrow. The individual single exon probes can be provided in the form of substantially isolated and purified nucleic acid, typically, but not necessarily, in a quantity

sufficient to perform a hybridization reaction.

Such nucleic acid can be in any form directly hybridizable to the message that contains the probe's ORF, such as double stranded DNA, single-stranded DNA, complementary to the message, single-stranded RNA complementary to the message, or chimeric DNA/RNA molecules so hybridizable. The nucleic acid can alternatively or additionally include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained. For example, probes can include phosphorothioates, methylphosphonates, morpholino analogs, and peptide nucleic acids (PNA), as are described, for example, in U.S. Patent Nos. 5,142,047; 5,235,033; 5,166,315; 5,217,866; 5,184,444; 5,861,250.

Usefully, however, such probes are provided in a form and quantity suitable for amplification, where the amplified product is thereafter to be used in the hybridization reactions that probe gene expression. Typically, such probes are provided in a form and quantity suitable for amplification by PCR or by other well known amplification technique. One such technique additional to PCR is rolling circle amplification, as is described, *inter alia*, in U.S. Patent Nos. 5,854,033 and 5,714,320 and international patent publications WO 97/19193 and WO 00/15779. As is well understood, where the probes are to be provided in a form suitable for amplification, the range of nucleic acid analogues and/or internucleotide linkages will be constrained by the requirements and nature of the amplification enzyme.

Where the probe is to be provided in form suitable for amplification, the quantity need not be sufficient for direct hybridization for gene expression analysis, and need be sufficient only to function as an amplification template, typically at least about 1, 10 or 100 pg or more.

Each discrete amplifiable probe can also be packaged with amplification primers, either in a single composition that comprises probe template and primers, or in a kit that comprises such primers separately packaged therefrom. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes. The probe composition and/or kit can also include buffers, enzyme, etc., required to effect amplification.

As mentioned earlier, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically average at least about 100, 200, 300, 400 or 500 bp in length, including (and typically, but not necessarily centered about) the ORF. Furthermore, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically not contain a detectable label.

When intended for use in solution phase hybridization, however – that is, for use in a hybridization reaction in which the probe is not first bound to a support substrate (although the target may indeed be so bound) – length constraints that are imposed in microarray-based hybridization approaches will be relaxed, and such probes will typically be labeled.

In such case, the only functional constraint that dictates the minimum size of such probe is that each such probe must be capable of specifically identifying in a hybridization reaction the exon from which it is drawn. In theory, a probe of as little as 17 nucleotides is capable

of uniquely identifying its cognate sequence in the human genome. For hybridization to expressed message – a subset of target sequence that is much reduced in complexity as compared to genomic sequence – even fewer nucleotides are
5 required for specificity.

Therefore, the probes of the present invention can include as few as 20, 25 or 50 bp or ORF, or more. In particular embodiments, the ORF sequences are given in SEQ ID NOS. 13,115 – 26,012, respectively, for probe SEQ ID
10 NOS. 1 – 13,114. The minimum amount of ORF required to be included in the probe of the present invention in order to provide specific signal in either solution phase or microarray-based hybridizations can readily be determined for each of ORF SEQ ID NOS. 13,115 – 26,012 individually
15 by routine experimentation using standard high stringency conditions.

Such high stringency conditions are described, *inter alia*, in Ausubel et al. and Maniatis et al. For microarray-based hybridization, standard high stringency
20 conditions can usefully be 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 µg/µl human c_{ot}1 DNA, and 0.5 % SDS, in a humid oven at 42°C overnight, followed by successive washes of the microarray in 1X SSC, 0.2% SDS at 55°C for 5 minutes, and then 0.1X SSC, 0.2% SDS, at 55°C for 20
25 minutes. For solution phase hybridization, standard high stringency conditions can usefully be aqueous hybridization at 65°C in 6X SSC. Lower stringency conditions, suitable for cross-hybridization to mRNA encoding structurally- and functionally-related proteins, can usefully be the same as
30 the high stringency conditions but with reduction in temperature for hybridization and washing to room temperature (approximately 25°C).

When intended for use in solution phase hybridization, the maximum size of the single exon probes
35 of the present invention is dictated by the proximity of

other expressed exons in genomic DNA: although each single exon probe can include intergenic and/or intronic material contiguous to the ORF in the human genome, each probe of the present invention will include portions of only one
5 expressed exon.

Thus, each single exon probe will include no more than about 25 kb of contiguous genomic sequence, more typically no more than about 20 kb of contiguous genomic sequence, more usually no more than about 15 kb, even more
10 usually no more than about 10 kb. Usually, probes that are maximally about 5 kb will be used, more typically no more than about 3 kb.

It will be appreciated that the Sequence Listing appended hereto presents, by convention, only that strand
15 of the probe and ORF sequence that can be directly translated reading from 5' to 3' end. As would be well understood by one of skill in the art, single stranded probes must be complementary in sequence to the ORF as present in an mRNA; it is well within the skill in the art
20 to determine such complementary sequence. It will further be understood that double stranded probes can be used in both solution-phase hybridization and microarray-based hybridization if suitably denatured.

Thus, it is an aspect of the present invention to
25 provide single-stranded nucleic acid probes that have sequence complementary to those described herein above and below, and double-stranded probes one strand of which has sequence complementary to the probes described herein.

The probes can, but need not, contain intergenic
30 and/or intronic material that flanks the ORF, on one or both sides, in the same linear relationship to the ORF that the intergenic and/or intronic material bears to the ORF in genomic DNA. The probes do not, however, contain nucleic acid derived from more than one expressed ORF.

35 And when intended for use in solution

hybridization, the probes of the present invention can usefully have detectable labels. Nucleic acid labels are well known in the art, and include, *inter alia*, radioactive labels, such as ^3H , ^{32}P , ^{33}P , ^{35}S , ^{125}I , ^{131}I ; fluorescent
5 labels, such as Cy3, Cy5, Cy5.5, Cy7, SYBR®

Green and other labels described in Haugland, *Handbook of Fluorescent Probes and Research Chemicals*, 7th ed., Molecular Probes Inc., Eugene, OR (2000), or fluorescence resonance energy transfer tandem conjugates
10 thereof; labels suitable for chemiluminescent and/or enhanced chemiluminescent detection; labels suitable for ESR and NMR detection; and labels that include one member of a specific binding pair, such as biotin, digoxigenin, or the like.

15 The probes, either in quantity sufficient for hybridization or sufficient for amplification, can be provided in individual vials or containers.

Alternatively, such probes can usefully be packaged as a plurality of such individual genome-derived
20 single exon probes.

When provided as a collection of plural individual probes, the probes are typically made available in amplifiable form in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96
25 well microtiter plate can be used, greater efficiency is obtained using higher density arrays.

If, as earlier mentioned, the ORF-specific 5' primers used for genomic amplification had a first common sequence added thereto, and the ORF-specific 3'
30 primers used for genomic amplification had a second, different, common sequence added thereto, a single set of 5' and 3' primers can be used to amplify all of the probes from the amplifiable ordered set.

Such collections of genome-derived single exon
35 probes can usefully include a plurality of probes chosen

for the common attribute of expression in the human bone marrow.

In such defined subsets, typically at least 50, 60, 75, 80, 85, 90 or 95% or more of the probes will be
5 chosen by their expression in the defined tissue or cell type.

The single exon probes of the present invention, as well as fragments of the single exon probes comprising selectively hybridizable portions of the probe ORF, can be
10 used to obtain the full length cDNA that includes the ORF by (i) screening of cDNA libraries; (ii) rapid amplification of cDNA ends ("RACE"); or (iii) other conventional means, as are described, *inter alia*, in Ausubel et al. and Maniatis et al.

15 It is another aspect of the present invention to provide genome-derived single exon nucleic acid microarrays useful for gene expression analysis, where the term "microarray" has the meaning given in the definitional section of this description, *supra*.

20 The invention particularly provides genome-derived single-exon nucleic acid microarrays comprising a plurality of probes known to be expressed in human bone marrow. In preferred embodiments, the present invention provides human genome-derived single exon microarrays
25 comprising a plurality of probes drawn from the group consisting of SEQ ID NOS.: 1 - 13,114.

When used for gene expression analysis, the genome-derived single exon microarrays provide greater physical informational density than do the genome-derived
30 single exon microarrays that have lower percentages of probes known to be expressed commonly in the tested tissue. At a fixed probe density, for example, a given microarray surface area of the defined subset genome-derived single exon microarray can yield a greater number of expression
35 measurements. Alternatively, at a given probe density, the

same number of expression measurements can be obtained from a smaller substrate surface area. Alternatively, at a fixed probe density and fixed surface area, probes can be provided redundantly, providing greater reliability in signal measurement for any given probe. Furthermore, with a higher percentage of probes known to be expressed in the assayed tissue, the dynamic range of the detection means can be adjusted to reveal finer levels discrimination among the levels of expression.

Although particularly described with respect to their utility as probes of gene expression, particularly as probes to be included on a genome-derived single exon microarray, each of the nucleic acids having SEQ ID NOS.: 1 - 13,114 contains an open-reading frame, set forth respectively in SEQ ID NOS.: 13,115 - 26,012, that encodes a protein domain. Thus, each of SEQ ID NOS. 1 - 13,114 can be used, or that portion thereof in SEQ ID NOS. 13,115 - 26,012 used, to express a protein domain by standard *in vitro* recombinant techniques. See Ausubel et al. and Maniatis et al.

Additionally, kits are available commercially that readily permit such nucleic acids to be expressed as protein in bacterial cells, insect cells, or mammalian cells, as desired (e.g., HAT[™] Protein Expression & Purification System, ClonTech Laboratories, Palo Alto, CA; Adeno-X[™] Expression System, ClonTech Laboratories, Palo Alto, CA; Protein Fusion & Purification (pMAL[™]) System, New England Biolabs, Beverley, MA)

Furthermore, shorter peptides can be chemically synthesized using commercial peptide synthesizing equipment and well known techniques. Procedures are described, *inter alia*, in Chan et al. (eds.), Fmoc Solid Phase Peptide Synthesis: A Practical Approach (Practical Approach Series, (Paper)), Oxford Univ. Press (March 2000) (ISBN: 0199637245); Jones, Amino Acid and Peptide Synthesis

(Oxford Chemistry Primers, No 7) , Oxford Univ. Press
(August 1992) (ISBN: 0198556683); and Bodanszky, Principles
of Peptide Synthesis (Springer Laboratory), Springer Verlag
(December 1993) (ISBN: 0387564314).

5 It is, therefore, another aspect of the invention
to provide peptides comprising an amino acid sequence
translated from SEQ ID NOS.: 13,115 - 26,012. Such amino
acid sequences are set out in SEQ ID NOS: 26,013 - 38,628.
Any such recombinantly-expressed or synthesized peptide of
10 at least 8, and preferably at least about 15, amino acids,
can be conjugated to a carrier protein and used to generate
antibody that recognizes the peptide. Thus, it is a
further aspect of the invention to provide peptides that
have at least 8, preferably at least 15, consecutive amino
15 acids.

The following examples are offered by way of
illustration and not by way of limitation.

20 EXAMPLE 1

Preparation of Single Exon Microarrays from ORFs Predicted
in Human Genomic Sequence

Bioinformatics Results

25 All human BAC sequences in fewer than 10 pieces
that had been accessioned in a five month period
immediately preceding this study were downloaded from
GenBank. This corresponds to ~2200 clones, totaling ~350
MB of sequence, or approximately 10% of the human genome.

30 After masking repetitive elements using the
program CROSS_MATCH, the sequence was analyzed for open
reading frames using three separate gene finding programs.
The three programs predict genes using independent
algorithmic methods developed on independent training sets:
35 GRAIL uses a neural network, GENEFINDER uses a hidden

Markoff model, and DICTION, a program proprietary to Genetics Institute, operates according to a different heuristic. The results of all three programs were used to create a prediction matrix across the segment of genomic
5 DNA.

The three gene finding programs yielded a range of results. GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed. GENEFINDER was second, calling 1%, and DICTION
10 yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

The consensus data were as follows. GRAIL and GENEFINDER agreed on 0.7% of genomic sequence, GRAIL and DICTION agreed on 0.5% of genomic sequence, and the three
15 programs together agreed on 0.25% of the data analyzed. That is, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

ORFs predicted by any two of the three programs
20 ("consensus ORFs") were assorted into "gene bins" using two criteria: (1) any 7 consecutive exons within a 25 kb window were placed together in a bin as likely contributing to a single gene, and (2) all ORFs within a 25-kb window were placed together in a bin as likely contributing to a single
25 gene if fewer than 7 exons were found within the 25 kb window.

PCR

The largest ORF from each gene bin that did not
30 span repetitive sequence was then chosen for amplification, as were all consensus ORFs longer than 500 bp. This method approximated one exon per gene; however, a number of genes were found to be represented by multiple elements.

Previously, we had determined that DNA fragments
35 fewer than 250 bp in length do not bind well to the amino-

modified glass surface of the slides used as support substrate for construction of microarrays; therefore, amplicons were designed in the present experiments to approximate 500 bp in length.

5 Accordingly, after selecting the largest ORF per gene bin, a 500 bp fragment of sequence centered on the ORF was passed to the primer picking software, PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>). A first
10 additional sequence was commonly added to each ORF-unique 5' primer, and a second, different, additional sequence was commonly added to each ORF-unique 3' primer, to permit subsequent reamplification of the amplicon using a single set of "universal" 5' and 3' primers, thus immortalizing
15 the amplicon. The addition of universal priming sequences also facilitates sequence verification, and can be used to add a cloning site should some ORFs be found to warrant further study.

 The ORFs were then PCR amplified from genomic
20 DNA, verified on agarose gels, and sequenced using the universal primers to validate the identity of the amplicon to be spotted in the microarray.

 Primers were supplied by Operon Technologies (Alameda, CA). PCR amplification was performed by standard
25 techniques using human genomic DNA (Clontech, Palo Alto, CA) as template. Each PCR product was verified by SYBR® green (Molecular Probes, Inc., Eugene, OR) staining of agarose gels, with subsequent imaging by Fluorimager (Molecular Dynamics, Inc., Sunnyvale, CA). PCR
30 amplification was classified as successful if a single band appeared.

 The success rate for amplifying ORFs of interest directly from genomic DNA using PCR was approximately 75%.
FIG. 5 graphs the distribution of predicted ORF (exon)
35 length and distribution of amplified PCR products, with ORF

length shown in red and PCR product length shown in blue (which may appear black in the figure). Although the range of ORF sizes is readily seen to extend to beyond 900 bp, the mean predicted exon size was only 229 bp, with a median
5 size of 150 bp (n=9498). With an average amplicon size of 475 ± 25 bp, approximately 50% of the average PCR amplification product contained predicted coding region, with the remaining 50% of the amplicon containing either intron, intergenic sequence, or both.

10 Using a strategy predicated on amplifying about 500 bp, it was found that long exons had a higher PCR failure rate. To address this, the bioinformatics process was adjusted to amplify 1000, 1500 or 2000 bp fragments from exons larger than 500 bp. This improved the rate of
15 successful amplification of exons exceeding 500 bp, constituting about 9.2% of the exons predicted by the gene finding algorithms.

Approximately 75% of the probes disposed on the array (90% of those that successfully PCR amplified) were
20 sequence-verified by sequencing in both the forward and reverse direction using MegaBACE sequencer (Molecular Dynamics, Inc., Sunnyvale, CA), universal primers, and standard protocols.

Some genomic clones (BACs) yielded very poor PCR
25 and sequencing results. The reasons for this are unclear, but may be related to the quality of early draft sequence or the inclusion of vector and host contamination in some submitted sequence data.

Although the intronic and intergenic material
30 flanking coding regions could theoretically interfere with hybridization during microarray experiments, subsequent empirical results demonstrated that differential expression ratios were not significantly affected by the presence of noncoding sequence. The variation in exon size was
35 similarly found not to affect differential expression

ratios significantly; however, variation in exon size was observed to affect the absolute signal intensity (data not shown).

The 350 MB of genomic DNA was, by the above-
5 described process, reduced to 9750 discrete probes, which
were spotted in duplicate onto glass slides using
commercially available instrumentation (MicroArray GenII
Spotter and/or MicroArray GenIII Spotter, Molecular
Dynamics, Inc., Sunnyvale, CA). Each slide additionally
10 included either 16 or 32 *E. coli* genes, the average
hybridization signal of which was used as a measure of
background biological noise.

Each of the probe sequences was BLASTed against
the human EST data set, the NR data set, and SwissProt
15 GenBank (May 7, 1999 release 2.0.9).

One third of the probe sequences (as amplified)
produced an exact match (BLAST Expect ("E") values less
than $1 e^{-100}$) to either an EST (20% of sequences) or a known
mRNA (13% of sequences). A further 22% of the probe
20 sequences showed some homology to a known EST or mRNA
(BLAST E values from $1 e^{-5}$ to $1 e^{-99}$). The remaining 45% of
the probe sequences showed no significant sequence homology
to any expressed, or potentially expressed, sequences
present in public databases.

25 All of the probe sequences (as amplified) were
then analyzed for protein similarities with the SwissProt
database using BLASTX, Gish et al., *Nature Genet.* 3:266
(1993). The predicted functional breakdowns of the 2/3 of
probes identical or homologous to known sequences are
30 presented in Table 1.

Table 1

| |
|---|
| Function of Predicted ORFs As Deduced From Comparative Sequence Analysis |
|---|

| Total | V6 chip | V7 chip | Function Predicted from Comparative Sequence Analysis |
|-------|---------|---------|---|
| 211 | 96 | 115 | Receptor |
| 120 | 43 | 77 | Zinc Finger |
| 30 | 11 | 19 | Homeobox |
| 25 | 9 | 16 | Transcription Factor |
| 17 | 11 | 7 | Transcription |
| 118 | 57 | 61 | Structural |
| 95 | 39 | 56 | Kinase |
| 36 | 18 | 18 | Phosphatase |
| 83 | 31 | 52 | Ribosomal |
| 45 | 19 | 26 | Transport |
| 21 | 17 | 14 | Growth Factor |
| 17 | 12 | 5 | Cytochrome |
| 50 | 33 | 17 | Channel |

As can be seen, the two most common types of genes were transcription factors and receptors, making up 2.2% and 1.8% of the arrayed elements, respectively.

5

EXAMPLE 2

Gene Expression Measurements From Genome-Derived Single Exon Microarrays

10

The two genome-derived single exon microarrays prepared according to Example 1 were hybridized in a series of simultaneous two-color fluorescence experiments to (1) 15 Cy3-labeled cDNA synthesized from message drawn individually from each of brain, heart, liver, fetal liver, placenta, lung, bone marrow, HeLa, BT 474, or HBL 100 cells, and (2) Cy5-labeled cDNA prepared from message

pooled from all ten tissues and cell types, as a control in each of the measurements. Hybridization and scanning were carried out using standard protocols and Molecular Dynamics equipment.

5 Briefly, mRNA samples were bought from commercial sources (Clontech, Palo Alto, CA and Amersham Pharmacia Biotech (APB)). Cy3-dCTP and Cy5-dCTP (both from APB) were incorporated during separate reverse transcriptions of 1 µg of polyA⁺ mRNA performed using 1 µg oligo(dT)12-18 primer
10 and 2 µg random 9mer primers as follows. After heating to 70°C, the RNA:primer mixture was snap cooled on ice. After snap cooling on ice, added to the RNA to the stated final concentration was: 1X Superscript II buffer, 0.01 M DTT, 100µM dATP, 100 µM dGTP, 100 µM dTTP, 50 µM dCTP, 50 µM
15 Cy3-dCTP or Cy5-dCTP 50 µM, and 200 U Superscript II enzyme. The reaction was incubated for 2 hours at 42°C. After 2 hours, the first strand cDNA was isolated by adding 1 U Ribonuclease H, and incubating for 30 minutes at 37°C. The reaction was then purified using a Qiagen PCR cleanup
20 column, increasing the number of ethanol washes to 5. Probe was eluted using 10 mM Tris pH 8.5.

Using a spectrophotometer, probes were measured for dye incorporation. Volumes of both Cy3 and Cy5 cDNA corresponding to 50 pmoles of each dye were then dried in a
25 Speedvac, resuspended in 30 µl hybridization solution containing 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 µg/µl human c₀t1 DNA, and 0.5 % SDS.

Hybridizations were carried out under a coverslip, with the array placed in a humid oven at 42°C
30 overnight. Before scanning, slides were washed in 1X SSC, 0.2% SDS at 55°C for 5 minutes, followed by 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. Slides were briefly dipped in water and dried thoroughly under a gentle stream of nitrogen.

35 Slides were scanned using a Molecular Dynamics

Gen3 scanner, as described. Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

5 Although the use of pooled cDNA as a reference permitted the survey of a large number of tissues, it attenuates the measurement of relative gene expression, since every highly expressed gene in the tissue/cell type-specific fluorescence channel will be present to a level of
10 at least 10% in the control channel. Because of this fact, both signal and expression ratios (the latter hereinafter, "expression" or "relative expression") for each probe were normalized using the average ratio or average signal, respectively, as measured across the whole slide.

15 Data were accepted for further analysis only when signal was at least three times greater than biological noise, the latter defined by the average signal produced by the *E. coli* control genes.

 The relative expression signal for these probes
20 was then plotted as function of tissue or cell type, and is presented in FIG. 6.

 FIG. 6 shows the distribution of expression across a panel of ten tissues. The graph shows the number of sequence-verified products that were either not
25 expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), and expressed in all tissues tested ("10").

 Of 9999 arrayed elements on the two microarrays (including positive and negative controls and "failed"
30 products), 2353 (51%) were expressed in at least one tissue or cell type. Of the gene elements showing significant signal - where expression was scored as "significant" if the normalized Cy3 signal was greater than 1, representing signal 5-fold over biological noise (0.2) - 39% (991) were
35 expressed in all 10 tissues. The next most common class

(15%) consisted of gene elements expressed in only a single tissue.

The genes expressed in a single tissue were further analyzed, and the results of the analyses are
5 compiled in FIG. 7.

FIG. 7A is a matrix presenting the expression of all verified sequences that showed expression greater than 3 in at least one tissue. Each clone is represented by a column in the matrix. Each of the 10 tissues assayed is
10 represented by a separate row in the matrix, and relative expression of a clone in that tissue is indicated at the respective node by intensity of green shading, with the intensity legend shown in panel B. The top row of the matrix ("EST Hit") contains "bioinformatic" rather than
15 "physical" expression data - that is, presents the results returned by query of EST, NR and SwissProt databases using the probe sequence. The legend for "bioinformatic expression" (i.e., degree of homology returned) is presented in panel C. Briefly, white is known, black is
20 novel, with gray depicting nonidentical with significant homology (white: E values < 1e-100; gray: E values from 1e-05 to 1e-99; black: E values > 1e-05).

As FIG. 7 readily shows, heart and brain were demonstrated to have the greatest numbers of genes that
25 were shown to be uniquely expressed in the respective tissue. In brain, 200 uniquely expressed genes were identified; in heart, 150. The remaining tissues gave the following figures for uniquely expressed genes: liver, 100; lung, 70; fetal liver, 150; bone marrow, 75; placenta, 100;
30 HeLa, 50; HBL, 100; and BT474, 50.

It was further observed that there were many more "novel" genes among those that were up-regulated in only one tissue, as compared with those that were down-regulated in only one tissue. In fact, it was found that ORFs whose
35 expression was measurable in only a single of the tested

tissues were represented in sequencing databases at a rate of only 11%, whereas 36% of the ORFs whose expression was measurable in 9 of the tissues were present in public databases. As for those ORFs expressed in all ten tissues, 5 fully 45% were present in existing expressed sequence databases. These results are not unexpected, since genes expressed in a greater number of tissues have a higher likelihood of being, and thus of having been, discovered by EST approaches.

10

Comparison of Signal from Known and Unknown Genes

The normalized signal of the genes found to have high homology to genes present in the GenBank human EST database were compared to the normalized signal of those 15 genes not found in the GenBank human EST database. The data are shown in FIG. 8.

FIG. 8 shows the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than $1e-30$ (designated "unknown") 20 upon query of existing EST, NR and SwissProt databases, and shows in blue the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect value of less than $1e-30$ ("known"). Note that biological background noise has an averaged normalized Cy3 signal intensity of 25 0.2.

As expected, the most highly expressed of the ORFs were "known" genes. This is not surprising, since very high signal intensity correlates with very commonly-expressed genes, which have a higher likelihood of being 30 found by EST sequence.

However, a significant point is that a large number of even the high expressers were "unknown". Since the genomic approach used to identify genes and to confirm their expression does not bias exons toward either the 3' 35 or 5' end of a gene, many of these high expression genes

will not have been detected in an end-sequenced cDNA library.

The significant point is that presence of the gene in an EST database is not a prerequisite for
5 incorporation into a genome-derived microarray, and further, that arraying such "unknown" exons can help to assign function to as-yet undiscovered genes.

Verification of Gene Expression

10 To ascertain the validity of the approach described above to identify genes from raw genomic sequence, expression of two of the probes was assayed using reverse transcriptase polymerase chain reaction (RT PCR) and northern blot analysis.

15 Two microarray probes were selected on the basis of exon size, prior sequencing success, and tissue-specific gene expression patterns as measured by the microarray experiments. The primers originally used to amplify the two respective ORFs from genomic DNA were used in RT PCR
20 against a panel of tissue-specific cDNAs (Rapid-Scan gene expression panel 24 human cDNAs) (OriGene Technologies, Inc., Rockville, MD).

Sequence AL079300_1 was shown by microarray hybridization to be present in cardiac tissue, and sequence
25 AL031734_1 was shown by microarray experiment to be present in placental tissue (data not shown). RT-PCR on these two sequences confirmed the tissue-specific gene expression as measured by microarrays, as ascertained by the presence of a correctly sized PCR product from the respective tissue
30 type cDNAs.

Clearly, all microarray results cannot, and indeed should not, be confirmed by independent assay methods, or the high throughput, highly parallel advantages of microarray hybridization assays will be lost. However,
35 in addition to the two RT-PCR results presented above, the

observation that 1/3 of the arrayed genes exist in expression databases provides powerful confirmation of the power of our methodology - which combines bioinformatic prediction with expression confirmation using genome-derived single exon microarrays - to identify novel genes from raw genomic data.

To verify that the approach further provides correct characterization of the expression patterns of the identified genes, a detailed analysis was performed of the microarrayed sequences that showed high signal in brain.

For this latter analysis, sequences that showed high (normalized) signal in brain, but which showed very low (normalized) signal (less than 0.5, determined to be biological noise) in all other tissues, were further studied. There were 82 sequences that fit these criteria, approximately 2% of the arrayed elements. The 10 sequences showing the highest signal in brain in microarray hybridizations are detailed in Table 2, along with assigned function, if known or reasonably predicted.

Table 2

| Function of the Most Highly Expressed Genes Expressed Only in Brain | | | | |
|---|-------------------|------------------|------------------------------------|---|
| Microarray Sequence Name | Normalized Signal | Expression Ratio | Homology to EST present in GenBank | Gene Function as described by GenBank |
| AP000217-1 | 5.2 | +7.7 | High | S-100 protein, b-chain, Ca ²⁺ binding protein expressed in central nervous |

| | | | | |
|------------|-----|------|------|---|
| | | | | system |
| AP000047-1 | 2.3 | | High | Unknown Function |
| AC006548-9 | 1.7 | | High | Similar to mouse membrane glyco-protein M6, expressed in central nervous system |
| AC007245-5 | 1.5 | | High | Similar to amphiphysin, a synaptic vesicle- associated protein. Ref 21 |
| L44140-4 | 1.2 | +2.0 | High | Endothelial actin-binding protein found in nonmuscle filamin |
| AC004689-9 | 1.2 | +3.5 | High | Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases |
| AL031657-1 | 1.2 | +3.0 | High | Unknown function/ Contains the anhyrin motif, a common protein sequence motif |
| AC009266-2 | 1.1 | +3.7 | Low | Low homology to |

| | | | | |
|------------|-----|------|------|---|
| | | | | the Synaptotagmin I protein in rat/present at low levels throughout rat brain |
| AP000086-1 | 1.0 | +2.7 | Low | Unknown, very poor homology to collagen |
| AC004689-3 | 1.0 | | High | Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases |

Of the ten sequences studied by these latter confirmatory approaches, eight were previously known. Of these eight, six had previously been reported to be
5 important in the central nervous system or brain. The exon giving the highest signal (AP00217-1) was found to be the gene encoding an S100B Ca^{2+} binding protein, reported in the literature to be highly and uniquely expressed in the central nervous system. Heizmann, *Neurochem. Res.* 9:1097
10 (1997).

A number of the brain-specific probe sequences (including AC006548-9, AC009266-2) did not have homology to any known human cDNAs in GenBank but did show homology to rat and mouse cDNAs. Sequences AC004689-9 and AC004689-3
15 were both found to be phosphatases present in neurons (Millward *et al.*, *Trends Biochem. Sci.* 24(5):186-191 (1999)). Two microarray sequences, AP000047-1 and AP000086-1 have unknown function, with AP000086-1 being absent from GenBank. Functionality can now be narrowed

down to a role in the central nervous system for both of these genes, showing the power of designing microarrays in this fashion.

Next, the function of the chip sequences with the highest (normalized) signal intensity in brain, regardless of expression in other tissues, was assessed. In this latter analysis, we found expression of many more common genes, since the sequences were not limited to those expressed only in brain. For example, looking at the 20 highest signal intensity spots in brain, 4 were similar to tubulin (AC00807905; AF146191-2; AC007664-4; AF14191-2), 2 were similar to actin (AL035701-2; AL034402-1), and 6 were found to be homologous to glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (AL035604-1; Z86090-1; AC006064-L, AC006064-K; AC035604-3; AC006064-L). These genes are often used as controls or housekeeping genes in microarray experiments of all types.

Other interesting genes highly expressed in brain were a ferritin heavy chain protein, which is reported in the literature to be found in brain and liver (Joshi et al., *J. Neurol. Sci.* 134(Suppl):52-56 (1995)), a result duplicated with the array. Other highly expressed chip sequences included a translation elongation factor 1 α (AC007564-4), a DEAD-box homolog (AL023804-4), and a Y-chromosome RNA-binding motif (Chai et al., *Genomics* 49(2):283-89 (1998)) (AC007320-3). A low homology analog (AP00123-1/2) to a gene, DSCR1, thought to be involved in trisomy 21 (Down's syndrome), showed high expression in both brain and heart, in agreement with the literature (Fuentes et al., *Mol. Genet.* 4(10):1935-44 (1995)).

As a further validation of the approach, we selected the BAC AC006064 to be included on the array. This BAC was known to contain the GAPDH gene, and thus could be used as a control for the ORF selection process. The gene finding and exon selection algorithms resulted in

choosing 25 exons from BAC AC006064 for spotting onto the array, of which four were drawn from the GAPDH gene. Table 3 shows the comparison of the average expression ratio for the 4 exons from BAC006064 compared with the average expression ratio for 5 different dilutions of a commercially available GAPDH cDNA (Clontech).

Table 3

| Comparison of Expression Ratio, for each tissue, of GAPDH | | |
|---|------------------|------------------|
| | AC006064 (n = 4) | Control (n = 5) |
| Bone Marrow | -1.81 \pm 0.11 | -1.85 \pm 0.08 |
| Brain | -1.41 \pm 0.11 | -1.17 \pm 0.05 |
| BT474 | 1.85 \pm 0.09 | 1.66 \pm 0.12 |
| Fetal Liver | -1.62 \pm 0.07 | -1.41 \pm 0.05 |
| HBL100 | 1.32 \pm 0.05 | 2.64 \pm 0.12 |
| Heart | 1.16 \pm 0.09 | 1.56 \pm 0.10 |
| HeLa | 1.11 \pm 0.06 | 1.30 \pm 0.15 |
| Liver | -1.62 \pm 0.22 | -2.07 \pm |
| Lung | -4.95 \pm 0.93 | -3.75 \pm 0.21 |
| Placenta | -3.56 \pm 0.25 | -3.52 \pm 0.43 |

10

Each tissue shows excellent agreement between the experimentally chosen exons and the control, again demonstrating the validity of the present exon mining approach. In addition, the data also show the variability of expression of GAPDH within tissues, calling into question its classification as a housekeeping gene and utility as a housekeeping control in microarray experiments.

20 EXAMPLE 3

Representation of Sequence and Expression Data as a
"Mondrian"

For each genomic clone processed for microarray
5 as above-described, a plethora of information was
accumulated, including full clone sequence, probe sequence
within the clone, results of each of the three gene finding
programs, EST information associated with the probe
sequences, and microarray signal and expression for
10 multiple tissues, challenging our ability to display the
information.

Accordingly, we devised a new tool for visual
display of the sequence with its attendant annotation
which, in deference to its visual similarity to the
15 paintings of Piet Mondrian, is hereinafter termed a
"Mondrian". FIGS. 3 and 4 present the key to the
information presented on a Mondrian.

FIG. 9 presents a Mondrian of BAC AC008172 (bases
25,000 to 130,000 shown), containing the carbamyl phosphate
20 synthetase gene (AF154830.1). Purple background within the
region shown as field 81 in FIG. 3 indicates all 37 known
exons for this gene.

As can be seen, GRAIL II successfully identified
27 of the known exons (73%), GENEFINDER successfully
25 identified 37 of the known exons (100%), while DICTION
identified 7 of the known exons (19%).

Seven of the predicted exons were selected for
physical assay, of which 5 successfully amplified by PCR
and were sequenced. These five exons were all found to be
30 from the same gene, the carbamyl phosphate synthetase gene
(AF154830.1).

The five exons were arrayed, and gene expression
measured across 10 tissues. As is readily seen in the
Mondrian, the five chip sequences on the array show
35 identical expression patterns, elegantly demonstrating the

reproducibility of the system.

FIG. 10 is a Mondrian of BAC AL049839. We selected 12 exons from this BAC, of which 10 successfully sequenced, which were found to form between 5 and 6 genes. Interestingly, 4 of the genes on this BAC are protease inhibitors. Again, these data elegantly show that exons selected from the same gene show the same expression patterns, depicted below the red line. From this figure, it is clear that our ability to find known genes is very good. A novel gene is also found from 86.6 kb to 88.6 kb, upon which all the exon finding programs agree. We are confident we have two exons from a single gene since they show the same expression patterns and the exons are proximal to each other. Backgrounds in the following colors indicate a known gene (top to bottom):

red = kallistatin protease inhibitor (P29622);
purple = plasma serine protease inhibitor (P05154);
turquoise = α 1 anti-chymotrypsin (P01011); mauve = 40S ribosomal protein (P08865). Note that chip sequence 8 and 12 did not sequence verify.

EXAMPLE 4

Genome-Derived Single Exon Probes Useful For Measuring Human Gene Expression

The protocols set forth in Examples 1 and 2, *supra*, were applied to additional human genomic sequence as it became newly available in GenBank to identify unique exons in the human genome that could be shown to be expressed at significant levels in bone marrow tissue.

These unique exons are within longer probe sequences. Each probe was completely sequenced on both strands prior to its use on a genome-derived single exon microarray; sequencing confirms the exact chemical

structure of each probe. An added benefit of sequencing is that it placed us in possession of a set of single base-incremented fragments of the sequenced nucleic acid, starting from the sequencing primer 3' OH. (Since the
5 single exon probes were first obtained by PCR amplification from genomic DNA, we were of course additionally in possession of an even larger set of single base incremented fragments of each of the 13,114 single exon probes, each fragment corresponding to an extension product from one of
10 the two amplification primers.)

The structures of the 13,114 unique single exon probes are clearly presented in the Sequence Listing as SEQ ID Nos.: 1 - 13,114. The 16 nt 5' primer sequence and 16 nt 3' primer sequence present on the amplicon are not
15 included in the sequence listing. The sequences of the exons present within each of these probes is presented in the Sequence Listing as SEQ ID Nos.: 13,115 - 26,012, respectively. It will be noted that some amplicons have more than one exon, some exons are contained in more than
20 one amplicon.

As detailed in Example 2, expression was demonstrated by disposing the amplicons as single exon probes on nucleic acid microarrays and then performing two-color fluorescent hybridization analysis; significant
25 expression is based on a statistical confidence that the signal is significantly greater than negative biological control spots. The negative biological control is formed from spotted DNA sequences from a different species. Here, 32 sequences from E.Coli were spotted in duplicate to give
30 a total of 64 spots.

For each hybridisation (each slide, each colour) the median value of the signal from all of the spots is determined. The normalised signal value is the arithmetic mean of the signal from duplicate spots divided by the
35 population median.

Control spots are eliminated if there is more than a five-fold difference between each one of the duplicate spots raw signals.

The median of the signal from the remaining
5 control spots is calculated and all subsequent calculations are done with normalised signals.

Control spots having a signal of greater than median + 2.4 (the value 2.4 is roughly 12 times the observed standard deviation of control spot populations)
10 are eliminated. Spots with such high signals are considered to be "outliers".

The mean and standard deviation of the modified control spot populations are calculated.

The mean + 3x the standard deviation (mean +
15 (3*SD)) is used as the signal threshold qualifier for that particular hybridisation. Thus, individual thresholds are determined for each channel and each hybridisation.

This means that, assuming that the data is distributed normally, there is a 99% confidence that any
20 signal exceeding the threshold is significant.

The probes and their expression data are presented in Table 4, set forth respectively in Example 5. Example 5 presents the subset of probes that is significantly expressed in the human bone marrow and thus
25 presents the subset of probes that was recognized to be useful for measuring expression of their cognate genes in human bone marrow tissue.

The sequence of each of the exon probes identified by SEQ ID NOS.: 13,115 - 26,012 was individually
30 used as a BLAST (or, for SWISSPROT, BLASTX) query to identify the most similar sequence in each of dbEST, SwissProt (BLASTX), and NR divisions of GenBank. Because the query sequences are themselves derived from genomic sequence in GenBank, only nongenomic hits from NR were
35 scored.

The smallest in value of the BLAST (or BLASTX) expect ("E") scores for each query sequence across the three database divisions was used as a measure of the "expression novelty" of the probe's ORF. Table 4 is sorted
5 in descending order based on this measure, reported as "Most Similar (top) Hit BLAST E Value". Those sequences for which no "Hit E Value" is listed are those exons which were found to have no similar sequences.

As sorted, Table 4 thus lists its respective
10 probes (by "AMPLICON SEQ ID NO.:" and additionally by the SEQ ID NO.: of the exon contained within the probe:"EXON SEQ ID NO.:") from least similar to sequences known to be expressed (i.e., highest BLAST E value), at the beginning of the table, to most similar to sequences known to be
15 expressed (i.e., lowest BLAST E value), at the bottom of the table.

Table 4 further provides, for each listed probe, the accession number of the database sequence that yielded the "Most Similar (top) Hit BLAST E Value", along with the
20 name of the database in which the database sequence is found ("Top Hit Database Source").

Table 4 further provides SEQ ID NOS.
corresponding to the predicted amino acid sequences where they have been determined for the probe and exon nucleotide
25 sequences. These are set out as PEPTIDE SEQ ID NOS.:. The peptide sequences for a given exon are predicted as follows: Since each chip exon is a consensus sequence drawn from predictions from various exon finding programs (i.e. Grail, GeneFinder and GenScan), the multiple initial ORFs
30 are first determined in a uniform way according to each prediction. In particular, the reading frame for predicting the first amino acid in the peptide sequence always starts with the first base of any codon and ends with the last base of non-termination codon. Next, for each strand of the
35 exon, initial ORFs are merged into one or more final ORFs

in an exhaustive process based on the following criteria:

1) the merging ORFs must be overlapping, and 2) the merging ORFs must be in the same frame.

The Sequence Listing, which is a superset of all
5 of the data presented in Table 4, further includes, for each probe, the most similar hit, with accession number and BLAST E value, from the each of the three queried databases.

Table 4 further lists, for each probe, a portion
10 of the descriptor for the top hit ("Top Hit Descriptor") as provided in the sequence database. For those ORFs that are similar in sequence, but nonidentical to known sequences (e.g., those with BLAST E values between about $1e-05$ and $1e-100$), the descriptor reveals the likely function of the
15 protein encoded by the probe's ORF.

Using BLAST E value cutoffs of $1e-05$ (i.e., 1×10^{-5}) and $1e-100$ (i.e., 1×10^{-100}) as evidence of similarity to sequences known to be expressed is of course arbitrary: in Example 2, *supra*, a BLAST E value of $1e-30$ was used as
20 the boundary when only two classes were to be defined for analysis (unknown, $>1e-30$; known $<1e-30$) (see also FIG. 8). Furthermore, even when the "Most Similar (Top) Hit BLAST E Value" is low, e.g., less than about $1e-100$ - which is probative evidence that the query sequence has previously
25 been shown to be expressed - the top hit is highly unlikely exactly to match the probe sequence.

First, such expression entries typically will not have the intronic and/or intergenic sequence present within the single exon probes listed in the Table. Second, even
30 the ORF itself is unlikely in such cases to be present identically in the databases, since most of the EST and mRNA clones in existing databases include multiple exons, without any indication of the location of exon boundaries.

As noted, the data presented in Table 4 represent
35 a proper subset of the data present within the attached

sequence listing. For each amplicon probe (SEQ ID NOs.: 1 - 13,114) and probe exon (SEQ ID NOs.: 13,115 - 26,012, respectively), the sequence listing further provides, through iterated annotation fields <220> and <223>:

5 (a) the accession number of the BAC from which the sequence was derived ("MAP TO"), thus providing a link to the chromosomal map location and other information about the genomic milieu of the probe sequence;

 (b) the most similar sequence provided by BLAST
10 query of the EST database, with accession number and BLAST E value for the "hit";

 (c) the most similar sequence provided by BLAST query of the GenBank NR database, with accession number and BLAST E value for the "hit"; and

15 (d) the most similar sequence provided by BLASTX query of the SWISSPROT database, with accession number and BLAST E value for the "hit".

20 EXAMPLE 5

Genome-Derived Single Exon Probes Useful For Measuring
Expression of Genes in Human Bone marrow

Table 4 (546 pages) presents expression, homology, and
25 functional information for the genome-derived single exon probes that are expressed significantly in human bone marrow.

CLAIMS

1. A spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human bone marrow comprising a plurality single exon nucleic probes, said probes comprising any one of the nucleotide sequences set out in SEQ ID NOS: 1 - 13,114 or a complementary sequence, or a portion of such a sequence.
2. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably amplifiable.
3. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably isolatable from said plurality.
4. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 3 wherein said probes comprise any one of the nucleotide sequences set out in SEQ ID NOS.: 13,115 - 26,012.
5. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 4, wherein each of said plurality of probes is amplifiable using at least one common primer.
6. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 5 wherein the set comprises between 50 - 20,000 single exon nucleic acid probes.
7. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 6, wherein the

average length of the single exon nucleic acid probes is between 200 and 500 bp.

8. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 7, wherein at least 50% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

9. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 8, wherein at least 50% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

10. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 9 characterised in that said set of probes is addressably disposed upon a substrate.

11. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 10 wherein said substrate is selected from glass, amorphous silicon, crystalline silicon and plastic.

12. A microarray comprising a spatially addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 11.

13. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human bone marrow comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 1 - 13,114 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid molecule expressed in the human bone marrow.

14. A single exon nucleic acid probe as claimed in claim 13 comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 13,115 - 26,012 or a complementary sequence or a fragment thereof.
- 5
15. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human bone marrow which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any
10 of SEQ ID NOs.: 26,013 - 38,628, or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human bone marrow.
- 15 16. A single exon nucleic acid probe as claimed in any one of claims 13 to 15 wherein said single exon nucleic acid probe comprises between 15 and 25 contiguous nucleotides of said SEQ ID NO.
- 20 17. A single exon nucleic acid probe as claimed in any one of claims 13 to 15, wherein said probe is between 3 - 25 kb in length.
18. A single exon nucleic acid probe as claimed in any one
25 of claims 13 - 17, wherein said probe is DNA, RNA or PNA.
19. A single exon nucleic acid probe as claimed in any one of claims 13 - 18, wherein said probe is detectably labeled.
- 30
20. A single exon nucleic acid probe as claimed in any one of claims 13 - 19, wherein said probe lacks prokaryotic and bacteriophage vector sequence.
- 35 21. A single exon nucleic acid probe as claimed in any one

of claims 13 - 20, wherein said probe lacks homopolymeric stretches of A or T.

22. A method of measuring gene expression in a sample
5 derived from human bone marrow, comprising:
 contacting the microarray of claim 12, with a first
 collection of detectably labeled nucleic acids,
 said first collection of nucleic acids derived
 from mRNA of human bone marrow; and then
10 measuring the label detectably bound to each probe of
 said microarray.

23. A method of identifying exons in a eukaryotic genome,
comprising:
15 algorithmically predicting at least one exon from
 genomic sequence of said eukaryote; and then
 detecting specific hybridization of detectably labeled
 nucleic acids to a single exon probe,
wherein said detectably labeled nucleic acids are derived
20 from mRNA from the bone marrow of said eukaryote, said
probe is a single exon probe having a fragment identical in
sequence to, or complementary in sequence to, said
predicted exon, said probe is included within a microarray
according to claim 12, and said fragment is selectively
25 hybridizable at high stringency.

24. A method of assigning exons to a single gene,
comprising:
 identifying a plurality of exons from genomic
30 sequence according to the method of claim 23; and
 then
 measuring the expression of each of said exons in a
 plurality of tissues and/or cell types using
 hybridization to single exon microarrays having a
35 probe with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

5 25. A nucleic acid sequence as set out in any of SEQ ID Nos: 1 - 26,012 which encodes a peptide.

26. A peptide encoded by a sequence as set out in any of SEQ ID Nos: 1 - 26,012.

10

27. A peptide comprising a sequence as set out in any of SEQ ID Nos: 26,013 - 38,628.

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--------------------|
| 450 | 13523 | 26465 | 4.57 | | | | |
| 880 | 13945 | 26803 | 10.46 | | | | |
| 1046 | 14092 | | 3.88 | | | | |
| 1305 | 14341 | 27306 | 7.19 | | | | |
| 1618 | 14650 | 27628 | 4.21 | | | | |
| 1842 | 14674 | 27647 | 6.05 | | | | |
| 1738 | 14768 | 27753 | 2.88 | | | | |
| 1764 | 14793 | 27778 | 1.27 | | | | |
| 1770 | 14799 | 27785 | 9.04 | | | | |
| 1908 | 14832 | 27828 | 1.24 | | | | |
| 1985 | 15016 | 28023 | 2.44 | | | | |
| 2175 | 15191 | 28212 | 2.92 | | | | |
| 2287 | 15300 | 28324 | 2.97 | | | | |
| 3200 | 16255 | 29176 | 3.13 | | | | |
| 3464 | 16510 | 29431 | 1.32 | | | | |
| 3527 | 16573 | 29496 | 10.05 | | | | |
| 3574 | 16619 | | 0.85 | | | | |
| 3968 | 17008 | | 1.15 | | | | |
| 4225 | 17254 | 30141 | 1.66 | | | | |
| 4280 | 17319 | 30198 | 6.25 | | | | |
| 4310 | 17339 | 30218 | 0.83 | | | | |
| 4310 | 17339 | 30218 | 0.83 | | | | |
| 4364 | 17391 | | 1.03 | | | | |
| 4420 | 17447 | 30338 | 0.63 | | | | |
| 4874 | 17891 | 30780 | 1.27 | | | | |
| 4959 | 17974 | 30865 | 0.74 | | | | |
| 5083 | 18093 | 30969 | 5.95 | | | | |
| 5095 | 18105 | 30980 | 1.42 | | | | |
| 5329 | 18435 | 31187 | 1.78 | | | | |
| 5329 | 18435 | 31188 | 1.78 | | | | |
| 5496 | 18596 | | 4.07 | | | | |
| 5678 | 18773 | | 7.77 | | | | |
| 5782 | 18596 | | 3.48 | | | | |
| 5824 | 18914 | 32097 | 0.65 | | | | |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 5830 | 18920 | 32103 | 3.19 | | | | |
| 6138 | 25655 | 32443 | 1.68 | | | | |
| 6187 | 18242 | 32473 | 2.11 | | | | |
| 6556 | 19616 | | 1.24 | | | | |
| 6700 | 19757 | 33034 | 0.89 | | | | |
| 6700 | 19757 | 33035 | 0.89 | | | | |
| 7332 | 20303 | 33647 | 1.52 | | | | |
| 7332 | 20303 | 33648 | 1.52 | | | | |
| 7642 | 20602 | 33966 | 1.45 | | | | |
| 7842 | 20602 | 33987 | 1.45 | | | | |
| 8114 | 21051 | | 0.61 | | | | |
| 8396 | 21365 | 34774 | 1.55 | | | | |
| 8830 | 21797 | 35218 | 1.21 | | | | |
| 9212 | 22178 | 35608 | 0.57 | | | | |
| 9212 | 22178 | 35609 | 0.57 | | | | |
| 9892 | 22845 | 36302 | 5.61 | | | | |
| 10124 | 23050 | 36529 | 0.69 | | | | |
| 10241 | 23166 | 36653 | 1.44 | | | | |
| 10383 | 23305 | 36782 | 0.91 | | | | |
| 10675 | 23597 | 37093 | 0.49 | | | | |
| 10675 | 23597 | 37094 | 0.49 | | | | |
| 10794 | 23715 | 37216 | 0.6 | | | | |
| 10794 | 23715 | 37217 | 0.6 | | | | |
| 11043 | 24007 | | 2.14 | | | | |
| 11366 | 24314 | | 1.61 | | | | |
| 11687 | 24653 | 38232 | 1.82 | | | | |
| 11829 | 24712 | | 1.84 | | | | |
| 12600 | 25302 | | 1.5 | | | | |
| 12888 | 25476 | 31730 | 1.34 | | | | |
| 6170 | 19245 | 32477 | 15.3 | 9.9E+00 | AJ239028.1 | NT | Homo sapiens LSS gene, partial, exons 15, 16, 17 and 18 |
| 8339 | 21308 | 34723 | 1.75 | 9.8E+00 | U32716.1 | NT | Haemophilus influenzae Rd section 31 of 163 of the complete genome |
| 10100 | 23026 | 36502 | 0.47 | 9.8E+00 | Y18930.1 | NT | Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2 |
| 10100 | 23026 | 36503 | 0.47 | 9.8E+00 | Y18930.1 | NT | Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2 |
| 7194 | 20218 | 33549 | 0.66 | 9.6E+00 | AF065630.1 | NT | Gallus gallus ornithine transcarbamylase (OTC) gene, exon 1 |

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Table 4
Single Exon Probes Expressed In Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 7194 | 20218 | 33550 | 0.66 | 9.6E+00 | AF065630.1 | NT | Gallus gallus ornithine transcarbamylase (OTC) gene, exon 1 |
| 10787 | 23708 | 37209 | 1.19 | 9.6E+00 | AF242432.1 | NT | Mus musculus Nalp3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Nalp1) and general transcription factor 1LH polypeptide 2 (Gtf2h2) genes, complete cds |
| 10787 | 23708 | 37210 | 1.19 | 9.6E+00 | AF242432.1 | NT | Mus musculus Nalp3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Nalp1) and general transcription factor 1LH polypeptide 2 (Gtf2h2) genes, complete cds |
| 2935 | 15993 | 28913 | 3.21 | 9.4E+00 | AB043785.1 | NT | Mus musculus Nalp3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Nalp1) and general transcription factor 1LH polypeptide 2 (Gtf2h2) genes, complete cds |
| 6457 | 19522 | 32773 | 0.54 | 9.4E+00 | P75130 | SWISSPROT | Mus musculus AT3 gene for antithrombin, complete cds |
| 11911 | 24792 | 38381 | 2.45 | 9.4E+00 | O99825 | SWISSPROT | HYPOTHETICAL PROTEIN MG447 HOMOLOG |
| 11911 | 24792 | 38382 | 2.45 | 9.4E+00 | O99825 | SWISSPROT | NADH:UBIQUINONE OXIDOREDUCTASE CHAIN 4 |
| 8435 | 21404 | 34817 | 0.86 | 9.3E+00 | AF130990.1 | NT | NADH:UBIQUINONE OXIDOREDUCTASE CHAIN 4 |
| 9356 | 22321 | 35748 | 3.15 | 9.3E+00 | P11210 | SWISSPROT | Homo sapiens ectodysplasin-A receptor protein (EDAR) gene, exons 2, 3, and 4 |
| 5369 | 18474 | 31346 | 2.66 | 9.1E+00 | AF095609.1 | NT | IMMEDIATE-EARLY PROTEIN 1 (IE1) (IMMEDIATE-EARLY PHOSPHOPROTEIN PP89) |
| 5369 | 18474 | 31347 | 2.66 | 9.1E+00 | AF095609.1 | NT | Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product |
| 9785 | 22726 | 32456 | 0.95 | 9.0E+00 | P09241 | SWISSPROT | Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product |
| 8162 | 19227 | 32456 | 5.62 | 8.9E+00 | BE971806.1 | EST_HUMAN | RHODOPSIN |
| 6517 | 19580 | 32837 | 2.21 | 8.7E+00 | AB019788.1 | NT | 601651038R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934562 3' |
| 6517 | 19580 | 32838 | 2.21 | 8.7E+00 | AB019788.1 | NT | Cynops pyrrhogaster CpTbx3 premature mRNA, partial cds |
| 440 | 13514 | 28445 | 1.03 | 8.4E+00 | 5031804 | NT | Cynops pyrrhogaster CpTbx3 premature mRNA, partial cds |
| 9810 | 21133 | 34538 | 3.58 | 8.1E+00 | AJ131719.1 | NT | Homo sapiens insulin receptor substrate 1 (IRS1) mRNA |
| 11504 | 24446 | | 1.54 | 8.0E+00 | P41820 | SWISSPROT | Zea mays mRNA for legumain-like protease (see2a) |
| 8491 | 21459 | | 0.82 | 7.6E+00 | Z21489.1 | NT | BREFELDIN A RESISTANCE PROTEIN |
| 7569 | 20532 | | 2.17 | 7.5E+00 | AL445065.1 | NT | African swine fever virus NP1450L gene encoding RNA polymerase largest subunit |
| 8704 | 21672 | 35096 | 1.58 | 7.5E+00 | P35441 | SWISSPROT | Thermoplasma acidophilum complete genome, segment 3/5 |
| 8704 | 21672 | 35096 | 1.58 | 7.5E+00 | P35441 | SWISSPROT | THROMBOSPONDIN 1 PRECURSOR |
| 5998 | 18985 | 32176 | 3.53 | 7.4E+00 | BF700517.1 | EST_HUMAN | THROMBOSPONDIN 1 PRECURSOR |
| 9106 | 22072 | 35498 | 2.72 | 7.4E+00 | P04929 | SWISSPROT | 602128876F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285506 5' |
| 9106 | 22072 | 35499 | 2.72 | 7.4E+00 | P04929 | SWISSPROT | HISTIDINE-RICH GLYCOPROTEIN PRECURSOR |
| 2990 | 16048 | 28968 | 4.7 | 7.2E+00 | L12051.1 | NT | HISTIDINE-RICH GLYCOPROTEIN PRECURSOR |
| 2990 | 16048 | 28969 | 4.7 | 7.2E+00 | L12051.1 | NT | Lycopodium esculentum Mill. GTPase (SAR2) mRNA, complete cds |
| 7230 | 20252 | 33586 | 1.12 | 7.2E+00 | BE179090.1 | EST_HUMAN | Lycopodium esculentum Mill. GTPase (SAR2) mRNA, complete cds |
| 7356 | 20326 | 33673 | 1.1 | 7.1E+00 | P28166 | SWISSPROT | RCO-HT0613-200300-031-a07 HT0613 Homo sapiens cDNA |
| 7356 | 20326 | 33674 | 1.1 | 7.1E+00 | P28166 | SWISSPROT | ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1) |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 9957 | 22884 | | 6.86 | 7.1E+00 | AL161595.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91 |
| 11716 | 24678 | 38258 | 2.96 | 7.1E+00 | P05850 | SWISSPROT | HYPOTHETICAL 17.3 KDA PROTEIN IN MRDA-PHPB INTERGENIC REGION |
| 11909 | 24790 | 38379 | 4.81 | 7.1E+00 | P06106 | SWISSPROT | MET17 PROTEIN [INCLUDES: O-ACETYLHOMOSERINE SULFHYDRYLASE (OAH SULFHYDRYLASE); O-ACETYL SERINE SULFHYDRYLASE (OAS SULFHYDRYLASE)] |
| 10341 | 23285 | 38744 | 3.43 | 7.0E+00 | P48610 | SWISSPROT | ARGININE KINASE (AK) |
| 11580 | 24518 | 38074 | 1.7 | 7.0E+00 | O22469 | SWISSPROT | WD-40 REPEAT PROTEIN MSI3 |
| 8626 | 21594 | 35014 | 3.94 | 6.9E+00 | P35679 | SWISSPROT | 60S RIBOSOMAL PROTEIN L4 (L2) |
| 10716 | 23638 | 37131 | 1.32 | 6.9E+00 | P44834 | SWISSPROT | DNA MISMATCH REPAIR PROTEIN MUTS |
| 10734 | 23666 | 37149 | 0.44 | 6.9E+00 | P34226 | SWISSPROT | SKT5 PROTEIN |
| 8240 | 21209 | 34613 | 1.31 | 6.8E+00 | W03412.1 | EST_HUMAN | zao7c11.1.1 Scores melanocyte 2NbrHM Homo sapiens cDNA clone IMAGE:291860 5' |
| 8240 | 21209 | 34614 | 1.31 | 6.8E+00 | W03412.1 | EST_HUMAN | zao7c11.1.1 Scores melanocyte 2NbrHM Homo sapiens cDNA clone IMAGE:291860 5' |
| 9488 | 22452 | | 1.35 | 6.8E+00 | P36307 | SWISSPROT | OUTER CAPSID PROTEIN VP4 (HEMAGGLUTININ) (OUTER LAYER PROTEIN VP4) [CONTAINS: OUTER CAPSID PROTEINS VP5 AND VP8] |
| 10569 | 23491 | 36983 | 3.31 | 6.8E+00 | Q03570 | SWISSPROT | HYPOTHETICAL 197.0 KDA PROTEIN C38C10.5 IN CHROMOSOME III |
| 5358 | 18461 | | 0.74 | 6.6E+00 | Q99028 | SWISSPROT | CATECHOL-O-METHYLTRANSFERASE, SOLUBLE FORM (S-COMT) |
| 6895 | 19752 | 33029 | 0.72 | 6.6E+00 | B1672121.1 | EST_HUMAN | 602152573F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4283427 5' |
| 10434 | 23356 | 36842 | 1.87 | 6.6E+00 | Q9ZE07 | SWISSPROT | URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE) |
| 10434 | 23356 | 36843 | 1.87 | 6.6E+00 | Q9ZE07 | SWISSPROT | URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE) |
| 11463 | 24406 | | 2.49 | 6.6E+00 | Q10309 | SWISSPROT | PROBABLE CATION-TRANSPORTING ATPASE C6C3.05C |
| 9535 | 22498 | 35946 | 7.17 | 6.5E+00 | P03374 | SWISSPROT | ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP36] |
| 10667 | 23589 | 37086 | 0.47 | 6.5E+00 | BE866001.1 | EST_HUMAN | 801678435F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3960969 5' |
| 10099 | 23025 | 36501 | 1.17 | 6.2E+00 | AY010901.1 | NT | Schizaphyllum commune unknown mRNA |
| 10927 | 23847 | 37362 | 0.55 | 6.2E+00 | 6754621 | NT | Mus musculus mannosidase 2, alpha B1 (Man2b1), mRNA |
| 7236 | 20257 | 33591 | 1.35 | 6.0E+00 | BE780163.1 | EST_HUMAN | 601468031F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3871303 5' |
| 10175 | 23100 | 36590 | 0.46 | 6.0E+00 | AP000008.1 | NT | Pyrococcus horikoshii OT3 genomic DNA, 1168001-1485000 nt, position (6/7) |
| 10880 | 23800 | 37302 | 0.63 | 6.0E+00 | AE001862.1 | NT | Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2 |
| 10880 | 23800 | 37303 | 0.63 | 6.0E+00 | AE001862.1 | NT | Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2 |
| 6670 | 19727 | 33003 | 6.7 | 5.9E+00 | AF155142.1 | NT | Mus musculus mixed lineage kinase 3 (Mlk3) and two pore domain K+ channel subunit (Kcnk6) genes, complete cds |
| 3536 | 16682 | | 0.88 | 5.8E+00 | 7661557 | NT | Homo sapiens DESC1 protein (DESC1), mRNA |
| 7369 | 20339 | 33690 | 0.65 | 5.7E+00 | AF302046.1 | NT | Mus musculus immunoglobulin scavenger receptor IgSR mRNA, complete cds |
| 7369 | 20339 | 33691 | 0.65 | 5.7E+00 | AF302046.1 | NT | Mus musculus immunoglobulin scavenger receptor IgSR mRNA, complete cds |
| 7819 | 20768 | | 1.5 | 5.6E+00 | P75080 | SWISSPROT | DNA POLYMERASE III, ALPHA CHAIN POLC-TYPE (POLIII) |
| 11805 | 23960 | 37485 | 2.98 | 5.6E+00 | Q55276 | SWISSPROT | LYCOPENE BETA CYCLASE |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 6380 | 19448 | 32689 | 0.78 | 5.5E+00 | P47447 | SWISSPROT | HEAT-INDUCIBLE TRANSCRIPTION REPRESSOR HRCA |
| 10138 | 23084 | | 0.47 | 5.9E+00 | P13983 | SWISSPROT | EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN) |
| 11803 | 23958 | 37482 | 2.35 | 5.3E+00 | P11990 | SWISSPROT | PNEUMOLYSIN (THIOL-ACTIVATED CYTOLYSIN) |
| 7115 | 20049 | 33351 | 1.1 | 5.4E+00 | X02212.1 | NT | Chicken alpha-cardiac actin gene |
| 7115 | 20049 | 33352 | 1.1 | 5.4E+00 | X02212.1 | NT | Chicken alpha-cardiac actin gene |
| 7562 | 20515 | | 0.84 | 5.4E+00 | Q89435 | SWISSPROT | NEL PROTEIN PRECURSOR (NEL-RELATED PROTEIN 2) |
| 8143 | 21080 | 34480 | 0.6 | 5.4E+00 | P50391 | SWISSPROT | NEUROPEPTIDE Y RECEPTOR TYPE 4 (NPY4-R) (PANCREATIC POLYPEPTIDE RECEPTOR 1) (PP1) |
| 8202 | 21172 | | 1.72 | 5.4E+00 | Q91062 | SWISSPROT | VITELLOGENIN PRECURSOR (VTG) [CONTAINS: LIPOVITELLIN LV-1N; LIPOVITELLIN LV-1C; LIPOVITELLIN LV-2] |
| 9151 | 22117 | 35543 | 0.73 | 5.4E+00 | P40379 | SWISSPROT | REP1 PROTEIN |
| 9151 | 22117 | 35544 | 0.73 | 5.4E+00 | P40379 | SWISSPROT | REP1 PROTEIN |
| 10396 | 23318 | 36789 | 1.41 | 5.4E+00 | Q17094 | SWISSPROT | RHODOPSIN |
| 10396 | 23318 | 36800 | 1.41 | 5.4E+00 | Q17094 | SWISSPROT | RHODOPSIN |
| 4824 | 17841 | 30739 | 1.22 | 5.3E+00 | L43126.1 | NT | Bovine immunodeficiency-like virus surface envelope gene, 5' end of cds |
| 6635 | 19693 | | 0.6 | 5.3E+00 | P41779 | SWISSPROT | HOMEOBOX PROTEIN CEH-20 |
| 8415 | 21384 | | 3.9 | 5.3E+00 | P54098 | SWISSPROT | DNA POLYMERASE GAMMA (MITOCHONDRIAL DNA POLYMERASE CATALYTIC SUBUNIT) |
| 9335 | 22300 | | 0.53 | 5.3E+00 | AB034990.1 | NT | Homo sapiens HERPUD1 gene for stress protein Herp, complete cds |
| 11950 | 24829 | 38425 | 1.84 | 5.3E+00 | Q27805 | SWISSPROT | PROBABLE ANTIBACTERIAL PEPTIDE POLYPEPTIDE PRECURSOR |
| 12093 | 24964 | 38559 | 2.34 | 5.3E+00 | Z72663.1 | NT | S.cerevisiae chromosome VII reading frame ORF YGL141w |
| 12093 | 24964 | 38560 | 2.34 | 5.3E+00 | Z72663.1 | NT | S.cerevisiae chromosome VII reading frame ORF YGL141w |
| 5539 | 18636 | | 1.22 | 5.2E+00 | BE184840.1 | EST_HUMAN | QV4-H10691-270400-186-09 H10691 Homo sapiens cDNA |
| 10738 | 23660 | | 0.78 | 5.2E+00 | AF248070.1 | NT | Drosophila orientacea R1B retrotransposable element reverse transcriptase gene, partial cds |
| 11527 | 24468 | | 1.46 | 5.2E+00 | Q10136 | SWISSPROT | HYPOTHETICAL 61.1 KD PROTEIN C23E2.03C IN CHROMOSOME I |
| 9313 | 22278 | 35709 | 0.85 | 5.1E+00 | Q16005 | SWISSPROT | RHODOPSIN |
| 10184 | 23109 | 36592 | 1.07 | 5.1E+00 | P09182 | SWISSPROT | COLICIN N IMMUNITY PROTEIN (MICROCIN N IMMUNITY PROTEIN) |
| 11617 | 24555 | 38117 | 3.01 | 5.1E+00 | P65200 | SWISSPROT | ZINC FINGER PROTEIN HRX (ALL-1) |
| 6418 | 19485 | 32734 | 0.65 | 5.0E+00 | BF310443.1 | EST_HUMAN | 601894910FT NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124114 5' |
| 10554 | 23476 | | 0.65 | 5.0E+00 | BF308561.1 | EST_HUMAN | 601890420FT NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131509 5' |
| 10706 | 23717 | 37219 | 3.79 | 5.0E+00 | AF182445.2 | NT | Canis familiaris skeletal muscle chloride channel CIC-1 (CLCN1) mRNA, complete cds |
| 11622 | 24560 | 38122 | 6.39 | 5.0E+00 | Z83960.1 | NT | Mycobacterium tuberculosis H37Rv complete genome; segment 103/162 |
| 10592 | 23514 | | 0.63 | 4.9E+00 | U91928.1 | NT | Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds |
| 4090 | 17124 | | 9.81 | 4.8E+00 | AF185255.1 | NT | Eunice australis histone H3 (H3) gene, partial cds |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 8494 | 21462 | 34878 | 0.53 | 4.8E+00 | BF367809.1 | EST_HUMAN | RC3-GN0042-100800-011-c10 GN0042 Homo sapiens cDNA |
| 8888 | 21862 | | 5.15 | 4.8E+00 | AW750067.1 | EST_HUMAN | PMO-BT0547-310100-002-b04 BT0547 Homo sapiens cDNA |
| 289 | 13384 | 26311 | 2.03 | 4.7E+00 | BF240552.1 | EST_HUMAN | 601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4089716 5' |
| 290 | 13384 | 26311 | 1.89 | 4.7E+00 | BF240552.1 | EST_HUMAN | 601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4089716 5' |
| 3287 | 16341 | 29260 | 1.66 | 4.7E+00 | AL163280.2 | NT | Homo sapiens chromosome 21 segment HS21C080 |
| 8064 | 21001 | 34397 | 0.55 | 4.6E+00 | U67569.1 | NT | Methanococcus jannaschii section 111 of 150 of the complete genome |
| 9551 | 22513 | 35963 | 1.12 | 4.6E+00 | BE646437.1 | EST_HUMAN | 7e88g10.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3282088 3' similar to TR:O75140 O75140 |
| 9551 | 22513 | 35964 | 1.12 | 4.6E+00 | BE646437.1 | EST_HUMAN | KIAA0945 PROTEIN; contains element PTR5 repetitive element; |
| 10755 | 23677 | | 0.6 | 4.6E+00 | AF240786.1 | NT | 7e88g10.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3282088 3' similar to TR:O75140 O75140 |
| 8047 | 20984 | | 0.61 | 4.5E+00 | AF126177.1 | NT | KIAA0645 PROTEIN; contains element PTR5 repetitive element; |
| 11930 | 24811 | 38408 | 2.19 | 4.5E+00 | AE001044.1 | NT | Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds |
| 12055 | 24928 | 36526 | 1.87 | 4.5E+00 | BF66841.1 | EST_HUMAN | Issatchenkia orientalis inositolphosphorylceramide synthase (IPC1) gene, complete cds |
| 3053 | 16110 | 29024 | 0.76 | 4.4E+00 | BF530893.1 | EST_HUMAN | Archaeoglobus fulgidus section 63 of 172 of the complete genome |
| 3053 | 16110 | 29025 | 0.78 | 4.4E+00 | BF530893.1 | EST_HUMAN | 602123238F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4280216 5' |
| 6326 | 19396 | | 1.69 | 4.4E+00 | X13414.1 | NT | 602072585F1 NCL_CGAP_Brm67 Homo sapiens cDNA clone IMAGE:4216284 5' |
| 6394 | 19462 | 32709 | 0.59 | 4.4E+00 | AF156896.1 | NT | 602072585F1 NCL_CGAP_Brm67 Homo sapiens cDNA clone IMAGE:4216284 5' |
| 6240 | 19313 | | 0.71 | 4.3E+00 | AF059879.1 | NT | Murine I gene for MHC class II(a) associated invariant chain |
| 7672 | 20630 | 33994 | 3.53 | 4.3E+00 | Y13402.1 | NT | Nicotiana tabacum inorganic phosphate transporter (PT1) mRNA, complete cds |
| 7874 | 20818 | 34198 | 0.81 | 4.3E+00 | AE001222.1 | NT | Homo sapiens neutrophil collagenase (CLGNA) gene, promoter region and 5'UTR |
| 11210 | 24164 | 37694 | 7.01 | 4.3E+00 | AF240786.1 | NT | Plasmodium falciparum R28R+var1 gene, exon 1 |
| 11279 | 24230 | | 1.93 | 4.3E+00 | 11526311 | NT | Treponema pallidum section 38 of 87 of the complete genome |
| 5595 | 18691 | | 3.57 | 4.2E+00 | P18444 | SWISSPROT | Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds |
| 5675 | 18770 | 31942 | 1.35 | 4.2E+00 | P51826 | SWISSPROT | Homo sapiens DiGeorge syndrome critical region gene 2 (DGCR2), mRNA |
| 5854 | 18845 | | 0.56 | 4.2E+00 | O27830 | SWISSPROT | MICROSOMAL DIPEPTIDASE PRECURSOR (MDP) (DEHYDROPEPTIDASE-I) (RENAL DIPEPTIDASE) (RDP) |
| 6938 | 20162 | 33483 | 1.69 | 4.2E+00 | P13983 | SWISSPROT | LAF-4 PROTEIN (LYMPHOID NUCLEAR PROTEIN) |
| 6938 | 20162 | 33484 | 1.69 | 4.2E+00 | P13983 | SWISSPROT | PUTATIVE ATP-DEPENDENT HELICASE MTH1802 |
| 9311 | 22278 | 35708 | 5.1 | 4.2E+00 | AI809013.1 | EST_HUMAN | EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN) |
| 10278 | 23203 | 36988 | 1.1 | 4.2E+00 | P31368 | SWISSPROT | EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN) |
| 10508 | 23430 | | 0.53 | 4.2E+00 | P40898 | SWISSPROT | wf67g03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360692 3' |
| | | | | | | | NUBBIN PROTEIN (TWIN PROTEIN) (POU DOMAIN PROTEIN 1) (PDM-1) (DPOU-19) (DOCT1) |
| | | | | | | | HEXOSE TRANSPORTER HXT8 |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 6046 | 25652 | 32334 | 0.84 | 4.1E+00 | O09185 | SWISSPROT | CELLULAR TUMOR ANTIGEN P53 |
| 6046 | 25652 | 32335 | 0.64 | 4.1E+00 | O09185 | SWISSPROT | CELLULAR TUMOR ANTIGEN P53 |
| 7319 | 20290 | 33633 | 0.76 | 4.1E+00 | BE25368.1 | EST_HUMAN | 801110727F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351534 5' |
| 7420 | 20387 | 33738 | 0.55 | 4.1E+00 | BF247939.1 | EST_HUMAN | 801859030F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4069758 5' |
| 7923 | 20866 | 34254 | 7.87 | 4.1E+00 | O23810 | SWISSPROT | YY1 PROTEIN PRECURSOR |
| 8051 | 20998 | | 0.64 | 4.1E+00 | AB041523.1 | NT | Patapacten yessoensis mRNA for calcineurin A, complete cds |
| 8055 | 21002 | 34398 | 3.95 | 4.1E+00 | P28984 | SWISSPROT | GENE 68 PROTEIN |
| 8065 | 21002 | 34399 | 3.95 | 4.1E+00 | P28984 | SWISSPROT | GENE 68 PROTEIN |
| 8249 | 21218 | 34628 | 2.5 | 4.1E+00 | U57503.1 | NT | Pan troglodytes novel repetitive solo LTR element in the RNU2 locus |
| 8898 | 22951 | 36310 | 0.52 | 4.1E+00 | P11253 | SWISSPROT | 50S RIBOSOMAL PROTEIN L4 |
| 10031 | 22958 | 36426 | 2.43 | 4.1E+00 | BF692425.1 | EST_HUMAN | 802247938F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333209 5' |
| 10669 | 23591 | | 0.45 | 4.1E+00 | P46414 | SWISSPROT | CYCLIN-DEPENDENT KINASE INHIBITOR 1B (CYCLIN-DEPENDENT KINASE INHIBITOR P27) (P27KIP1) |
| 10981 | 23901 | 37414 | 0.47 | 4.1E+00 | O84242 | SWISSPROT | 3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE III (BETA-KETOACYL-ACP SYNTHASE III) (KAS III) |
| 11231 | 24184 | | 2.3 | 4.1E+00 | P09716 | SWISSPROT | HYPOTHETICAL PROTEIN HVL1 |
| 11317 | 24267 | | 13.22 | 4.1E+00 | BE85880.1 | EST_HUMAN | 601507510F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909051 5' |
| 3556 | 16602 | | 0.7 | 4.0E+00 | P38229 | SWISSPROT | GLC7-INTERACTING PROTEIN 1 |
| 5534 | 20057 | 33361 | 0.94 | 4.0E+00 | O62653 | SWISSPROT | SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE ; ISOMALTASE] |
| 5534 | 20057 | 33362 | 0.94 | 4.0E+00 | O62653 | SWISSPROT | SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE ; ISOMALTASE] |
| 7123 | 20057 | 33361 | 1.01 | 4.0E+00 | O62653 | SWISSPROT | SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE ; ISOMALTASE] |
| 7123 | 20057 | 33362 | 1.01 | 4.0E+00 | O62653 | SWISSPROT | SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE ; ISOMALTASE] |
| 7395 | 20363 | 33715 | 1.47 | 4.0E+00 | O33010 | SWISSPROT | CELL DIVISION PROTEIN FT5V HOMOLOG |
| 9225 | 22191 | 35621 | 0.44 | 4.0E+00 | Q14157 | SWISSPROT | HYPOTHETICAL PROTEIN KIAA0144 |
| 10303 | 23228 | 36711 | 0.43 | 4.0E+00 | O61309 | SWISSPROT | NITRIC-OXIDE SYNTHASE (NOS, TYPE I) (NEURONAL NOS) (NNOS) |
| 10526 | 23448 | 36946 | 0.6 | 4.0E+00 | AE002132.1 | NT | Ureaplasma urealyticum section 33 of 59 of the complete genome |
| 10620 | 23542 | 37041 | 0.49 | 4.0E+00 | Q00511 | SWISSPROT | URICASE (URATE OXIDASE) |
| 10620 | 23542 | 37042 | 0.49 | 4.0E+00 | Q00511 | SWISSPROT | URICASE (URATE OXIDASE) |
| 11802 | 23957 | 37481 | 1.67 | 4.0E+00 | P14546 | SWISSPROT | CYTOCHROME C OXIDASE POLYPEPTIDE III |
| 11875 | 24757 | 38340 | 2.68 | 4.0E+00 | P07564 | SWISSPROT | GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)] |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 11875 | 24757 | 38341 | 2.68 | 4.0E+00 | P07564 | SWISSPROT | GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS (NS1, NS2A, NS2B, NS4A AND NS4B); HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)] |
| 3513 | 16559 | 29483 | 4.65 | 3.9E+00 | X64518.1 | NT | N. tabacum chitinase gene 50 for class I chitinase C |
| 4349 | 17376 | | 0.96 | 3.9E+00 | AF055466.1 | NT | Mus musculus seminal vesicle secretory protein 98 (MSVSP98) gene, promoter region |
| 5741 | 18835 | 32015 | 2.98 | 3.9E+00 | BE814357.1 | EST_HUMAN | MRO-BN0070-300500-028-h05 BN0070 Homo sapiens cDNA |
| 5741 | 18835 | 32016 | 2.98 | 3.9E+00 | BE814357.1 | EST_HUMAN | MRO-BN0070-300500-028-h05 BN0070 Homo sapiens cDNA |
| 6791 | 19845 | 33129 | 0.95 | 3.9E+00 | AF298209.1 | NT | Dicotyledonous discoidium non-LTR retrotransposon TRE5-B, polyprotein (gag) and group-specific antigen (pol) genes, complete cds |
| 6848 | 19901 | 33195 | 0.67 | 3.9E+00 | U91328.1 | NT | Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds |
| 7057 | 20079 | 33388 | 4.24 | 3.9E+00 | P39299 | SWISSPROT | HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN AIDB-RPSF INTERGENIC REGION |
| 7587 | 20548 | 33908 | 4.15 | 3.9E+00 | M23907.1 | NT | Human MHC class II lymphocyte antigen (DPw4-beta-1) gene, exon 2 |
| 8660 | 21628 | 35049 | 2.34 | 3.9E+00 | X65865.1 | NT | X.laevis mRNA for M4 muscarinic receptor |
| 11720 | 23917 | 37434 | 2.93 | 3.9E+00 | Y18000.1 | NT | Homo sapiens NF2 gene |
| 11742 | 24627 | 38206 | 1.89 | 3.9E+00 | AA661489.1 | EST_HUMAN | nr18a12.st NCI CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1168318 similar to gb:A10416 |
| 2637 | 18638 | | 1.27 | 3.8E+00 | AE001562.1 | NT | METALLOPROTEINASE INHIBITOR 1 PRECURSOR (HUMAN); Helicobacter pylori, strain J99 section 123 of 132 of the complete genome |
| 5530 | 18593 | 32654 | 0.93 | 3.8E+00 | Q57830 | SWISSPROT | HYPOTHETICAL PROTEIN MJ0385 |
| 6937 | 20161 | 33482 | 0.59 | 3.8E+00 | AI493849.1 | EST_HUMAN | q25107.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2030437 3' |
| 8775 | 21742 | 35164 | 1.03 | 3.8E+00 | D44725.1 | EST_HUMAN | HUMSUPY135 Human brain cDNA Homo sapiens cDNA clone 148 |
| 10154 | 23079 | | 0.59 | 3.8E+00 | AJ390981.1 | NT | Streptococcus oralis partial xpt gene for xanthine phosphoribosyltransferase, strain NCTC7864 |
| 12119 | 24989 | | 15.21 | 3.8E+00 | 9631294 | NT | Melanoplus sanguinipes entomopoxvirus, complete genome |
| 4049 | 17088 | 29882 | 9.75 | 3.7E+00 | AL161539.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39 |
| 7372 | 20342 | | 0.9 | 3.7E+00 | AL445066.1 | NT | Thermoplasma acidophilum complete genome; segment 3/5 |
| 9056 | 22022 | | 0.49 | 3.7E+00 | 4503950 | NT | Homo sapiens glucokinase (hexokinase 4, maturity onset diabetes of the young 2) (GCK), nuclear gene encoding mitochondrial protein, mRNA |
| 9532 | 22495 | 35943 | 0.92 | 3.7E+00 | U43541.1 | NT | Mus musculus laminin beta 2 gene, exons 17-33, and complete cds |
| 11760 | 24688 | 38269 | 1.73 | 3.7E+00 | BF669279.1 | EST_HUMAN | 602120551F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277748 5' |
| 11760 | 24688 | 38270 | 1.73 | 3.7E+00 | BF669279.1 | EST_HUMAN | 602120551F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277748 5' |
| 12256 | 25082 | | 2.5 | 3.7E+00 | AB013748.3 | NT | Gallus gallus mRNA for hypoxia-inducible factor-1 alpha, complete cds |
| 595 | 13662 | 26575 | 4.04 | 3.6E+00 | AV761055.1 | EST_HUMAN | AV761055 MDS Homo sapiens cDNA clone MDSBUE10 5' |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 5286 | 18292 | 31153 | 0.63 | 3.6E+00 | Z89109.1 | NT | Bacillus subtilis complete genome (section 6 of 21): from 999501 to 1209040 |
| 5327 | 18433 | 31185 | 0.73 | 3.6E+00 | BF316316.1 | EST_HUMAN | 601901866F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4131016 5' |
| 8897 | 21863 | 35285 | 0.93 | 3.6E+00 | D12367.1 | EST_HUMAN | HUM000TB08 Liver HepG2 cell line. Homo sapiens cDNA clone hb08 |
| 8897 | 21863 | 35286 | 0.93 | 3.6E+00 | D12367.1 | EST_HUMAN | HUM000TB08 Liver HepG2 cell line. Homo sapiens cDNA clone hb08 |
| 8992 | 21958 | 35383 | 4.21 | 3.6E+00 | AE004447.1 | NT | Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome |
| 8992 | 21958 | 35384 | 4.21 | 3.6E+00 | AE004447.1 | NT | Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome |
| 10022 | 22949 | 36416 | 0.44 | 3.6E+00 | U72775.1 | NT | Ciconia episcopus cytochrome b gene, mitochondrial gene encoding mitochondrial protein, partial cds |
| 10022 | 22949 | 36417 | 0.44 | 3.6E+00 | U72775.1 | NT | Ciconia episcopus cytochrome b gene, mitochondrial gene encoding mitochondrial protein, partial cds |
| 11200 | 24155 | | 3.18 | 3.6E+00 | M96795.1 | NT | Escherichia coli glycerophosphate dehydrogenase (gldD) gene, partial cds; and the translation start site has been verified (gldE), the translation start site has been verified (gldG), and repressor protein (gldR) genes, complete cds |
| 6115 | 19193 | | 1.1 | 3.5E+00 | L42898.1 | NT | Borrelia burgdorferi (strain 25015) outer surface protein (ospC) gene, partial cds |
| 6337 | 19406 | 32647 | 0.96 | 3.5E+00 | R19745.1 | EST_HUMAN | Y440C08.r1 Soares Infant brain IN1B Homo sapiens cDNA clone IMAGE:34940 5' |
| 8087 | 21023 | 34422 | 0.5 | 3.5E+00 | P97608 | SWISSPROT | 5-OXOPROLINASE (5-OXO-L-PROLINASE) (PYROGLUTAMASE) (5-OPASE) |
| 8094 | 21030 | 34428 | 0.54 | 3.5E+00 | AA992102.1 | EST_HUMAN | o37f10.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1618987 3' similar to gb:J04213 |
| 8124 | 21081 | 34459 | 0.56 | 3.5E+00 | 4505264 | NT | CELLULAR RETINALDEHYDE-BINDING PROTEIN (HUMAN); |
| 8829 | 21796 | | 0.6 | 3.5E+00 | P24557 | SWISSPROT | Homo sapiens macrophage stimulating 1 receptor (c-met-related tyrosine kinase) (MST1R) mRNA |
| 9387 | 22352 | 35782 | 0.91 | 3.5E+00 | AA190998.1 | EST_HUMAN | THROMBOXANE-A SYNTHASE (TXA SYNTHASE) (TXS) |
| 9387 | 22352 | 35783 | 0.91 | 3.5E+00 | AA190998.1 | EST_HUMAN | zp86b04.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627055 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element; |
| 9850 | 22786 | 36240 | 0.96 | 3.5E+00 | AL161553.2 | NT | zp86b04.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627055 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element; |
| 1514 | 14546 | 27517 | 5.3 | 3.4E+00 | AF254577.1 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 53 |
| 6893 | 19945 | 33241 | 0.49 | 3.4E+00 | U77617.1 | NT | Brassic napus RPB5d mRNA, complete cds |
| 7586 | 20547 | 33907 | 2.99 | 3.4E+00 | P04052 | SWISSPROT | Chloramphenicol transferase (ChlA) gene, complete cds |
| 7668 | 20907 | 34298 | 0.9 | 3.4E+00 | P04052 | SWISSPROT | DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT |
| 9025 | 21991 | | 0.68 | 3.4E+00 | U65406.1 | NT | Human alternatively spliced potassium channels ROM-K1, ROM-K2, ROM-K3, ROM-K4, ROM-K5, and ROM-K6 (KCNJ1) gene, complete cds |
| 9428 | 22392 | 35831 | 0.73 | 3.4E+00 | AJ220042.1 | NT | ROM-K6 (KCNJ1) gene, complete cds |
| 9487 | 22431 | 35889 | 0.55 | 3.4E+00 | AJ250567.1 | NT | Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3 |
| 10627 | 23549 | 37049 | 2.59 | 3.4E+00 | AF013167.1 | NT | Homo sapiens partial TM4SF2 gene for tetraspanin protein, exon 6 |
| | | | | | | | Saccharomyces cerevisiae MSS1 gene, complete cds |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 11881 | 24743 | 38327 | 2.86 | 3.4E+00 | L77570.1 | NT | Homo sapiens DiGeorge syndrome critical region, centromeric end |
| 6186 | 19261 | 32496 | 1.03 | 3.3E+00 | Q08669 | SWISSPROT | PUTATIVE IRON ALCOHOL DEHYDROGENASE |
| 6186 | 19261 | 32497 | 1.03 | 3.3E+00 | Q08669 | SWISSPROT | PUTATIVE IRON ALCOHOL DEHYDROGENASE |
| 8225 | 21194 | 34601 | 0.9 | 3.3E+00 | AF111168.2 | NT | Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds, and unknown genes |
| 10830 | 23761 | 37250 | 0.9 | 3.3E+00 | AP001511.1 | NT | Bacillus halodurans genomic DNA, section 5/14 |
| 10830 | 23761 | 37251 | 0.9 | 3.3E+00 | AP001511.1 | NT | Bacillus halodurans genomic DNA, section 5/14 |
| 501 | 13573 | 26495 | 1.85 | 3.2E+00 | X98422.1 | NT | D. rerio zp-50 POU gene |
| 4066 | 13573 | 26495 | 0.89 | 3.2E+00 | X98422.1 | NT | D. rerio zp-50 POU gene |
| 4769 | 17779 | 30674 | 1.35 | 3.2E+00 | 450240.4 | NT | Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) (CEACAM1), mRNA |
| 5648 | 18744 | 31910 | 1.2 | 3.2E+00 | P54924 | SWISSPROT | SQUALENE-HOPENE CYCLASE |
| 5648 | 18744 | 31911 | 1.2 | 3.2E+00 | P54924 | SWISSPROT | SQUALENE-HOPENE CYCLASE |
| 5683 | 18778 | 31950 | 2.79 | 3.2E+00 | P12783 | SWISSPROT | PHOSPHOGLYCERATE KINASE, CYTOSOLIC |
| 5683 | 18778 | 31951 | 2.79 | 3.2E+00 | P12783 | SWISSPROT | PHOSPHOGLYCERATE KINASE, CYTOSOLIC |
| 6439 | 19504 | 32754 | 1.66 | 3.2E+00 | P18931 | SWISSPROT | NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 |
| 6439 | 19504 | 32755 | 1.66 | 3.2E+00 | P18931 | SWISSPROT | NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 |
| 7863 | 20807 | 34185 | 0.71 | 3.2E+00 | P04275 | SWISSPROT | VON WILLEBRAND FACTOR PRECURSOR (VWF) |
| 8052 | 20989 | 34386 | 2.47 | 3.2E+00 | Y13655.1 | NT | Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 genes |
| 8052 | 20989 | 34387 | 2.47 | 3.2E+00 | Y13655.1 | NT | Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 genes |
| 9385 | 22350 | 36298 | 4.78 | 3.2E+00 | P13061 | SWISSPROT | PERIPLASMIC [NIFE] HYDROGENASE SMALL SUBUNIT (NIFE HYDROGENLYASE SMALL CHAIN) |
| 9888 | 22841 | 36298 | 1.87 | 3.2E+00 | M36383.1 | NT | S. cerevisiae threonine deaminase (ILD1) gene, complete cds |
| 10500 | 23422 | 36821 | 2 | 3.2E+00 | AB016081.2 | NT | Oryzias latipes OIGC6 gene for guanylyl cyclase C, complete cds |
| 12217 | 25055 | | 2.84 | 3.2E+00 | L33836.1 | NT | Sus scrofa choline acetyltransferase gene, promoter region |
| 5975 | 19080 | 32261 | 2.25 | 3.1E+00 | Q10135 | SWISSPROT | HYPOTHETICAL 142.5 KD PROTEIN C23E2.02 IN CHROMOSOME 1 |
| 7618 | 20578 | 33941 | 0.9 | 3.1E+00 | P52178 | SWISSPROT | TRIOSE PHOSPHATE PHOSPHATE TRANSLOCATOR, NON-GREEN PLASTID PRECURSOR (CTPT) |
| 7998 | 20938 | | 1 | 3.1E+00 | AF303225.1 | NT | Bacillus subtilis pectate lyase (pelE) gene, complete cds |
| 8424 | 21393 | 34804 | 0.43 | 3.1E+00 | P40985 | SWISSPROT | PROBABLE UBIQUITIN-PROTEIN LIGASE HUL4 |
| 8949 | 21915 | 35338 | 4.37 | 3.1E+00 | P49894 | SWISSPROT | TYPE I IODOHYDRONINE DEIODINASE (TYPE-I 5DEIODINASE) (DIOI) (TYPE 1 DIO) (5DI) |
| 8949 | 21915 | 35339 | 4.37 | 3.1E+00 | P49894 | SWISSPROT | TYPE I IODOHYDRONINE DEIODINASE (TYPE-I 5DEIODINASE) (DIOI) (TYPE 1 DIO) (5DI) |
| 9614 | 22618 | | 3.9 | 3.1E+00 | Q14957 | SWISSPROT | GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C) |
| 9880 | 22633 | 35089 | 0.48 | 3.1E+00 | Q01149 | SWISSPROT | COLLAGEN ALPHA 2(I) CHAIN PRECURSOR |
| 10256 | 23181 | 36668 | 0.86 | 3.1E+00 | 7624759 | NT | Chlorella vulgaris chloroplast, complete genome |
| 10347 | 23271 | | 0.61 | 3.1E+00 | Q10125 | SWISSPROT | HYPOTHETICAL 56.3 KD PROTEIN F52C9.5 IN CHROMOSOME III |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 10700 | 23622 | 37118 | 5.2 | 3.1E+00 | P49365 | SWISSPROT | DEOXYHYDROLYSINE SYNTHASE (DHS) |
| 11781 | 23946 | | 1.96 | 3.1E+00 | P33515 | SWISSPROT | GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS6)] |
| 11811 | 24696 | | 2.76 | 3.1E+00 | S56980.1 | NT | retinoid acid nuclear receptor isoform beta 2 [mice, embryonal carcinoma cell line, PCC7-MZ1, mRNA, 2871 nt] |
| 2849 | 15909 | 28833 | 1.5 | 3.0E+00 | 8923984 | NT | Homo sapiens hypothetical protein PRO0889 (PRO0889), mRNA |
| 5411 | 18514 | 31392 | 1.33 | 3.0E+00 | X53096.1 | NT | S. aureus genes encoding Sau961 DNA methyltransferase and Sau961 restriction endonuclease |
| 6708 | 19784 | 33043 | 0.79 | 3.0E+00 | X56037.1 | NT | Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2) |
| 6708 | 19784 | 33044 | 0.79 | 3.0E+00 | X56037.1 | NT | Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2) |
| 7363 | 20333 | | 9.68 | 3.0E+00 | P18406 | SWISSPROT | CYR61 PROTEIN PRECURSOR (3CH61) |
| 7402 | 20370 | | 0.59 | 3.0E+00 | Q13201 | SWISSPROT | ENDOTHELIAL CELL MULTIMERIN PRECURSOR |
| 9268 | 22224 | | 1.21 | 3.0E+00 | X67838.1 | NT | B. napus DNA for myosinase |
| 10657 | 23579 | 37076 | 0.54 | 3.0E+00 | Q58605 | SWISSPROT | S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE) |
| 11008 | 23973 | 37497 | 1.65 | 3.0E+00 | Q16181 | SWISSPROT | CDC10 PROTEIN HOMOLOG |
| 11351 | 24301 | 37827 | 4.84 | 3.0E+00 | P51842 | SWISSPROT | RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GC-F) |
| 11351 | | | | | | | RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GC-F) |
| 11351 | 24301 | 37828 | 4.84 | 3.0E+00 | P51842 | SWISSPROT | RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GC-F) |
| 2026 | 15046 | 28059 | 2.33 | 2.9E+00 | AE002225.2 | NT | Chlamydomonas reinhardtii mitochondrial DNA for 16S ribosomal RNA |
| 6192 | 19266 | | 0.6 | 2.9E+00 | A8026033.1 | NT | Bonapartia pedaliata mitochondrial DNA for 16S ribosomal RNA |
| 7094 | 20028 | 33332 | 1.97 | 2.9E+00 | Z36879.1 | NT | F. pinguei gdcA gene for P-protein of the glycine cleavage system |
| 7418 | 20385 | 33734 | 6.15 | 2.9E+00 | O14514 | SWISSPROT | BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR |
| 7418 | 20385 | 33735 | 5.15 | 2.9E+00 | O14514 | SWISSPROT | BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR |
| 7689 | 20547 | 34011 | 5.32 | 2.9E+00 | P46589 | SWISSPROT | ADHERENCE FACTOR (ADHESION AND AGGREGATION MEDIATING SURFACE ANTIGEN) |
| 8200 | 21170 | 34580 | 0.61 | 2.9E+00 | P05844 | SWISSPROT | STRUCTURAL POLYPROTEIN [CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; MINOR STRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3] |
| 8200 | 21170 | 34581 | 0.61 | 2.9E+00 | P05844 | SWISSPROT | STRUCTURAL POLYPROTEIN [CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; MINOR STRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3] |
| 8434 | 21403 | 34816 | 0.82 | 2.9E+00 | BF344171.1 | EST_HUMAN | NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3 |
| 1451 | 14484 | 27460 | 4.16 | 2.8E+00 | AF186398.1 | NT | 602017413F1 NC1 CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4153059 5' |
| | | | | | | | Buxus harlandii maturase K (matK) gene, partial cds, chloroplast gene for chloroplast product |

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Table 4
Single Exon Probes Expressed In Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 1637 | 14669 | | 2.57 | 2.8E+00 | AL161552.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52 |
| 7529 | 20492 | 33854 | 4.93 | 2.8E+00 | 8393724 | NT | Mus musculus endonuclease (LOC53423), mRNA |
| 8972 | 22898 | | 0.56 | 2.8E+00 | BE565182.1 | EST_HUMAN | 601342758F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3684807 5' |
| 11048 | 20492 | 33854 | 1.73 | 2.8E+00 | 8393724 | NT | Mus musculus endonuclease (LOC53423), mRNA |
| 233 | 13333 | 26256 | 13.36 | 2.7E+00 | 6878306 | NT | Mus musculus per-hexamer repeat gene 3 (Phx3), mRNA |
| 233 | 13333 | 26257 | 13.36 | 2.7E+00 | 6878306 | NT | Mus musculus per-hexamer repeat gene 3 (Phx3), mRNA |
| 5631 | 18727 | 31888 | 1.11 | 2.7E+00 | L14005.1 | NT | Homo sapiens apolipoprotein A polymorphism Kringle IV gene, exons 1 and 2 |
| 8485 | 21453 | | 0.66 | 2.7E+00 | U15947.1 | NT | Ipomoea purpurea chalcone synthase (CHS) gene including complete 5'UTR and complete cds |
| 8319 | 22284 | | 1.69 | 2.7E+00 | AL116459.1 | NT | Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation |
| 9787 | 21110 | 34510 | 0.64 | 2.7E+00 | AW088191.1 | EST_HUMAN | xc88612x1 NCI_CGAP_Brn35 Homo sapiens cDNA clone IMAGE:2691374 3' similar to gb:M17793 |
| 10866 | 23786 | | 1.69 | 2.7E+00 | BE03527.1 | EST_HUMAN | THYMOSIN BETA-4 (HUMAN); |
| 4701 | 17722 | 30615 | 6.29 | 2.6E+00 | AF068749.1 | NT | CMO-BT0281-031198-087-H04 BT0281 Homo sapiens cDNA |
| 5627 | 18723 | 31883 | 2.06 | 2.6E+00 | 6755601 | NT | Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds |
| 5627 | 18723 | 31884 | 2.06 | 2.6E+00 | 6755601 | NT | Mus musculus SRY-box containing gene 13 (Sox13), mRNA |
| 5925 | 19011 | | 3.9 | 2.6E+00 | Y17052.1 | NT | Mus musculus SRY-box containing gene 13 (Sox13), mRNA |
| 7803 | 26002 | | 0.7 | 2.6E+00 | AJ224639.1 | NT | Mycobacterium fortuitum furA II gene |
| 7967 | 20906 | | 32.15 | 2.6E+00 | AF235502.1 | NT | Homo sapiens Surf-5 and Surf-6 genes |
| 8394 | 21363 | 34770 | 1.12 | 2.6E+00 | AJ132180.1 | NT | Mus musculus SH2-containing inositol 5-phosphatase (SHIP) gene, exons 16 through 27, and complete cds |
| 8394 | 21363 | 34771 | 1.12 | 2.6E+00 | AJ132180.1 | NT | faba bean necrotic yellows virus C2-Eg gene, isolate Egyptian EV1-93 |
| 10015 | 22942 | 36408 | 3.12 | 2.6E+00 | AL161540.2 | NT | faba bean necrotic yellows virus C2-Eg gene, isolate Egyptian EV1-93 |
| 10720 | 23842 | | 1.61 | 2.6E+00 | 9055193 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40 |
| 12841 | 25877 | | 2.58 | 2.6E+00 | 11419220 | NT | Mus musculus cleavage and polyadenylation specificity factor 3 (Cpsf3), mRNA |
| 1460 | 14493 | 27466 | 3.73 | 2.5E+00 | AJ271844.1 | NT | Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), mRNA |
| 1460 | 14493 | 27467 | 3.73 | 2.5E+00 | AJ271844.1 | NT | Aspergillus nidulans recQ gene for DNA helicase, exons 1-4 |
| 5911 | 18997 | 32186 | 2.32 | 2.5E+00 | P13485 | SWISSPROT | TEICHOIC ACID BIOSYNTHESIS PROTEIN F |
| 5911 | 18997 | 32187 | 2.32 | 2.5E+00 | P13485 | SWISSPROT | TEICHOIC ACID BIOSYNTHESIS PROTEIN F |
| 6601 | 18997 | 32186 | 1.49 | 2.5E+00 | P13485 | SWISSPROT | TEICHOIC ACID BIOSYNTHESIS PROTEIN F |
| 6601 | 18997 | 32187 | 1.49 | 2.5E+00 | P13485 | SWISSPROT | TEICHOIC ACID BIOSYNTHESIS PROTEIN F |
| 6892 | 19944 | 33240 | 0.66 | 2.5E+00 | D30052.1 | NT | Vibrio cholerae ctaA gene and ctaB gene for cholera toxins, complete cds |
| 7960 | 20901 | 34293 | 0.55 | 2.5E+00 | P17598 | SWISSPROT | LATENCY-RELATED PROTEIN 1 |
| 8035 | 20972 | 34366 | 0.97 | 2.5E+00 | AW949158.1 | EST_HUMAN | QV4-F10005-110500-205-q07 F10005 Homo sapiens cDNA |
| 8095 | 21031 | 34429 | 0.51 | 2.5E+00 | 4502902 | NT | Homo sapiens clathrin, heavy polypeptide-like 1 (CLTCL1) mRNA |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 9459 | 22423 | 35861 | 1.49 | 2.5E+00 | D50307.1 | NT | Rice DNA for aldolase C-1, complete cds |
| 10211 | 23136 | 36623 | 0.73 | 2.5E+00 | BE287758.1 | EST_HUMAN | 601175779F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531090 5' |
| 12214 | 25053 | | 2.5 | 2.5E+00 | AF289665.1 | NT | Mus musculus EIF4H gene, partial cds; LIMK1 gene, complete cds; and ELN gene, partial cds |
| 3026 | 16083 | 29006 | 1.1 | 2.4E+00 | M24282.1 | NT | Chicken alpha-3 collagen type VI mRNA, 3' end |
| 4944 | 17960 | 30851 | 5.31 | 2.4E+00 | 4503352 | NT | Homo sapiens double C2-like domains, alpha (DOC2A) mRNA |
| 6126 | 19204 | 32427 | 3.62 | 2.4E+00 | P02843 | SWISSPROT | VITELLOGENIN I PRECURSOR (YOLK PROTEIN 1) |
| 7606 | 20567 | 33927 | 0.71 | 2.4E+00 | BF667502.1 | EST_HUMAN | 602120856F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278012 5' |
| 7608 | 20567 | 33928 | 0.71 | 2.4E+00 | BF667502.1 | EST_HUMAN | 602120856F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278012 5' |
| 8479 | 21448 | 34984 | 2.08 | 2.4E+00 | P26842 | SWISSPROT | CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14) |
| 8479 | 21448 | 34985 | 2.08 | 2.4E+00 | P26842 | SWISSPROT | CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14) |
| 8554 | 21522 | | 2.92 | 2.4E+00 | AE001496.1 | NT | Helicobacter pylori, strain J99 section 47 of 132 of the complete genome |
| 8998 | 21984 | | 1.46 | 2.4E+00 | AW875126.1 | EST_HUMAN | RC2.PT0004-031289.011-405 PT0004 Homo sapiens cDNA |
| 9180 | 22146 | 35573 | 9.52 | 2.4E+00 | P24091 | SWISSPROT | ENDOCHITINASE B PRECURSOR (CHN-B) |
| 10398 | 23320 | 36803 | 2.34 | 2.4E+00 | P13673 | SWISSPROT | SKIN GRANULE PROTEIN PRECURSOR |
| 10398 | 23320 | 36804 | 2.34 | 2.4E+00 | P13673 | SWISSPROT | SKIN GRANULE PROTEIN PRECURSOR |
| 10466 | 23388 | 36882 | 2.1 | 2.4E+00 | X92511.1 | NT | H. sapiens CTGF gene and promoter region |
| 10604 | 23526 | | 6.1 | 2.4E+00 | P09099 | SWISSPROT | XYLULOSE KINASE (XYLULOKINASE) |
| 10685 | 23607 | 37100 | 1.67 | 2.4E+00 | BE326702.1 | EST_HUMAN | hr63f06.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133187 3' |
| 10685 | 23607 | 37101 | 1.67 | 2.4E+00 | BE326702.1 | EST_HUMAN | hr63f06.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133187 3' |
| 10955 | 23875 | 37389 | 1.14 | 2.4E+00 | Q31481 | SWISSPROT | DENITRIFICATION REGULATORY PROTEIN NIRQ |
| 11415 | 24359 | 37894 | 2.2 | 2.4E+00 | Y14079.1 | NT | Bacillus subtilis chromosomal DNA, region 75 degrees: glpPKD operon and downstream |
| 11517 | 24458 | | 1.66 | 2.4E+00 | AF096872.1 | NT | Capra hircus alphaS2-casein type C gene, intron 15 |
| 11686 | 24652 | 38231 | 2.14 | 2.4E+00 | AF159652.2 | NT | Fragaria x ananassa cytosolic ascorbate peroxidase (ApxSC) gene, ApxSC-c allele, complete cds |
| 1258 | 14293 | 27257 | 11.33 | 2.3E+00 | Z46724.1 | NT | G domesticus artificial single chain antibody gene (L3) |
| 4147 | 17178 | | 1.45 | 2.3E+00 | A1401081.1 | NT | Bos taurus partial cysb gene for cytochrome b |
| 5934 | 19020 | | 0.99 | 2.3E+00 | N86245.1 | EST_HUMAN | J7340F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J7340 5' similar to PROLYCABOXYPEPTIDASE |
| 7687 | 20845 | 34009 | 2.42 | 2.3E+00 | 6978554 | NT | Rattus norvegicus ATPase, Car++ transporting, ubiquitous (Atp2a3), mRNA |
| 7653 | 26003 | | 2.79 | 2.3E+00 | P07199 | SWISSPROT | MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B) |
| 8059 | 20996 | 34392 | 1.12 | 2.3E+00 | X60265.1 | NT | M. maezi dnaK and dnaJ genes homologues coding for DnaK and DnaJ |
| 9465 | 22429 | 35868 | 0.54 | 2.3E+00 | 5835317 | NT | Polyporus ornaiipinnis mitochondrion, complete genome |
| 9525 | 22488 | 35936 | 2.03 | 2.3E+00 | Q11127 | SWISSPROT | ALPHA-(1,3)-FUCOSYLTRANSFERASE (GALACTOSIDE 3-L-FUCOSYLTRANSFERASE) (FUCOSYLTRANSFERASE 4) (FUCT-IV) |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 10958 | 23878 | 37390 | 0.45 | 2.3E+00 | P02461 | SWISSPROT | COLLAGEN ALPHA 1(III) CHAIN PRECURSOR |
| 11153 | 24113 | 37838 | 7.84 | 2.3E+00 | Q07076 | SWISSPROT | ANNEXIN VII (SYNEXIN) |
| 11897 | 24778 | 38364 | 1.59 | 2.3E+00 | P45931 | SWISSPROT | HYPOPHOSPHATASE 1 171.0 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION |
| 12072 | 24945 | 38539 | 2.34 | 2.3E+00 | BF541987.1 | EST_HUMAN | 602069121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5' |
| 12072 | 24945 | 38540 | 2.34 | 2.3E+00 | BF541987.1 | EST_HUMAN | 602069121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5' |
| 12443 | 25205 | 31828 | 6.31 | 2.3E+00 | BE895237.1 | EST_HUMAN | 601433673F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918843 5' |
| 13077 | 25609 | | 1.3 | 2.3E+00 | AF281862.1 | NT | Neurospora crassa G protein alpha subunit GNA-3 (gna-3) gene, complete cds |
| 4046 | 17084 | 29981 | 1.42 | 2.2E+00 | AF020528.1 | NT | Magnaporthe grisea Class IV chitin synthase (chs4) gene, complete cds |
| 4342 | 17369 | 30251 | 3.8 | 2.2E+00 | D67071.1 | NT | Rat gene for regucalcin, exon1 (non-coding exon) |
| 4342 | 17369 | 30252 | 3.8 | 2.2E+00 | D67071.1 | NT | Rat gene for regucalcin, exon1 (non-coding exon) |
| 5415 | 18518 | 31395 | 11.02 | 2.2E+00 | O88307 | SWISSPROT | SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) (> |
| 5415 | 18518 | 31396 | 11.02 | 2.2E+00 | O88307 | SWISSPROT | SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) (> |
| 5953 | 19038 | 32234 | 1.83 | 2.2E+00 | BE927220.1 | EST_HUMAN | RC3-CT0254-300800-022-e06 CT0254 Homo sapiens cDNA |
| 5953 | 19038 | 32235 | 1.83 | 2.2E+00 | BE927220.1 | EST_HUMAN | RC3-CT0254-300800-022-e06 CT0254 Homo sapiens cDNA |
| 6180 | 19255 | 32488 | 8.78 | 2.2E+00 | BE260383.1 | EST_HUMAN | 600943401T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2959777 3' |
| 6489 | 19554 | 32804 | 3.91 | 2.2E+00 | Q00335 | SWISSPROT | MINOR VIRION STRUCTURAL PROTEIN MU-2 |
| 6750 | 19804 | 33085 | 3.14 | 2.2E+00 | P51459 | SWISSPROT | INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SOMATOMEDIN A) |
| 7149 | 18381 | | 3.5 | 2.2E+00 | AA594574.1 | EST_HUMAN | nt85b02.s1 NCL_CGAP_Cot0 Homo sapiens cDNA clone IMAGE:1058379 3' |
| 7539 | 20502 | 33861 | 0.95 | 2.2E+00 | AA137027.1 | EST_HUMAN | zn97f04.r1 Stragene fetal retina 837202 Homo sapiens cDNA clone IMAGE:566143 5' |
| 7865 | 20809 | 34187 | 18.24 | 2.2E+00 | AA449012.1 | EST_HUMAN | zn05g10.r1 Soares fetal testis Nb2HF8_gw Homo sapiens cDNA clone IMAGE:785634 5' |
| 7953 | 20894 | 34287 | 0.66 | 2.2E+00 | P54918 | SWISSPROT | ALANINE RACEMASE |
| 8439 | 21408 | 34820 | 0.69 | 2.2E+00 | BE301560.1 | EST_HUMAN | bb17h12.x1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2963207 3' similar to gb:D45838 Mouse mRNA for nuclear pore-targeting-complex component of (MOUSE); |
| 8439 | 21408 | 34821 | 0.69 | 2.2E+00 | BE301560.1 | EST_HUMAN | bb17h12.x1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2963207 3' similar to gb:D45838 Mouse mRNA for nuclear pore-targeting-complex component of (MOUSE); |
| 9697 | 22850 | | 11.22 | 2.2E+00 | BE741678.1 | EST_HUMAN | 601594733F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948561 5' |
| 9927 | 25698 | | 2.53 | 2.2E+00 | Q04706 | SWISSPROT | TRANSPONSON TY1 PROTEIN A |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 10413 | 23335 | 36819 | 1.57 | 2.2E+00 | AI290373.1 | EST_HUMAN | qm69b03.x1 Soares_placenta_8to9weeks_2NbHP8b0W Homo sapiens cDNA clone IMAGE:1893965 3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN); |
| 10413 | 23335 | 36820 | 1.57 | 2.2E+00 | AI290373.1 | EST_HUMAN | qm69b03.x1 Soares_placenta_8to9weeks_2NbHP8b0W Homo sapiens cDNA clone IMAGE:1893965 3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN); |
| 10456 | 23378 | 36871 | 2.22 | 2.2E+00 | BF246782.1 | EST_HUMAN | 901855591F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075391 5' |
| 10922 | 23743 | 37244 | 3.06 | 2.2E+00 | AF183416.1 | NT | Homo sapiens ovarian granulosa cell 13.0 kDa protein hGR74 homolog mRNA, complete cds |
| 11768 | 23923 | 37442 | 3.23 | 2.2E+00 | P07911 | SWISSPROT | UROMODULIN PRECURSOR (TAMM-HORSFALL URINARY GLYCOPROTEIN) (THP) |
| 11937 | 24818 | 38415 | 6.31 | 2.2E+00 | P10407 | SWISSPROT | EARLY E1A 28 KD PROTEIN |
| 571 | 15844 | 26555 | 12.39 | 2.1E+00 | AF132612.2 | NT | Mus musculus pre-T cell receptor alpha gene, enhancer region and upstream region |
| 3601 | 16646 | | 0.83 | 2.1E+00 | AW449366.1 | EST_HUMAN | U1-H-513-akt-e-08-0-U1.s1 NCI CGAP Sub5 Homo sapiens cDNA clone IMAGE:2734550 3' |
| 6255 | 19328 | | 0.86 | 2.1E+00 | P75357 | SWISSPROT | HYPOTHETICAL PROTEIN MG302 HOMOLOG |
| 6980 | 20203 | 33532 | 3.45 | 2.1E+00 | O70159 | SWISSPROT | ALPHA-2HS-GLYCOPROTEIN PRECURSOR (FETUIN-A) |
| 7225 | 20247 | 33581 | 0.61 | 2.1E+00 | 4503430 | NT | Homo sapiens dysferlin, limb girdle muscular dystrophy 2B (autosomal recessive) (DYSF) mRNA, and translated products |
| 7246 | 19981 | 33278 | 5.97 | 2.1E+00 | N29575.1 | EST_HUMAN | yy08a10.s1 Soares_melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270618 3' similar to gb:M55654 TRANSCRIPTION INITIATION FACTOR TFIIID (HUMAN); |
| 8842 | 21809 | | 1.82 | 2.1E+00 | AU123630.1 | EST_HUMAN | AU123630 NT2RM2 Homo sapiens cDNA clone NT2RM2000671 5' |
| 1201 | 14240 | 27197 | 1.39 | 2.0E+00 | AF180527.1 | NT | Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds |
| 1201 | 14240 | 27198 | 1.39 | 2.0E+00 | AF180527.1 | NT | Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds |
| 1338 | 14372 | 27342 | 1.19 | 2.0E+00 | AF204927.1 | NT | Oryctolagus cuniculus Ner.K*-ATPase beta 1 subunit mRNA, complete cds |
| 1578 | 14611 | | 3.42 | 2.0E+00 | P25582 | SWISSPROT | PUTATIVE RRNA METHYLTRANSFERASE SPB1 |
| 2159 | 15175 | 28195 | 4.98 | 2.0E+00 | Z78279.1 | NT | R.norvegicus mRNA for collagen alpha1 type I |
| 2159 | 15175 | 28196 | 4.98 | 2.0E+00 | Z78279.1 | NT | R.norvegicus mRNA for collagen alpha1 type I |
| 4127 | 17160 | 30048 | 2.24 | 2.0E+00 | AW664496.1 | EST_HUMAN | h13c05.x1 NCI CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972168 3' similar to gb:X01677 GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN); |
| 4127 | 17160 | 30049 | 2.24 | 2.0E+00 | AW664496.1 | EST_HUMAN | h13c05.x1 NCI CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972168 3' similar to gb:X01677 GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN); |
| 7798 | 20750 | | 0.85 | 2.0E+00 | P07566 | SWISSPROT | STRUCTURAL POLYPEPTIDE [CONTAINS: NUCLEOCAPSID PROTEIN C; MEMBRANE GLYCOPROTEINS E1 AND E2] |
| 8358 | 21327 | 34738 | 3.84 | 2.0E+00 | AB008676.1 | NT | Escherichia coli 0157 DNA, map position at 46 min., complete cds |
| 8358 | 21327 | 34739 | 3.84 | 2.0E+00 | AB008676.1 | NT | Escherichia coli 0157 DNA, map position at 46 min., complete cds |
| 8358 | 21327 | 34740 | 3.84 | 2.0E+00 | AB008676.1 | NT | Escherichia coli 0157 DNA, map position at 46 min., complete cds |
| 9274 | 22240 | 35668 | 3.22 | 2.0E+00 | F31500.1 | EST_HUMAN | HSPD22703 HM3 Homo sapiens cDNA clone s4000117808 |
| 12756 | 25898 | 31427 | 4.52 | 2.0E+00 | 5834943 | NT | Gallus gallus mitochondrion, complete genome |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 4829 | 17846 | 30748 | 0.98 | 1.9E+00 | AF209468.1 | NT | Danio rerio Rb50-like protein mRNA, complete cds |
| 5679 | 18774 | 31945 | 4.52 | 1.9E+00 | 6754389 | NT | Mus musculus inositol 1,4,5-triphosphate receptor 1 (Itp1), mRNA |
| 5679 | 18774 | 31946 | 4.52 | 1.9E+00 | 6754389 | NT | Mus musculus inositol 1,4,5-triphosphate receptor 1 (Itp1), mRNA |
| 6219 | 19293 | 32527 | 1.05 | 1.9E+00 | BE968695.1 | EST_HUMAN | 601679636F1 NIH_MGC_78 Homo sapiens cDNA clone IMAGE:3949881 5' |
| 6810 | 19864 | | 1.19 | 1.9E+00 | AW845889.1 | EST_HUMAN | MRO-CT0063-071099-002-g02 CT0063 Homo sapiens cDNA |
| 6912 | 19964 | | 2.37 | 1.9E+00 | Q63827 | SWISSPROT | CTD-BINDING SR-LIKE PROTEIN RA4 |
| 8802 | 21769 | 35193 | 1.72 | 1.9E+00 | P02467 | SWISSPROT | COLLAGEN ALPHA 2(I) CHAIN PRECURSOR |
| 8802 | 21769 | 35194 | 1.72 | 1.9E+00 | P02467 | SWISSPROT | COLLAGEN ALPHA 2(I) CHAIN PRECURSOR |
| 9008 | 21972 | | 3.6 | 1.9E+00 | BF380208.1 | EST_HUMAN | CM3-MT0114-010600-323-h12 MT0114 Homo sapiens cDNA |
| 9245 | 22211 | | 1.52 | 1.9E+00 | O51781 | SWISSPROT | ARGININE DEIMINASE (ADI) (ARGININE DIHYDROLASE) (AD) |
| 9988 | 22915 | 36380 | 0.53 | 1.9E+00 | AA669125.1 | EST_HUMAN | ab94a04 s1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:854574 3' similar to contains Alu repetitive element; contains element L1 L1 repetitive element; |
| 10929 | 23849 | 37364 | 0.63 | 1.9E+00 | AF248269.1 | NT | Homo sapiens gag-pro-pd precursor protein gene, partial cds |
| 3109 | 16166 | 29077 | 1.5 | 1.8E+00 | P21004 | SWISSPROT | PROTEIN B8 PRECURSOR |
| 3137 | 16194 | 29103 | 10.81 | 1.8E+00 | U04356.1 | NT | Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds |
| 3137 | 16194 | 29104 | 10.81 | 1.8E+00 | U04356.1 | NT | Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds |
| 5967 | 19052 | | 1.84 | 1.8E+00 | P18502 | SWISSPROT | HEDGEHOG RECEPTOR (PATCHED PROTEIN) |
| 6224 | 19288 | 32532 | 2.2 | 1.8E+00 | BF311999.1 | EST_HUMAN | 601897854F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127364 5' |
| 6638 | 19600 | | 1.19 | 1.8E+00 | BF683327.1 | EST_HUMAN | 602139470F1 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:4298272 5' |
| 6904 | 19956 | 33253 | 1.02 | 1.8E+00 | BF305652.1 | EST_HUMAN | 601893489F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4135038 5' |
| 7260 | 19995 | 33292 | 1.07 | 1.8E+00 | P21249 | SWISSPROT | MAJOR ANTIGEN |
| 7476 | 20442 | | 0.7 | 1.8E+00 | P27127 | SWISSPROT | LIPOPOLYSACCHARIDE 1,6-GALACTOSYLTRANSFERASE (UDP-D-GALACTOSE--(GLUCOSYL)-LIPOPOLYSACCHARIDE-ALPHA-1,3-D-GALACTOSYLTRANSFERASE) |
| 8454 | 21423 | 34838 | 0.9 | 1.8E+00 | P11369 | SWISSPROT | RETROVIRUS-RELATED POL POLYPYRIMIDIN [CONTAINS: REVERSE TRANSCRIPTASE ; |
| 8454 | 21423 | 34839 | 0.9 | 1.8E+00 | P11369 | SWISSPROT | RETROVIRUS-RELATED POL POLYPYRIMIDIN [CONTAINS: REVERSE TRANSCRIPTASE ; |
| 8812 | 21779 | 35204 | 0.46 | 1.8E+00 | P48634 | SWISSPROT | LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2) |
| 8812 | 21779 | 35205 | 0.46 | 1.8E+00 | P48634 | SWISSPROT | LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2) |
| 8812 | 21779 | 35206 | 0.46 | 1.8E+00 | P48634 | SWISSPROT | LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2) |
| 9206 | 21779 | 35803 | 2.21 | 1.8E+00 | O43281 | SWISSPROT | EMBRYONAL FYN-ASSOCIATED SUBSTRATE (HEFS) |
| 9530 | 22493 | 35941 | 0.66 | 1.8E+00 | R31042.1 | EST_HUMAN | yht2c08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:135278 5' |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 9617 | 22561 | 36009 | 0.64 | 1.8E+00 | AW880004.1 | EST_HUMAN | QV0-OT030-070300-148-e03 OT0300 Homo sapiens cDNA |
| 10208 | 23133 | 36620 | 0.93 | 1.8E+00 | P27050 | SWISSPROT | CHITINASE D PRECURSOR |
| 10846 | 23568 | | 2.88 | 1.8E+00 | AF111849.1 | NT | Homo sapiens PRO0530 mRNA, complete cds |
| 10919 | 23839 | | 0.75 | 1.8E+00 | P44325 | SWISSPROT | CYTIDINE DEAMINASE (CYTIDINE AMINOHYDROLASE) (CDA) |
| 12563 | 25808 | | 8.17 | 1.8E+00 | AF314254.1 | NT | Chlamydomonas reinhardtii alternative oxidase 1 (AOX1) gene, nuclear gene encoding mitochondrial protein |
| 12842 | 25326 | | 5.63 | 1.8E+00 | 9506404 | NT | Rattus norvegicus Actin-related protein complex 1b (Atpclb), mRNA |
| 1110 | 14154 | 27104 | 2.43 | 1.7E+00 | Q60114 | SWISSPROT | LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE) |
| 2279 | 15292 | 28317 | 3.08 | 1.7E+00 | AL163280.2 | NT | Homo sapiens chromosome 21 segment HS21C080 |
| 2382 | 15390 | 28415 | 1.67 | 1.7E+00 | A1141067.1 | EST_HUMAN | oz43h05.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1678137 3' |
| 4487 | 17512 | 30400 | 0.9 | 1.7E+00 | Q60114 | SWISSPROT | LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE) |
| 5694 | 18789 | 31959 | 1.66 | 1.7E+00 | BE063546.1 | EST_HUMAN | CM0-BT0282-171299-127-e05 BT0282 Homo sapiens cDNA |
| 5894 | 18789 | 31960 | 1.66 | 1.7E+00 | BE063546.1 | EST_HUMAN | CM0-BT0282-171299-127-e05 BT0282 Homo sapiens cDNA |
| 5955 | 19040 | 32238 | 0.49 | 1.7E+00 | R58748.1 | EST_HUMAN | G4846 Fetal heart Homo sapiens cDNA clone G4846 5' end |
| 6133 | 19210 | 32436 | 3.14 | 1.7E+00 | Q9TTR8 | SWISSPROT | COUP TRANSCRIPTION FACTOR 1 (COUP-TF1) (COUP-TF I) |
| 6703 | 19759 | 33038 | 0.59 | 1.7E+00 | P35816 | SWISSPROT | (PYRUVATE DEHYDROGENASE (LIPOAMIDE) PHOSPHATASE, MITOCHONDRIAL PRECURSOR (PDP) (PYRUVATE DEHYDROGENASE PHOSPHATASE, CATALYTIC SUBUNIT) (PDPC) |
| 7428 | 20395 | 33746 | 1.01 | 1.7E+00 | Q03703 | SWISSPROT | HYPOTHEITICAL 38.0 KD PROTEIN IN CAT2-AMD1 INTERGENIC REGION |
| 7428 | 20395 | 33747 | 1.01 | 1.7E+00 | Q03703 | SWISSPROT | HYPOTHEITICAL 38.0 KD PROTEIN IN CAT2-AMD1 INTERGENIC REGION |
| 8187 | 21157 | 34566 | 0.81 | 1.7E+00 | AF021335.1 | NT | Mus musculus T cell receptor gamma locus, TCR gamma 2 and gamma 4 gene clusters |
| 8367 | 21368 | 34748 | 1.21 | 1.7E+00 | 6755715 | NT | Mus musculus T-cell acute lymphocytic leukemia 1 (Tlal1), mRNA |
| 8397 | 21366 | 34775 | 0.54 | 1.7E+00 | BF530630.1 | EST_HUMAN | 602071917F1 NC1 CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4214669 5' |
| 8887 | 21853 | 35273 | 0.45 | 1.7E+00 | AF245513.1 | NT | Hippoglossus hippoglossus interferon inducible Mx protein (Mx) mRNA, complete cds |
| 8974 | 21940 | | 1.92 | 1.7E+00 | BF308000.1 | EST_HUMAN | 601894255F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4140084 5' |
| 9052 | 22018 | 35442 | 0.51 | 1.7E+00 | X69063.1 | NT | M.musculus Ank-1 mRNA for erythroid ankyrin |
| 9052 | 22018 | 35443 | 0.51 | 1.7E+00 | X69063.1 | NT | M.musculus Ank-1 mRNA for erythroid ankyrin |
| 9166 | 22132 | 35558 | 0.43 | 1.7E+00 | U19832.1 | NT | Rattus norvegicus SA gene, partial cds |
| 9504 | 25697 | 35909 | 2.37 | 1.7E+00 | Q60479 | SWISSPROT | HOMEBOX PROTEIN DLX-3 |
| 9504 | 25697 | 35910 | 2.37 | 1.7E+00 | Q60479 | SWISSPROT | HOMEBOX PROTEIN DLX-3 |
| 9965 | 22892 | | 1.4 | 1.7E+00 | AF161380.1 | NT | Homo sapiens HSPC262 mRNA, partial cds |
| 10532 | 23454 | | 0.5 | 1.7E+00 | AW953681.1 | EST_HUMAN | EST365751 IMAGE resequences, MAGC Homo sapiens cDNA |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 12518 | 25249 | 31803 | 1.78 | 1.7E+00 | A1878443.1 | EST_HUMAN | tu82d07.x1 NCI CGAP Gas4 Homo sapiens cDNA clone IMAGE:2287649 3' similar to contains MSR1.11 |
| 2049 | 15068 | 28088 | 14.89 | 1.6E+00 | AF199339.1 | NT | MSR1 repetitive element; |
| 2059 | 15078 | 28097 | 3.29 | 1.6E+00 | AF077374.1 | NT | Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds |
| 2065 | 15083 | 28102 | 1.62 | 1.6E+00 | Y11344.1 | NT | Homo sapiens small proline-rich protein (SPRR3) gene, exons 1, 2, and 3 and complete cds |
| 2292 | 15304 | | 1.33 | 1.6E+00 | X98373.1 | NT | Mus musculus ST6GalNAcII gene, exon 2 |
| | | | | | | NT | B. napus gene encoding endo-polygalacturonase |
| 2872 | 16030 | 28953 | 1.88 | 1.6E+00 | W58426.1 | EST_HUMAN | zid25f01.11 Soares_fetal_heart_NBHH19W Homo sapiens cDNA clone IMAGE:341689 5' similar to |
| 4063 | 17099 | | 7.07 | 1.6E+00 | BF570077.1 | EST_HUMAN | gb:D29805 N-ACETYLACTOSAMINE SYNTHASE (HUMAN); |
| 4379 | 17407 | 30287 | 1.29 | 1.6E+00 | AF158827.1 | NT | 602186085T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310591 3' |
| 4379 | 17407 | 30288 | 1.29 | 1.6E+00 | AF158827.1 | NT | Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds |
| 5120 | 18130 | 31006 | 2.98 | 1.6E+00 | Y11344.1 | NT | Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds |
| 5120 | 18130 | 31007 | 2.98 | 1.6E+00 | Y11344.1 | NT | Mus musculus ST6GalNAcII gene, exon 2 |
| 5926 | 18012 | 32204 | 2.21 | 1.6E+00 | L04808.1 | NT | Mus musculus ST6GalNAcII gene, exon 2 |
| 6020 | 19103 | 32305 | 0.82 | 1.6E+00 | AF005631.1 | NT | Brachydanio rerio MHC class II DA-beta-2*01 gene, 3' end |
| 6614 | 19672 | 32950 | 0.83 | 1.6E+00 | BF380703.1 | EST_HUMAN | Homo sapiens transglutaminase type I (TgaseI) gene, promoter region |
| 6968 | 19921 | 33217 | 0.97 | 1.6E+00 | AW294881.1 | EST_HUMAN | IL2-UT0073-060900-145-E02 UT0073 Homo sapiens cDNA |
| 7456 | 20422 | 33777 | 2.47 | 1.6E+00 | BE697287.1 | EST_HUMAN | UI-HB12-ant-b-04-0-UJ.st NCI CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727511 3' |
| 8364 | 21333 | | 1.1 | 1.6E+00 | Q46378 | SWISSPROT | RCO-CT0415-200700-032-e10 CT0415 Homo sapiens cDNA |
| 8722 | 21690 | 35117 | 3.42 | 1.6E+00 | AJ297131.1 | NT | VIRULENCE FACTOR MVIN HOMOLOG |
| 9251 | 22217 | 35847 | 0.9 | 1.6E+00 | 11437222 | NT | Mus musculus SIL, MAP_17, CYP_a, SCL & CYP_b genes |
| 9251 | 22217 | 35848 | 0.9 | 1.6E+00 | 11437222 | NT | Homo sapiens hypothetical protein PRO0971 (PRO0971), mRNA |
| 9815 | 25695 | 34540 | 1.54 | 1.6E+00 | X52046.1 | NT | Homo sapiens hypothetical protein PRO0971 (PRO0971), mRNA |
| 9815 | 25695 | 34541 | 1.54 | 1.6E+00 | X52046.1 | NT | M. musculus COL3A1 gene for collagen alpha-1 |
| 9945 | 22872 | | 0.48 | 1.6E+00 | AF043466.1 | NT | M. musculus COL3A1 gene for collagen alpha-1 |
| 10091 | 23017 | 36463 | 1.23 | 1.6E+00 | T41290.1 | EST_HUMAN | Thermotoga bacter ethanolicus D-xylose-binding protein (xyf) gene, complete cds |
| 10506 | 23428 | 36825 | 0.48 | 1.6E+00 | AF121361.1 | NT | ph6b6_19/1TV Outward Alu-primed hncDNA library Homo sapiens cDNA clone ph6b6_19/1TV |
| 10545 | 23467 | 36961 | 1.12 | 1.6E+00 | AW835644.1 | EST_HUMAN | Drosophila melanogaster signal transducing adaptor protein (STAM), serine threonine kinase Ial (IAL), and zinc finger protein (DNZ1) genes, complete cds |
| 10545 | 23467 | 36962 | 1.12 | 1.6E+00 | AW835644.1 | EST_HUMAN | QV4-LT0016-090200-100-d07 LT0016 Homo sapiens cDNA |
| 10709 | 23631 | 37126 | 0.78 | 1.6E+00 | AF037552.1 | NT | QV4-LT0016-090200-100-d07 LT0016 Homo sapiens cDNA |
| 11123 | 24083 | 37609 | 1.73 | 1.6E+00 | P64817 | SWISSPROT | Mus musculus T cell receptor gamma locus, TCR gamma 1 and gamma 3 gene clusters |
| 11192 | 19103 | 32305 | 5.78 | 1.6E+00 | AF005631.1 | NT | CAPSID PROTEIN P40 [CONTAINS: ASSEMBLIN (PROTEASE); CAPSID ASSEMBLY PROTEIN] |
| 12017 | 24894 | 38491 | 2.83 | 1.6E+00 | AF104313.1 | NT | Homo sapiens transglutaminase type I (TgaseI) gene, promoter region |
| | | | | | | NT | Homo sapiens unknown mRNA |

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Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 35 | 13155 | 26056 | 3.54 | 1.5E+00 | U53449.1 | NT | Rattus norvegicus jun dimerization protein 2 (jdp-2) mRNA, complete cds |
| 234 | 13334 | 26258 | 2.63 | 1.5E+00 | AE002201.2 | NT | Chlamydia pneumoniae AR39, section 32 of 94 of the complete genome |
| 622 | 13687 | | 2.04 | 1.5E+00 | 6752961 | NT | Mus musculus a disintegrin and metalloproteinase domain (ADAM) 15 (metargidin) (Adam15), mRNA |
| 2420 | 15427 | 28450 | 3.2 | 1.5E+00 | AJ131402.1 | NT | Potato virus A RNA, complete genome, isolate U |
| 2522 | 15525 | 28547 | 2.17 | 1.5E+00 | 6678350 | NT | Mus musculus T-cell lymphoma invasion and metastasis 1 (Tiam1), mRNA |
| 3155 | 15427 | 28450 | 2.96 | 1.5E+00 | AJ131402.1 | NT | Potato virus A RNA, complete genome, isolate U |
| 3386 | 16435 | 28362 | 0.92 | 1.5E+00 | AE001945.1 | NT | Deinococcus radiodurans R1 section 82 of 229 of the complete chromosome 1 |
| 5817 | 18907 | 32090 | 0.82 | 1.5E+00 | A1655301.1 | EST_HUMAN | h12f10.x1 NCI_CGAP_GCS Homo sapiens cDNA clone IMAGE:2240587 3' similar to TR:000237 O00237 HKF-1.1 |
| 5817 | 18907 | 32091 | 0.82 | 1.5E+00 | A1655301.1 | EST_HUMAN | h12f10.x1 NCI_CGAP_GCS Homo sapiens cDNA clone IMAGE:2240587 3' similar to TR:000237 O00237 HKF-1.1 |
| 6546 | 18607 | 32869 | 2.71 | 1.5E+00 | R17879.1 | EST_HUMAN | 9810e02.1 Soares infant brain T1B Homo sapiens cDNA clone IMAGE:31693 5' |
| 7335 | 20308 | | 1.48 | 1.5E+00 | BE785356.1 | EST_HUMAN | 601478745F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3881555 5' |
| 7368 | 20338 | 33688 | 16.72 | 1.5E+00 | P47179 | SWISSPROT | HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR |
| 7368 | 20338 | 33689 | 16.72 | 1.5E+00 | P47179 | SWISSPROT | HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR |
| 7568 | 20531 | 33890 | 0.6 | 1.5E+00 | AA889259.1 | EST_HUMAN | ak26f10.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1407115 3' |
| 7850 | 20796 | 34172 | 0.73 | 1.5E+00 | A1003254.1 | EST_HUMAN | an07b11.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684893 3' similar to gb:S95936 SEROTRANSFERRIN PRECURSOR (HUMAN); |
| 8144 | 21081 | | 0.67 | 1.5E+00 | AB039887.1 | NT | Homo sapiens WDR4 gene for WD repeat protein, complete cds |
| 8459 | 21428 | 34845 | 0.91 | 1.5E+00 | BE897446.1 | EST_HUMAN | 601509586F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911181 5' |
| 8514 | 21482 | 34896 | 0.48 | 1.5E+00 | AB040887.1 | NT | Homo sapiens mRNA for KIAA1454 protein, partial cds |
| 8991 | 21957 | 35382 | 1.08 | 1.5E+00 | K02138.1 | NT | Mouse germline IgM chain gene, mu-delta region |
| 9370 | 22335 | | 0.47 | 1.5E+00 | AB038516.1 | NT | Homo sapiens hGPIb alpha gene for platelet glycoprotein Ib alpha, complete cds |
| 9489 | 22453 | 35893 | 0.55 | 1.5E+00 | BF217818.1 | EST_HUMAN | 601882662F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095135 5' |
| 9838 | 22774 | 36229 | 0.91 | 1.5E+00 | R81928.1 | EST_HUMAN | y03h01.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:147697 5' |
| 9993 | 22820 | 36387 | 1.09 | 1.5E+00 | AW379697.1 | EST_HUMAN | QV3-CT0192-26 1099-008-d09 CT0192 Homo sapiens cDNA |
| 10219 | 23144 | 36633 | 6.14 | 1.5E+00 | BF376754.1 | EST_HUMAN | RC0-TN0078-150900-034-g05 TN0078 Homo sapiens cDNA |
| 10412 | 23334 | | 1.42 | 1.5E+00 | BF37944.1 | EST_HUMAN | 602035771F1 NCI_CGAP Bm64 Homo sapiens cDNA clone IMAGE:4183865 5' |
| 10556 | 23478 | 36972 | 2.92 | 1.5E+00 | AA017689.1 | EST_HUMAN | z638g06.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361306 5' |
| 10556 | 23478 | 36973 | 2.92 | 1.5E+00 | AA017689.1 | EST_HUMAN | z638g06.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361306 5' |
| 11727 | 24613 | 38190 | 5.98 | 1.5E+00 | AL134197.1 | EST_HUMAN | DKFZp547P243.s1 547 (synonym: hfbt1) Homo sapiens cDNA clone DKFZp547P243 3' |
| 11889 | 24751 | | 6.39 | 1.5E+00 | X07380.1 | NT | Malze mitochondrial tRNA-Ser gene and tRNA-Phe pseudogene |
| 12112 | 24982 | 38583 | 1.53 | 1.5E+00 | BE257552.1 | EST_HUMAN | 601109621F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350477 5' |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 1262 | 25151 | | 1.87 | 1.5E+00 | 6753287 | NT | Mus musculus caspase 9 associated protein 2 (Casp8ap2), mRNA |
| 12510 | 25899 | 31420 | 1.51 | 1.5E+00 | D63480.1 | NT | Human mRNA for KIAA0146 gene, partial cds |
| 12723 | 25376 | | 4.94 | 1.5E+00 | AL445085.1 | NT | Thermoplasma acidophilum complete genome; segment 3/5 |
| 12821 | 25443 | | 1.33 | 1.5E+00 | 6978492 | NT | Rattus norvegicus 5'-Lipoxygenase (Alox5), mRNA |
| 32 | 13152 | 26052 | 1.41 | 1.4E+00 | 7661685 | NT | Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA |
| 32 | 13152 | 26053 | 1.41 | 1.4E+00 | 7661685 | NT | Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA |
| 2285 | 15298 | | 0.9 | 1.4E+00 | AF053357.1 | NT | Helicobacter pylori glutamine synthetase (gha) gene, complete cds |
| 2341 | 15351 | | 8.77 | 1.4E+00 | U67922.1 | NT | Ovis aries prion protein gene, complete cds |
| 2677 | 15673 | 28693 | 1.83 | 1.4E+00 | X74463.1 | NT | Human papillomavirus type 7 genomic DNA |
| 2784 | 15776 | 28794 | 2.75 | 1.4E+00 | AF064584.2 | NT | Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds |
| 2784 | 15776 | 28795 | 2.75 | 1.4E+00 | AF064584.2 | NT | Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds |
| 3345 | 16396 | | 0.63 | 1.4E+00 | 5453733 | NT | WSB1 protein (WSB1) genes, complete cds |
| 4284 | 17313 | 30191 | 1.38 | 1.4E+00 | AW900455.1 | EST_HUMAN | Homo sapiens Mad4 homolog (MAD4) mRNA |
| 4284 | 17313 | 30192 | 1.38 | 1.4E+00 | AW900455.1 | EST_HUMAN | CMO-NN1005-140300-286-h06 NN1005 Homo sapiens cDNA |
| 4590 | 16144 | 28056 | 0.92 | 1.4E+00 | AE002324.2 | NT | CMO-NN1005-140300-286-h06 NN1005 Homo sapiens cDNA |
| 4590 | 16144 | 28057 | 0.92 | 1.4E+00 | AE002324.2 | NT | Chlamydia muridarum, section 55 of 85 of the complete genome |
| 4615 | 17636 | | 1.71 | 1.4E+00 | BF681547.1 | EST_HUMAN | Chlamydia muridarum, section 55 of 85 of the complete genome |
| 5446 | 18548 | 31461 | 1.58 | 1.4E+00 | AW054976.1 | EST_HUMAN | 602166887F1 NIH_MGC_93 Homo sapiens cDNA clone IMAGE:4297556 5' |
| 5606 | 18702 | | 5.52 | 1.4E+00 | AB032983.1 | NT | w45g07.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510460 3' |
| 6410 | 19478 | 32725 | 3.06 | 1.4E+00 | Q13472 | SWISSPROT | Homo sapiens mRNA for KIAA1157 protein, partial cds |
| 6427 | 25996 | | 4.2 | 1.4E+00 | AB020712.1 | NT | DNA TOPOISOMERASE III ALPHA |
| 6552 | 19613 | 32875 | 2.65 | 1.4E+00 | Q92777 | SWISSPROT | Homo sapiens mRNA for KIAA0905 protein, complete cds |
| 6552 | 19613 | 32876 | 2.65 | 1.4E+00 | Q92777 | SWISSPROT | SYNAPSIN II |
| 6781 | 19836 | 33119 | 0.56 | 1.4E+00 | BE007870.1 | EST_HUMAN | SYNAPSIN II |
| 6781 | 19836 | 33120 | 0.56 | 1.4E+00 | BE007870.1 | EST_HUMAN | QV0-BN0148-050500-215-b11 BN0148 Homo sapiens cDNA |
| 6906 | 20122 | 33436 | 0.86 | 1.4E+00 | AW893057.1 | EST_HUMAN | QV0-BN0148-050500-215-b11 BN0148 Homo sapiens cDNA |
| | | | | | | | CM3-NN0006-300300-132-b12 NN0006 Homo sapiens cDNA |
| | | | | | | | Homo sapiens caveolin-1/-2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2) |
| 7503 | 20468 | 33829 | 2.02 | 1.4E+00 | AJ133269.1 | NT | h23f05.x1 NCL_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2918873 3' similar to contains Alu repetitive element |
| 7521 | 20486 | 33848 | 1.15 | 1.4E+00 | AW467760.1 | EST_HUMAN | LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) |
| 7582 | 20544 | 33904 | 0.58 | 1.4E+00 | P55268 | SWISSPROT | LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) |
| 7582 | 20544 | 33905 | 0.58 | 1.4E+00 | P55268 | SWISSPROT | LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 7611 | 20571 | 33935 | 0.66 | 1.4E+00 | Q80905 | SWISSPROT | MINOR CAPSID PROTEIN L2 |
| 8678 | 21646 | | 0.6 | 1.4E+00 | P07683 | SWISSPROT | GLUCOAMYLASE PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE) |
| 9146 | 22112 | | 4.6 | 1.4E+00 | AJ271735.1 | NT | Homo sapiens Xq pseudautosomal region; segment 1/2 |
| 9449 | 22413 | 35849 | 1.56 | 1.4E+00 | R20459.1 | EST_HUMAN | yg33f12.1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34345 5' |
| 9552 | 22514 | 35965 | 3.46 | 1.4E+00 | BE064667.1 | EST_HUMAN | RC1-BT0313-301299-012-05 BT0313 Homo sapiens cDNA |
| 9587 | 22649 | 36000 | 0.45 | 1.4E+00 | AF134844.1 | NT | Sceloporus undulatus ornithine transcarbamylase (OTC) mRNA, complete cds |
| 10568 | 23490 | 36982 | 0.89 | 1.4E+00 | BF575545.1 | EST_HUMAN | 602133135F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288137 5' |
| 10613 | 23535 | 37032 | 0.69 | 1.4E+00 | BE145374.1 | EST_HUMAN | IL5-HT0198-291099-008-C04 HT0198 Homo sapiens cDNA |
| 10613 | 23535 | 37033 | 0.69 | 1.4E+00 | BE145374.1 | EST_HUMAN | IL5-HT0198-291099-008-C04 HT0198 Homo sapiens cDNA |
| 10892 | 23812 | 37319 | 0.92 | 1.4E+00 | D63441.1 | NT | Pandorina colemaniae chloroplast rbcL gene for ribulose biphosphate carboxylase, partial cds |
| 10892 | 23812 | 37320 | 0.92 | 1.4E+00 | D63441.1 | NT | Pandorina colemaniae chloroplast rbcL gene for ribulose biphosphate carboxylase, partial cds |
| 11559 | 24499 | 38055 | 4.43 | 1.4E+00 | AB006682.1 | NT | Homo sapiens APECED mRNA for AIRE-1, complete cds |
| 11733 | 24619 | 38186 | 2.83 | 1.4E+00 | BE962107.2 | EST_HUMAN | 601655184R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3' |
| 11733 | 24619 | 38197 | 2.83 | 1.4E+00 | BE962107.2 | EST_HUMAN | 601655184R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3' |
| 11756 | 24684 | 38263 | 2.15 | 1.4E+00 | U30790.1 | NT | Pneumocystis carinii f. sp. ratii guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds |
| 11756 | 24684 | 38264 | 2.15 | 1.4E+00 | U30790.1 | NT | Pneumocystis carinii f. sp. ratii guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds |
| 12360 | 25827 | | 1.7 | 1.4E+00 | AL161500.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 12 |
| 13068 | 25602 | | 1.4 | 1.4E+00 | 7657624 | NT | Homo sapiens staufen (Drosophila, RNA-binding protein) homolog 2 (STAU2), mRNA |
| 572 | 13641 | | 1.56 | 1.3E+00 | Z73640.1 | NT | M. musculo gene encoding 4-Dihydropyrimidin-trisporate dehydrogenase |
| 903 | 13958 | 26915 | 3.12 | 1.3E+00 | AJ271192.1 | NT | Cantharellus sp. partial 25S rRNA gene, isolate Tibet |
| 1131 | 14174 | | 32.4 | 1.3E+00 | Y19213.1 | NT | Homo sapiens putative psihbA pseudogene for hair keratin, exons 2 to 7 |
| 1300 | 14336 | 27299 | 19.22 | 1.3E+00 | 4507998 | NT | Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA |
| 1300 | 14336 | 27300 | 19.22 | 1.3E+00 | 4507998 | NT | Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA |
| 1358 | 14393 | | 0.99 | 1.3E+00 | U61730.2 | NT | Cox lacryme-fdb dihydrodipicolinate synthase (dapA) gene, complete cds |
| 1614 | 14646 | | 2.59 | 1.3E+00 | AE002338.2 | NT | Chlamydia muridarum, section 66 of 85 of the complete genome |
| 2255 | 15269 | | 1.22 | 1.3E+00 | AB030447.1 | NT | Cyprinus carpio MRPb and MASPb genes for mannose-binding lectin-associated serine protease (MASP) and MASP-related protein, complete cds |
| 2416 | 15422 | 28445 | 1.03 | 1.3E+00 | P25391 | SWISSPROT | LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN) |
| 2557 | 15559 | | 2.6 | 1.3E+00 | BE966735.2 | EST_HUMAN | 601661233R1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915945 3' |
| 2950 | 16007 | 28931 | 0.67 | 1.3E+00 | 6755621 | NT | Mus musculus alpha-spectrin 1, erythroid (Spha1), mRNA |

Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 3611 | 16656 | 29574 | 1.02 | 1.3E+00 | AF016494.1 | NT | Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P55), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete c> |
| 5284 | 18290 | 31152 | 0.9 | 1.3E+00 | AJ390500.1 | NT | Candida albicans partial mRNA for ribonucleotide reductase large subunit (mr1 gene) |
| 5592 | 18688 | 31657 | 1.08 | 1.3E+00 | P19732 | SWISSPROT | PHENOL HYDROXYLASE P3 PROTEIN (PHENOL 2-MONO OXYGENASE P3 COMPONENT) |
| 5794 | 18998 | 32067 | 0.52 | 1.3E+00 | M27138.1 | NT | Human estradiol 17 beta-dehydrogenase gene, complete cds |
| 6063 | 19144 | 32355 | 0.54 | 1.3E+00 | BF683825.1 | EST_HUMAN | 602145264F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4309095 5' |
| 6134 | 19211 | 32437 | 8.25 | 1.3E+00 | AW362834.1 | EST_HUMAN | PM0-CT0289-291199-004-408 CT0289 Homo sapiens cDNA |
| 6134 | 19211 | 32438 | 8.25 | 1.3E+00 | AW362834.1 | EST_HUMAN | PM0-CT0289-291199-004-408 CT0289 Homo sapiens cDNA |
| 6557 | 19617 | 32882 | 1.14 | 1.3E+00 | M33496.1 | NT | D.melanogaster no-on-transient A gene product, complete cds |
| 6914 | 19966 | | 0.69 | 1.3E+00 | Q00156 | SWISSPROT | HYPOTHETICAL GENE 84 PROTEIN |
| 6956 | 20181 | | 0.54 | 1.3E+00 | P49940 | SWISSPROT | SPORE GERMINATION PROTEIN KB |
| 7014 | 20140 | 33457 | 0.81 | 1.3E+00 | M13918.2 | NT | Homo sapiens fibronectin receptor alpha-subunit precursor (ITGA5) mRNA, partial cds |
| 7124 | 25673 | 33363 | 0.52 | 1.3E+00 | AW821580.1 | EST_HUMAN | IL2-ST0311-020200-040-G12 ST0311 Homo sapiens cDNA |
| 7141 | 20117 | 33430 | 1.04 | 1.3E+00 | BE558819.1 | EST_HUMAN | 601061420F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447965 5' |
| 7307 | 20278 | 33616 | 0.8 | 1.3E+00 | BE243571.1 | EST_HUMAN | TCBAP-1D0959 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project TCBA Homo sapiens cDNA clone TCBAP0959 |
| 7691 | 20649 | 34013 | 0.72 | 1.3E+00 | P24540 | SWISSPROT | ACYLPHOSPHATASE, ORGAN-COMMON TYPE ISOZYMES A AND B (ACYLPHOSPHATE PHOSPHOHYDROLASE) |
| 8641 | 21609 | 35032 | 1.09 | 1.3E+00 | AJ099912.1 | NT | Sus scrofa plp gene |
| 8790 | 21757 | 35179 | 2.29 | 1.3E+00 | BE963379.2 | EST_HUMAN | 601657145R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3886195 3' |
| 8907 | 21873 | 35299 | 0.87 | 1.3E+00 | BE974280.1 | EST_HUMAN | 601680250R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950532 3' |
| 9059 | 22025 | | 1.88 | 1.3E+00 | 9810247 | NT | Homo sapiens GL004 protein (GL004), mRNA |
| 9142 | 22108 | 35534 | 0.92 | 1.3E+00 | A1927629.1 | EST_HUMAN | wo85a07.xt NCJ_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462100 3' |
| 9873 | 22826 | | 4.88 | 1.3E+00 | AF042084.1 | NT | Homo sapiens heparan glucosaminyl N-deacetylase/N-sulfotransferase-2 gene, complete cds |
| 9882 | 22835 | 36288 | 2.2 | 1.3E+00 | X72019.1 | NT | S.alba pht-1 mRNA for photolyase |
| 9882 | 22835 | 36289 | 2.2 | 1.3E+00 | X72019.1 | NT | S.alba pht-1 mRNA for photolyase |
| 9882 | 22909 | 36374 | 1.02 | 1.3E+00 | AF059250.1 | NT | Homo sapiens lipoxigenase (ALOX12B) mRNA, complete cds |
| 10029 | 22856 | 36424 | 1.57 | 1.3E+00 | O00754 | SWISSPROT | LYSOSOMAL ALPHA-MANNOSIDASE PRECURSOR (MANNOSIDASE, ALPHA B) (LYSOSOMAL ACID ALPHA-MANNOSIDASE) (LAMAN) |
| 10108 | 23034 | 36511 | 1.32 | 1.3E+00 | A1927629.1 | EST_HUMAN | wo85a07.xt NCJ_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462100 3' |
| 10185 | 23110 | 36593 | 0.83 | 1.3E+00 | AJ223982.1 | NT | Lactococcus lactis cremoris NCDO-lrv1 chromosomal inversion junction DNA |
| 10185 | 23110 | 36594 | 0.83 | 1.3E+00 | AJ223982.1 | NT | Lactococcus lactis cremoris NCDO-lrv1 chromosomal inversion junction DNA |
| 10225 | 23150 | 36639 | 3.75 | 1.3E+00 | BE963379.2 | EST_HUMAN | 601657145R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3886195 3' |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 10286 | 23211 | | 0.64 | 1.3E+00 | AI659944.1 | EST_HUMAN | ig77a12.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2214814 3' similar to gb:X14723 |
| 10509 | 23431 | 36927 | 0.45 | 1.3E+00 | AF061251.1 | NT | CLUSTERIN PRECURSOR (HUMAN); |
| 10509 | 23431 | 36928 | 0.45 | 1.3E+00 | AF061251.1 | NT | Escherichia coli serotype O157:H7 O antigen gene cluster |
| 10574 | 23496 | 36989 | 1.24 | 1.3E+00 | AE004392.1 | NT | Escherichia coli serotype O157:H7 O antigen gene cluster |
| 10591 | 23513 | 37006 | 1.53 | 1.3E+00 | M29953.1 | NT | Vibrio cholerae chromosome II, section 49 of 93 of the complete chromosome |
| 10948 | 23888 | | 0.85 | 1.3E+00 | AL163302.2 | NT | Campylobacter jejuni kanamycin phosphotransferase (aphA-7) gene, complete cds |
| 10975 | 23895 | 37409 | 0.49 | 1.3E+00 | AI890846.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C102 |
| 10987 | 23907 | | 0.43 | 1.3E+00 | 8923637 | NT | ws32e10.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2498922 3' similar to SW:TRXB_HUMAN |
| 11052 | 24015 | | 3.63 | 1.3E+00 | Q14117 | SWISSPROT | Q16881 THIOREDOXIN REDUCTASE ; |
| 11252 | 24205 | 37727 | 2.35 | 1.3E+00 | P25299 | SWISSPROT | Homo sapiens hypothetical protein FLJ20707 (FLJ20707), mRNA |
| 11273 | 24225 | 37751 | 1.71 | 1.3E+00 | Z18892.2 | NT | DIHYDROPYRIMIDINASE (DHPASE) (HYDANTOINASE) (DHP) |
| 11867 | 24749 | 38331 | 2.61 | 1.3E+00 | D42042.1 | NT | MRNA 3'-END PROCESSING PROTEIN RNA15 |
| 11945 | 24825 | 38420 | 2.1 | 1.3E+00 | Z98682.1 | NT | Mus musculus desmin gene |
| 12001 | 24878 | | 1.55 | 1.3E+00 | L31891.1 | NT | Human mRNA for KIAA0085 gene, partial cds |
| 12498 | 25239 | | 3.37 | 1.3E+00 | AF187873.1 | NT | Bacillus subtilis genomic DNA 23 9kB fragment |
| 12659 | 25344 | 31762 | 6.47 | 1.3E+00 | BF348043.1 | EST_HUMAN | Arabidopsis thaliana 3-ketacyl-acyl carrier protein synthase III (KAS III) mRNA, complete cds |
| 12679 | 25724 | | 3.24 | 1.3E+00 | P33464 | SWISSPROT | Cavia porcellus inwardly-rectifying potassium channel Kir2.2 (KCNU12) gene, complete cds |
| 12765 | 25407 | | 1.68 | 1.3E+00 | AF187035.1 | NT | 602023185F1 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4158452 5' |
| 651 | 13717 | 26639 | 13.29 | 1.2E+00 | AA676246.1 | EST_HUMAN | E1 GLYCOPROTEIN PRECURSOR (MATRIX GLYCOPROTEIN) (MEMBRANE GLYCOPROTEIN) |
| 824 | 13882 | 26833 | 1.37 | 1.2E+00 | P05228 | SWISSPROT | Stumira illium cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product |
| 824 | 13882 | 26834 | 1.37 | 1.2E+00 | P05228 | SWISSPROT | z122d08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431535 3' |
| 824 | 13882 | 26835 | 1.37 | 1.2E+00 | P05228 | SWISSPROT | HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-II) |
| 879 | 13934 | | 0.95 | 1.2E+00 | 8924234 | NT | HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III) |
| 1165 | 14206 | 27160 | 7.4 | 1.2E+00 | AF080245.2 | NT | HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III) |
| 1210 | 14246 | 27206 | 1.43 | 1.2E+00 | AJ252242.1 | NT | HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III) |
| 1210 | 14246 | 27207 | 1.43 | 1.2E+00 | AJ252242.1 | NT | HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III) |
| 2025 | 15045 | 28058 | 1.06 | 1.2E+00 | AF140631.1 | NT | Homo sapiens hypothetical protein PRO3077 (PRO3077), mRNA |
| 3127 | 16184 | 29093 | 0.99 | 1.2E+00 | AB020681.1 | NT | Elaeis oleifera sesquiterpene synthase mRNA, complete cds |
| 3179 | 16234 | 29151 | 6.14 | 1.2E+00 | AL161563.2 | NT | pea seed-borne mosaic virus complete genome |
| 3179 | 16234 | 29152 | 6.14 | 1.2E+00 | AL161563.2 | NT | pea seed-borne mosaic virus complete genome |
| 3299 | 16352 | | 3.07 | 1.2E+00 | P54910 | SWISSPROT | Homo sapiens G-protein coupled receptor 14 (GPR14) gene, complete cds |
| 3367 | 16417 | 29343 | 0.78 | 1.2E+00 | AF188740.1 | NT | Homo sapiens mRNA for KIAA0874 protein, partial cds |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 3725 | 16787 | 29878 | 5.46 | 1.2E+00 | U75902.1 | NT | Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds |
| 4012 | 17051 | 29857 | 1.76 | 1.2E+00 | BF373570.1 | EST_HUMAN | MR0-FT0175-050900-203-g06_1 FT0175 Homo sapiens cDNA |
| 4327 | 16417 | 29343 | 1.09 | 1.2E+00 | AF188740.1 | NT | Homo sapiens LHX3 gene, intron 2 |
| 4498 | 17523 | | 2.12 | 1.2E+00 | M87060.1 | NT | Rattus rattus cardiac AE3 gene, exons 1-23 |
| 4551 | 17574 | 30484 | 1.33 | 1.2E+00 | AL161509.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 21 |
| 4582 | 17613 | 30507 | 2.1 | 1.2E+00 | AF156495.1 | NT | Homo sapiens post-synaptic density 95 (DLG4) gene, complete cds |
| 4619 | 17640 | | 6.6 | 1.2E+00 | Y09200.1 | NT | T. pinnaeum chloroplast rbcL gene, partial |
| 5052 | 18084 | 30942 | 2.38 | 1.2E+00 | P05228 | SWISSPROT | HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III) |
| 5052 | 18084 | 30943 | 2.36 | 1.2E+00 | P05228 | SWISSPROT | HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III) |
| 5052 | 18084 | 30944 | 2.36 | 1.2E+00 | P05228 | SWISSPROT | HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III) |
| 5512 | 18612 | 31544 | 1.08 | 1.2E+00 | U20760.1 | NT | Human extracellular calcium-sensing receptor mRNA, complete cds |
| 5634 | 18730 | 31892 | 1.89 | 1.2E+00 | AW813276.1 | EST_HUMAN | MR3-ST0191-140200-013-c05 ST0191 Homo sapiens cDNA |
| 5894 | 18882 | | 0.57 | 1.2E+00 | X81879.1 | NT | Calicivirus cDNA for orf1, orf2 and orf3 |
| 5974 | 19059 | 32260 | 0.78 | 1.2E+00 | AF016052.1 | NT | Homo sapiens zinc finger protein ZNF191 (ZNF191) gene, complete cds |
| 6275 | 19348 | 32580 | 2.39 | 1.2E+00 | X74885.1 | NT | D. hydei ayl repeat cluster DNA, fragment D |
| 6338 | 19407 | 32648 | 4.12 | 1.2E+00 | BE003113.1 | EST_HUMAN | QV4-BN0090-270400-190-a03 BN0090 Homo sapiens cDNA |
| 6423 | 19490 | 32741 | 1.41 | 1.2E+00 | X89084.1 | NT | C. glutamicum pla gene and ackA gene |
| 6423 | 19490 | 32742 | 1.41 | 1.2E+00 | X89084.1 | NT | C. glutamicum pla gene and ackA gene |
| 6467 | 19532 | 32780 | 38.6 | 1.2E+00 | AA759254.1 | EST_HUMAN | eh84g12 st Soares_testis_NHT Homo sapiens cDNA clone 1322374 3' |
| 6575 | 19635 | 32901 | 0.6 | 1.2E+00 | N33295.1 | EST_HUMAN | W39b12.61 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:273598 3' similar to |
| 6650 | 19708 | 32884 | 0.71 | 1.2E+00 | P17671 | SWISSPROT | gblM87935HUMAAU472 Human carcinoma cell-derived Alu RNA transcript, (rRNA); gb:J04970 |
| 6654 | 19711 | 32988 | 2.01 | 1.2E+00 | AW813276.1 | EST_HUMAN | CARBOXYPEPTIDASE M PRECURSOR (HUMAN); |
| 7100 | 20034 | 33337 | 1.17 | 1.2E+00 | AB026010.1 | NT | ECDYSONE-INDUCIBLE PROTEIN E75-A |
| 7113 | 20047 | 33349 | 2.68 | 1.2E+00 | AJ002141.1 | NT | MR3-ST0191-140200-013-c05 ST0191 Homo sapiens cDNA |
| 7465 | 20431 | | 0.64 | 1.2E+00 | AJ271735.1 | NT | Homo sapiens mRNA for KIAA1087 protein, partial cds |
| 7610 | 25685 | 33934 | 1.64 | 1.2E+00 | AV734585.1 | EST_HUMAN | Mus musculus DSPP gene |
| 7912 | 20855 | 34243 | 2.6 | 1.2E+00 | X74207.1 | NT | Homo sapiens Xq pseudautosomal region; segment 1/2 |
| 8122 | 21059 | 34457 | 0.53 | 1.2E+00 | BE787846.1 | EST_HUMAN | AV734585 cDNA Homo sapiens cDNA clone cdaAFH03 5' |
| 8915 | 21881 | 35307 | 3.24 | 1.2E+00 | AB033030.1 | NT | L. lactis pyrD and pyrF genes |
| | | | | | | | Homo sapiens mRNA for KIAA1204 protein, partial cds |
| | | | | | | | ALPHA,ALPHA-TREHALOSE-PHOSPHATE SYNTHASE (UDP-FORMING) 123 KD SUBUNIT (TREHALOSE-6-PHOSPHATE SYNTHASE) (UDP-GLUCOSE-GLUCOSEPHOSPHATE |
| 9010 | 21976 | 35396 | 0.65 | 1.2E+00 | P38427 | SWISSPROT | GLUCOSYLTRANSFERASE) |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 9228 | 22194 | | 0.58 | 1.2E+00 | 7706271 | NT | Homo sapiens CGI-30 protein (LOC51611), mRNA |
| 9380 | 22345 | 35777 | 1.88 | 1.2E+00 | AW377210.1 | EST_HUMAN | MR2-CT0222-201099-001-e07 CT0222 Homo sapiens cDNA |
| 9594 | 22556 | 36006 | 0.47 | 1.2E+00 | H48599.1 | EST_HUMAN | yq80a06.r1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:202086 5' |
| 9753 | 22694 | 36150 | 3.63 | 1.2E+00 | Z32850.1 | NT | R. communis gene for pyrophosphate-dependent phosphofructokinase beta subunit |
| 9964 | 22891 | 36353 | 1.71 | 1.2E+00 | D11745.1 | EST_HUMAN | HUMHM01A01 Liver HepG2 cell line. Homo sapiens cDNA clone hm01a01 |
| 10291 | 23216 | 36700 | 3.52 | 1.2E+00 | X56832.1 | NT | H. sapiens ENO3 gene for muscle specific enolase |
| 10689 | 23611 | | 0.73 | 1.2E+00 | AB009666.1 | NT | Homo sapiens kldho gene, exon 1 |
| 11674 | 24640 | 38219 | 1.89 | 1.2E+00 | AW817817.1 | EST_HUMAN | PMO-ST0264-161199-001-d01 ST0264 Homo sapiens cDNA |
| 11713 | 24676 | | 7.68 | 1.2E+00 | BE160761.1 | EST_HUMAN | PM1-HT0422-160200-007-g10 HT0422 Homo sapiens cDNA |
| 11785 | 23940 | 37462 | 2.59 | 1.2E+00 | U50147.1 | NT | Rattus norvegicus synapse-associated protein 102 mRNA, complete cds |
| 12466 | 25799 | 31524 | 18.09 | 1.2E+00 | AL163203.2 | NT | Homo sapiens chromosome 21 segment HS21C003 |
| 12487 | 25232 | | 2.7 | 1.2E+00 | AP001515.1 | NT | Bacillus halodurans genomic DNA, section 9/14 |
| 464 | 13537 | 26463 | 1.43 | 1.1E+00 | D86980.1 | NT | Human mRNA for KIAA0227 gene, partial cds |
| 1777 | 14806 | 27792 | 1.97 | 1.1E+00 | AW995393.1 | EST_HUMAN | QV0-BN0042-170300-163-g12 BN0042 Homo sapiens cDNA |
| 1915 | 14839 | 27835 | 1.08 | 1.1E+00 | AW578889.1 | EST_HUMAN | U1-HF-BR0p-alk-f-02-0-U1.s1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3074834 3' |
| 3341 | 16392 | 29313 | 7.34 | 1.1E+00 | AL163213.2 | NT | Homo sapiens chromosome 21 segment HS21C013 |
| 3341 | 16392 | 29314 | 7.34 | 1.1E+00 | AL163213.2 | NT | Homo sapiens chromosome 21 segment HS21C013 |
| 3498 | 16545 | 29471 | 0.79 | 1.1E+00 | 8922841 | NT | Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA |
| 3593 | 16638 | 29568 | 3.34 | 1.1E+00 | AI808360.1 | EST_HUMAN | wf54h11.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359461 3' similar to SW:P531_HUMAN Q12888 P53-BINDING PROTEIN 53BP1 ; |
| 3731 | 16773 | 29684 | 1.52 | 1.1E+00 | AE003886.1 | NT | Xyella fastidiosa, section 32 of 229 of the complete genome |
| 3731 | 16773 | 29685 | 1.52 | 1.1E+00 | AE003886.1 | NT | Xyella fastidiosa, section 32 of 229 of the complete genome |
| 3831 | 16871 | | 0.86 | 1.1E+00 | X85374.1 | NT | H. parahaeemolyticus hphIM(A), hphIM(C), hphIR and menB genes |
| 3984 | 17004 | 29918 | 0.87 | 1.1E+00 | 8922841 | NT | Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA |
| 4050 | 17087 | 29983 | 1.02 | 1.1E+00 | 6755205 | NT | Mus musculus proteasome (prosome, macropain) subunit, beta type 7 (Pamb7), mRNA |
| 4243 | 17272 | | 6.78 | 1.1E+00 | 5835331 | NT | R. uniconis complete mitochondrial genome |
| 5028 | 18042 | 30925 | 3.15 | 1.1E+00 | U18466.1 | NT | African swine fever virus, complete genome |
| 5085 | 18093 | 30971 | 3.91 | 1.1E+00 | U34740.1 | NT | Emertella nidulans sterigmabovysin biosynthetic gene cluster: (stcA), (stcB), (stcC), (stcD), (stcE), (stcF), (stcG), (stcH), (stcI), (stcL), (stcO), (stcP), (stcQ), (stcR), (stcS), (stcT), (stcU), (stcV) and (stcW) genes, complete cds |
| 5109 | 18119 | 30993 | 1.04 | 1.1E+00 | X78425.1 | NT | E. faecalis pbp5 gene |
| 5289 | 18276 | 31139 | 0.9 | 1.1E+00 | 6880080 | NT | Homo sapiens putative GR6 protein (GR6), mRNA |
| 5380 | 18484 | 31359 | 1.53 | 1.1E+00 | 6978530 | NT | Rattus norvegicus Aquaporin 4 (Aqp4), mRNA |
| 5695 | 18790 | 31961 | 13.39 | 1.1E+00 | BE960184.1 | EST_HUMAN | 601652776R1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3825835 3' |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 5715 | 18809 | 31987 | 0.99 | 1.1E+00 | AI138582.1 | EST_HUMAN | qds5c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1736260 3' |
| 6211 | 19285 | 32517 | 1.93 | 1.1E+00 | 11419739 | NT | Homo sapiens solute carrier family 6 (neurotransmitter transporter), member 14 (SLC6A14), mRNA |
| 6405 | 19473 | 32721 | 0.94 | 1.1E+00 | AF197861.1 | NT | Macgregoria pulchra cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product |
| 6547 | 19608 | 32870 | 0.83 | 1.1E+00 | R06037.1 | EST_HUMAN | ye89e03.r1 Soares fetal liver spleen TNFSL Homo sapiens cDNA clone IMAGE:124924 5' |
| 6876 | 19929 | 33226 | 1.21 | 1.1E+00 | AJ404004.1 | NT | Mus musculus mRNA for ER protein 58 (EP58 gene) |
| 7468 | 20434 | | 0.88 | 1.1E+00 | AF101091.1 | NT | Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exons 25 through 28 |
| 7514 | 20479 | 33840 | 0.82 | 1.1E+00 | X55981.1 | NT | Maize mRNA for endase (2-phospho-D-glycerate hydrolase) |
| 7732 | 20687 | 34050 | 1.83 | 1.1E+00 | Z72338.1 | NT | Herpes simplex virus type 1 (strain KOS) UL41 gene |
| 7732 | 20687 | 34051 | 1.83 | 1.1E+00 | Z72338.1 | NT | Herpes simplex virus type 1 (strain KOS) UL41 gene |
| 7754 | 20707 | 34076 | 8.13 | 1.1E+00 | AL161588.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84 |
| 7833 | 25691 | 34158 | 0.94 | 1.1E+00 | 11967960 | NT | Mus musculus silent mating type information regulation 2, (S.cerevisiae, homolog)-like (Sir2), mRNA |
| 8470 | 21439 | 34857 | 2.95 | 1.1E+00 | BF693996.1 | EST_HUMAN | 602082582F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246828 5' |
| 8563 | 21531 | 34951 | 0.73 | 1.1E+00 | AI478339.1 | EST_HUMAN | bm39h11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2160549 3' |
| 9089 | 22055 | 35479 | 0.63 | 1.1E+00 | AB003088.1 | NT | Acetabularia caliculus mitochondrial COXI-like gene |
| 9167 | 22133 | 35559 | 1.42 | 1.1E+00 | S80750.1 | NT | VH-anti-cytomegalovirus glycoprotein B antibody 4D4 heavy chain variable region [human, mRNA Partial, 375 nt] |
| 9278 | 22244 | 35673 | 0.45 | 1.1E+00 | AI079946.1 | EST_HUMAN | cc24f05.x1 Soares_NHIMPu_S1 Homo sapiens cDNA clone IMAGE:1677249 3' |
| 9792 | 21115 | | 0.64 | 1.1E+00 | BE384876.1 | EST_HUMAN | 601276278F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3617418 5' |
| 9886 | 22913 | 36378 | 0.95 | 1.1E+00 | AJ245772.1 | NT | Mus musculus mRNA for stretch responsive musole (X-chromosome) protein (Srmx gene) |
| 10040 | 22867 | | 0.69 | 1.1E+00 | Y12227.1 | NT | Arabidopsis thaliana DNA, 24 kb surrounding PFL locus |
| 10130 | 23056 | 36834 | 0.95 | 1.1E+00 | L76301.1 | NT | Yersinia pseudotuberculosis psaE, psaF, adhesin (psaA), chaperone (psaB), and usher (psaC) genes, complete cds |
| 10192 | 23117 | 36801 | 1.38 | 1.1E+00 | AB023151.1 | NT | Homo sapiens mRNA for KIAA0934 protein, partial cds |
| 10297 | 23222 | 36706 | 5.66 | 1.1E+00 | AL161515.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27 |
| 10357 | 23281 | 36757 | 20.52 | 1.1E+00 | 6754021 | NT | Mus musculus guanine nucleotide binding protein (G protein), gamma 3 subunit (Gng3), mRNA |
| 10867 | 23787 | 37287 | 1.09 | 1.1E+00 | P73769 | SWISSPROT | DNA MISMATCH REPAIR PROTEIN MUTS |
| 10989 | 23909 | 37422 | 0.63 | 1.1E+00 | BF343644.1 | EST_HUMAN | 602014488F1 NCI_CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4150508 5' |
| 10989 | 23909 | 37423 | 0.63 | 1.1E+00 | BF343644.1 | EST_HUMAN | 602014488F1 NCI_CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4150508 5' |
| 11012 | 23977 | 37502 | 2.03 | 1.1E+00 | 11067364 | NT | Homo sapiens KIAA0626 gene product (KIAA0626), mRNA |
| 11064 | 24027 | | 3.83 | 1.1E+00 | AF068942.1 | NT | Klebsoridium fluitans cytochrome c oxidase subunit 2 (cox2) gene, mitochondrial gene encoding mitochondrial protein, partial cds |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 11435 | 18340 | | 4.65 | 1.1E+00 | 8822973 | NT | Homo sapiens hypothetical protein FLJ11280 (FLJ11280), mRNA |
| 11439 | 24382 | 37821 | 3.12 | 1.1E+00 | AF012862.1 | NT | Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds |
| 11439 | 24382 | 37822 | 3.12 | 1.1E+00 | AF012862.1 | NT | Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds |
| 11683 | 24649 | 38227 | 3.44 | 1.1E+00 | AB09699.1 | EST_HUMAN | wf76e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2361548 3' |
| 12439 | 25202 | | 3.12 | 1.1E+00 | P07866 | SWISSPROT | LOW TEMPERATURE ESSENTIAL PROTEIN |
| 12539 | 25263 | 31807 | 1.55 | 1.1E+00 | AF216996.1 | NT | Taenia solium immunogenic protein Ts78 mRNA, partial cds |
| 12681 | 25798 | | 2.28 | 1.1E+00 | AF234169.1 | NT | Dicystidium discoidum isopenicillin N pyrophosphate isomerase (Dip) mRNA, complete cds |
| 98 | 13215 | | 1.55 | 1.0E+00 | U23808.1 | NT | Xenopus laevis rhodopsin gene, complete cds |
| 113 | 13224 | 28148 | 1.66 | 1.0E+00 | D88425.1 | NT | Cavia cobaya mRNA for serine/threonine kinase, complete cds |
| 418 | 13491 | | 3.03 | 1.0E+00 | AB021684.1 | NT | Marchantia polymorpha genes for 26S rRNA, 5S rRNA, 18S rRNA, 5.8S rRNA and 26S rRNA |
| 578 | 13647 | 26560 | 2.22 | 1.0E+00 | AJ251660.1 | NT | Glardia tigrina mRNA for homeodomain transcription factor (so gene) |
| 678 | 13741 | 28668 | 6.74 | 1.0E+00 | AL163218.2 | NT | Homo sapiens chromosome 21 segment HS21C018 |
| 678 | 13742 | | 1.35 | 1.0E+00 | AF125984.1 | NT | Aedes aegypti mucin-like protein MUC1 mRNA, complete cds |
| 1388 | 15866 | | 3.53 | 1.0E+00 | X80418.1 | NT | V. carteri Algat-CAM mRNA |
| 1771 | 14800 | 27786 | 0.97 | 1.0E+00 | AB006531.1 | NT | Plautia stali Intestine virus RNA for nonstructural polyprotein, capsid protein precursor, complete cds |
| 2493 | 15496 | 28521 | 1.42 | 1.0E+00 | P48355 | SWISSPROT | DNA GYRASE SUBUNIT B |
| 2493 | 15496 | 28522 | 1.42 | 1.0E+00 | P48355 | SWISSPROT | DNA GYRASE SUBUNIT B |
| 2887 | 15946 | 28861 | 4.42 | 1.0E+00 | P24008 | SWISSPROT | 3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1) |
| 2887 | 15946 | 28862 | 4.42 | 1.0E+00 | P24008 | SWISSPROT | 3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1) |
| 2978 | 16036 | | 0.81 | 1.0E+00 | O14226 | SWISSPROT | HYPOTHETICAL 67.9 KD PROTEIN C6F12.08C IN CHROMOSOME I |
| 3212 | 16287 | 29190 | 1.08 | 1.0E+00 | AA628453.1 | EST_HUMAN | af26g08.s1 Soares_tet1_tet1 Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1032830 3' similar to |
| 3613 | 13215 | | 0.93 | 1.0E+00 | U23808.1 | NT | WP:C42D8.3 CE04204; contains element MER22 MER22 repetitive element ; |
| 3683 | 16736 | 28649 | 1.33 | 1.0E+00 | AJ23816.1 | NT | Xenopus laevis rhodopsin gene, complete cds |
| 4097 | 17131 | 30024 | 1.16 | 1.0E+00 | AF223391.1 | NT | Agaricus bisporus mRNA for tyrosinase |
| 4304 | 17333 | | 0.73 | 1.0E+00 | 8922245 | NT | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced |
| 4843 | 17860 | 30755 | 1.54 | 1.0E+00 | AL163247.2 | NT | Homo sapiens hypothetical protein FLJ10139 (FLJ10139), mRNA |
| 5053 | 18065 | | 0.9 | 1.0E+00 | D10852.1 | NT | Homo sapiens chromosome 21 segment HS21C047 |
| | | | | | | | Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 5354 | 18459 | 31328 | 3.23 | 1.0E+00 | Z97022.1 | NT | Hordeum vulgare gene encoding cysteine proteinase |
| 5949 | 19035 | 32228 | 5.05 | 1.0E+00 | AF248054.1 | NT | Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds |
| 5949 | 19035 | 32229 | 5.05 | 1.0E+00 | AF248054.1 | NT | Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds |
| 6067 | 19148 | 32360 | 1.44 | 1.0E+00 | Z97341.2 | NT | Arabidopsis thaliana DNA chromosome 4, ESSA FCA contig fragment No. 6 |
| 6236 | 18309 | 32541 | 4.52 | 1.0E+00 | P04501 | SWISSPROT | FIBER PROTEIN |
| 6243 | 18316 | 32548 | 1.77 | 1.0E+00 | AW452782.1 | EST_HUMAN | UI-H-BIG-4-09-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068969 3' |
| 6637 | 19695 | 32972 | 2.12 | 1.0E+00 | U75902.1 | NT | Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds |
| 6691 | 19748 | 33025 | 0.68 | 1.0E+00 | AF104869.1 | NT | Homo sapiens cell cycle protein (PA2G4) gene, exons 2 through 5 |
| 6788 | 19841 | | 0.98 | 1.0E+00 | P48506 | SWISSPROT | SRB-11 PROTEIN |
| 6813 | 19867 | 33155 | 0.71 | 1.0E+00 | BE797716.1 | EST_HUMAN | 601581891F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936382 5' |
| 6813 | 19867 | 33156 | 0.71 | 1.0E+00 | BE797716.1 | EST_HUMAN | 601581891F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936382 5' |
| 6944 | 20168 | 33481 | 1.17 | 1.0E+00 | Y11204.1 | NT | V. carteri gene encoding vdxopsin |
| 7033 | 18365 | 31252 | 0.64 | 1.0E+00 | U63721.1 | NT | Human elastin (ELN) gene, partial cds, and LIM-kinase (LIMK1) gene, complete cds |
| 7345 | 20316 | 33661 | 1 | 1.0E+00 | S52770.1 | NT | Insulin-like growth factor-binding protein 4 [cattle, pulmonary artery endothelial cells, mRNA, 2028 nt] |
| 7719 | 20676 | | 8.7 | 1.0E+00 | P20273 | SWISSPROT | B-CELL RECEPTOR CD22 PRECURSOR (LEU-14) (B-LYMPHOCYTE CELL ADHESION MOLECULE) |
| 7979 | 20918 | 34309 | 1.52 | 1.0E+00 | AF192531.1 | NT | Homo sapiens endothelin-converting enzyme 2 (ECE2) mRNA, complete cds |
| 7997 | 20936 | 34330 | 6.07 | 1.0E+00 | AA775191.1 | EST_HUMAN | ac79b08.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:868791 3' |
| 8165 | 21103 | | 0.57 | 1.0E+00 | BF679213.1 | EST_HUMAN | 602153792F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294727 5' |
| 8294 | 21263 | 34673 | 1.49 | 1.0E+00 | BE868267.1 | EST_HUMAN | 601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848005 5' |
| 8294 | 21263 | 34674 | 1.49 | 1.0E+00 | BE868267.1 | EST_HUMAN | 601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848005 5' |
| 8491 | 18065 | | 1.22 | 1.0E+00 | D10852.1 | NT | Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds |
| 8693 | 21661 | 35084 | 2.31 | 1.0E+00 | Q02207 | SWISSPROT | PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE; D-3-HYDROXYACYL COA DEHYDROGENASE] |
| 8693 | 21661 | 35085 | 2.31 | 1.0E+00 | Q02207 | SWISSPROT | PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE; D-3-HYDROXYACYL COA DEHYDROGENASE] |
| 8821 | 21788 | | 0.83 | 1.0E+00 | P51784 | SWISSPROT | UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 11 (UBIQUITIN THIOLESTERASE 11) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 11) (DEUBIQUITINATING ENZYME 11) |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 8855 | 21822 | 35242 | 0.44 | 1.0E+00 | Q9Y5T5 | SWISSPROT | UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (UBIQUITIN THIOLESTERASE 16) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN PROCESSING PROTEASE UBP-M) |
| 8855 | 21822 | 35243 | 0.44 | 1.0E+00 | Q9Y5T5 | SWISSPROT | UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (UBIQUITIN THIOLESTERASE 16) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN PROCESSING PROTEASE UBP-M) |
| 8883 | 25698 | | 2.37 | 1.0E+00 | BE147331.1 | EST_HUMAN | RC1-HT0229-181089-011-e06 HT0229 Homo sapiens cDNA |
| 8923 | 21889 | 35316 | 0.89 | 1.0E+00 | U42720.2 | NT | Simian immunodeficiency virus Gag protein (gag) gene, complete cds; Pol protein (pol) gene, partial cds; and Vif protein (vif), Vpr protein (vpr), Tat protein (tat), Rev protein (rev), Vpu protein (vpu), Env protein (env), and Nef protein (nef) genes, > |
| 9075 | 22041 | 35484 | 1.55 | 1.0E+00 | M39427.1 | NT | Human immunodeficiency virus type 1 (HIV-1), isolate SF33, |
| 9828 | 22570 | 36019 | 2.14 | 1.0E+00 | BE907592.1 | EST_HUMAN | 601497581F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899421 5' |
| 9838 | 22772 | 36227 | 1.25 | 1.0E+00 | 6753429 | NT | Mus musculus chloride channel calcium activated 1 (Clcat1), mRNA |
| 9838 | 22772 | 36228 | 1.25 | 1.0E+00 | 6753429 | NT | Mus musculus chloride channel calcium activated 1 (Clcat1), mRNA |
| 9899 | 22898 | 36359 | 1.94 | 1.0E+00 | AV689554.1 | EST_HUMAN | AV689554 GKG Homo sapiens cDNA clone GKCCYA11 5' |
| 9874 | 22901 | 36364 | 1.23 | 1.0E+00 | U44952.1 | NT | Xenopus laevis zona pellucida C glycoprotein precursor (XZPC) mRNA, complete cds |
| 9874 | 22901 | 36365 | 1.23 | 1.0E+00 | U44952.1 | NT | Xenopus laevis zona pellucida C glycoprotein precursor (XZPC) mRNA, complete cds |
| 10212 | 23137 | 36624 | 0.56 | 1.0E+00 | X15498.1 | NT | Human Coronavirus gene for membrane protein |
| 10212 | 23137 | 36625 | 0.56 | 1.0E+00 | X15498.1 | NT | Human Coronavirus gene for membrane protein |
| 10471 | 23393 | 36899 | 0.72 | 1.0E+00 | 5174562 | NT | Human Coronavirus gene for membrane protein |
| 10471 | 23393 | 36899 | 0.72 | 1.0E+00 | 5174562 | NT | Human Coronavirus gene for membrane protein |
| 10564 | 23486 | 36980 | 0.68 | 1.0E+00 | AI077920.1 | EST_HUMAN | Homo sapiens MHC binding factor, beta (MHCBBF) mRNA |
| 10690 | 23612 | 37108 | 3.7 | 1.0E+00 | AV758825.1 | EST_HUMAN | 6y15d07.s1 Soares_senescent_fibroblasts_NbH5F Homo sapiens cDNA clone IMAGE:1665901 3' |
| 10842 | 23762 | 37262 | 20.08 | 1.0E+00 | AA004982.1 | EST_HUMAN | AV758825 BM Homo sapiens cDNA clone BMFAW C04 5' |
| 10842 | 23762 | 37263 | 20.08 | 1.0E+00 | AA004982.1 | EST_HUMAN | zH94a02.1f1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428908 5' |
| 10876 | 23796 | 37297 | 1.18 | 1.0E+00 | L11910.1 | NT | zH94a02.1f1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428906 5' |
| 12046 | 18459 | 31326 | 1.66 | 1.0E+00 | Z97022.1 | NT | Human retinoblastoma susceptibility gene exons 1-27, complete cds |
| 12327 | 25129 | | 3.26 | 1.0E+00 | P15306 | SWISSPROT | Hordeum vulgare gene encoding cysteine protease |
| 12650 | 25333 | | 2.49 | 1.0E+00 | AW976184.1 | EST_HUMAN | THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM) |
| 1575 | 14608 | 27580 | 3.22 | 9.9E-01 | AF245455.1 | NT | EST388293 MAGE resequences; MAGN Homo sapiens cDNA |
| 1575 | 14608 | 27581 | 3.22 | 9.9E-01 | AF245455.1 | NT | Drosophila melanogaster regulator of G-protein signalling LOCO III mRNA, complete cds |
| 2845 | 15642 | 28666 | 1 | 9.9E-01 | AL163302.2 | NT | Drosophila melanogaster regulator of G-protein signalling LOCO III mRNA, complete cds |
| 3619 | 16693 | | 1.1 | 9.9E-01 | AF174585.1 | NT | Homo sapiens chromosome 21 segment HS21C102 |
| 5717 | 18811 | 31990 | 8.62 | 9.9E-01 | P49657 | SWISSPROT | Apple mosaic virus RNA 2 putative polymerase gene, complete cds |
| | | | | | | | SERINE/THREONINE PROTEIN KINASE MINIBRAIN |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 5969 | 18054 | 32254 | 0.79 | 9.8E-01 | Q09632 | SWISSPROT | PROBABLE OXIDOREDUCTASE ZK1290.5 IN CHROMOSOME II |
| 9616 | 22560 | | 1.4 | 9.8E-01 | U65667.1 | NT | Lyoporsicon esculentum putative Mt1 copy 1 nematode-resistance gene |
| 9913 | 22734 | | 3.02 | 9.8E-01 | Q28642 | SWISSPROT | B2 BRADYKININ RECEPTOR (BK-2 RECEPTOR) |
| 11069 | 24032 | 37556 | 1.48 | 9.8E-01 | AJ005029.1 | NT | Danio rerio mRNA for Eph-like receptor tyrosine kinase rtk8 |
| 524 | 13596 | 26513 | 1.12 | 9.8E-01 | P22567 | SWISSPROT | AMINO-ACID ACETYLTRANSFERASE (N-ACETYLGLUTAMATE SYNTHASE) (AGS) (NAGS) |
| 2305 | 15317 | | 1.28 | 9.8E-01 | AJ003108.1 | NT | Callitrix jacchus UBE1 gene derived retroposon on the Y chromosome |
| 2813 | 15805 | | 1.29 | 9.8E-01 | AF174644.1 | NT | Xenopus laevis rac GTPase mRNA, complete cds |
| 7406 | 20374 | 33725 | 4.12 | 9.8E-01 | AJ302158.1 | NT | Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983 |
| 7406 | 20374 | 33726 | 4.12 | 9.8E-01 | AJ302158.1 | NT | Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983 |
| 7807 | 20850 | 34236 | 0.89 | 9.8E-01 | BF034016.1 | EST_HUMAN | 601456337F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3860049 5' |
| 7807 | 20850 | 34237 | 0.99 | 9.8E-01 | BF034016.1 | EST_HUMAN | 601456337F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3860049 5' |
| 9069 | 22035 | 35458 | 0.88 | 9.8E-01 | P38652 | SWISSPROT | PHOSPHOGLUCOMUTASE (GLUCOSE PHOSPHOMUTASE) (PGM) |
| 10804 | 23725 | | 0.53 | 9.8E-01 | AA825565.1 | EST_HUMAN | cd55804.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1371847 3' |
| 11339 | 24289 | 37813 | 2.06 | 9.8E-01 | BE258705.1 | EST_HUMAN | 601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350760 5' |
| 11339 | 24289 | 37814 | 2.06 | 9.8E-01 | BE258705.1 | EST_HUMAN | 601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350760 5' |
| 12545 | 25268 | | 1.41 | 9.8E-01 | U52111.2 | NT | Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMK1), creatine transporter (CRT1), CDM protein (CDM), adrenergic dystrophy protein > |
| 7366 | 20336 | 33686 | 2.3 | 9.7E-01 | U26716.1 | NT | Drosophila melanogaster sodium channel protein (para) gene, exons 9, 10, 11, 12 and optional segments b, c, d and e, partial cds |
| 8848 | 21815 | 35235 | 1.81 | 9.7E-01 | AF149112.1 | NT | Triticum aestivum stripe rust resistance protein Yr10 (Yr10) gene, complete cds |
| 8854 | 21821 | 35241 | 1.33 | 9.7E-01 | M90544.1 | NT | Salmonella typhimurium adenine-methyltransferase (mod) and restriction endonuclease (res) |
| 11505 | 24447 | | 3.87 | 9.7E-01 | BF511209.1 | EST_HUMAN | UIH-BI4-ed-e-07-Q-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085140 3' |
| 12117 | 24987 | 38569 | 2.29 | 9.7E-01 | U87514.1 | NT | Dicotyledon discoidium CAR3 gene, promoter region |
| 4486 | 17511 | 30399 | 1.68 | 9.6E-01 | AW798674.1 | EST_HUMAN | PM2-UM0053-240300-005-f12 UM0053 Homo sapiens cDNA |
| 5179 | 18188 | 31065 | 0.9 | 9.6E-01 | 7682375 | NT | Homo sapiens KIAA0914 gene product (KIAA0914), mRNA |
| 5847 | 18937 | 32121 | 3.85 | 9.6E-01 | Z70556.1 | NT | Parvovirus B19 DNA, patient C, genome position 2448-2994 |
| 5847 | 18937 | 32122 | 3.85 | 9.6E-01 | Z70556.1 | NT | Parvovirus B19 DNA, patient C, genome position 2448-2994 |
| 6910 | 19662 | 33258 | 0.57 | 9.6E-01 | Z97341.2 | NT | Arabidopsis thaliana DNA chromosome 4, ESSA1 FCA contig fragment No. 6 |
| 8735 | 21703 | | 1.21 | 9.6E-01 | X95275.1 | NT | P. talciparum complete gene map of plasid-like DNA (IR-A) |
| 9203 | 22169 | 35599 | 0.51 | 9.6E-01 | L81138.1 | NT | Rattus norvegicus (strain R21) Rps2r gene, complete cds |

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 9446 | 22410 | 35847 | 0.44 | 9.6E-01 | AF228943.1 | NT | Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene |
| 11848 | 24731 | 38317 | 3.04 | 9.6E-01 | AV752605.1 | EST_HUMAN | AV752605 NPD Homo sapiens cDNA clone NPDBAG06 5' |
| 11848 | 24731 | 38318 | 3.04 | 9.6E-01 | AV752605.1 | EST_HUMAN | AV752605 NPD Homo sapiens cDNA clone NPDBAG06 5' |
| 12223 | 25060 | | 2.19 | 9.6E-01 | 11421722 | NT | Homo sapiens centrosomal protein 2 (CEP2), mRNA |
| 12839 | 25874 | 31416 | 3.03 | 9.6E-01 | U91423.1 | NT | Sphynx fibro NADH dehydrogenase subunit 2 (NADH2) gene, mitochondrial gene encoding mitochondrial protein, partial cds |
| 2484 | 15488 | 28512 | 1.03 | 9.5E-01 | 7705991 | NT | Homo sapiens CGI-125 protein (LOC51003), mRNA |
| 3796 | 16838 | 29741 | 2.39 | 9.5E-01 | BE902340.1 | EST_HUMAN | 601675639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5' |
| 3796 | 16838 | 29742 | 2.39 | 9.5E-01 | BE902340.1 | EST_HUMAN | 601675639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5' |
| 8364 | 22319 | 35745 | 0.68 | 9.5E-01 | AI90162.1 | EST_HUMAN | q57d07.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1733581 3' |
| 9461 | 22425 | 35863 | 1.1 | 9.5E-01 | AW861102.1 | EST_HUMAN | RC1-CT0286-241199-011-502 CT0286 Homo sapiens cDNA |
| 11574 | 24512 | 38069 | 1.5 | 9.5E-01 | BF218771.1 | EST_HUMAN | 601885163F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103030 5' |
| 11780 | 23935 | 37456 | 1.52 | 9.5E-01 | AW263799.1 | EST_HUMAN | UH-H-B12-shp-f-03-Q-U1-s1 NCI_OGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727677 3' |
| 3214 | 16269 | | 3.77 | 9.4E-01 | AF165990.1 | NT | Bartonella clarridgeiae RNA polymerase beta subunit (rpoB) gene, partial cds |
| 3231 | 16288 | | 1.93 | 9.4E-01 | AF080595.1 | NT | Pimpla brachycarpa zinc finger protein (ZFP1) mRNA, complete cds |
| 9217 | 22183 | 35616 | 0.69 | 9.4E-01 | M90724.1 | NT | Human Fc-gamma-receptorIIA (FCGR2A) gene, exon 4 |
| 12480 | 25235 | | 2.09 | 9.4E-01 | BE781251.1 | EST_HUMAN | 601466703F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3869929 5' |
| 12838 | 25790 | | 1.83 | 9.4E-01 | 11419857 | NT | Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR), mRNA |
| 1745 | 14774 | | 1.34 | 9.3E-01 | AF24282.1 | NT | Homo sapiens phytoeyl-CoA hydroxylase (PHYH) gene, exon 5 |
| 2841 | 15639 | 28663 | 1.01 | 9.3E-01 | BE071172.1 | EST_HUMAN | RC5-BT0503-271199-011-B01 BT0503 Homo sapiens cDNA |
| 4066 | 17102 | 29993 | 0.82 | 9.3E-01 | M20219.1 | NT | Bovine papillomavirus type 2, complete genome |
| 4066 | 17102 | 29994 | 0.82 | 9.3E-01 | M20219.1 | NT | Bovine papillomavirus type 2, complete genome |
| 5673 | 18768 | 31940 | 1.47 | 9.3E-01 | AF213884.1 | NT | Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds |
| 5761 | 18854 | 32034 | 3.92 | 9.3E-01 | L36189.1 | NT | Spodoptera frugiperda methylenetetrahydrofolate dehydrogenase mRNA, complete cds |
| 7554 | 20517 | | 0.76 | 9.3E-01 | AF270648.1 | NT | Plasmodium falciparum mature parasite-infected erythrocyte surface antigen (MESA) gene, complete cds |
| 8402 | 21371 | 34779 | 1.75 | 9.3E-01 | AA847040.1 | EST_HUMAN | 0609P03.s1 NCI_OGAP_OV2 Homo sapiens cDNA clone IMAGE:1385357 |
| 9165 | 22131 | | 0.95 | 9.3E-01 | AF081981.1 | NT | Xenopus laevis CCGH zinc finger protein C3H-2 (C3H-2) mRNA, complete cds |
| 9289 | 22255 | 35685 | 0.91 | 9.3E-01 | AL161534.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 34 |
| 12953 | 25528 | 31713 | 1.34 | 9.3E-01 | 11440298 | NT | Homo sapiens Inositol 1,4,5-triphosphate receptor, type 2 (ITPR2), mRNA |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 12965 | 25534 | | 3.29 | 9.3E-01 | AF271207.1 | NT | Aedes triseriatus putative large subunit ribosomal protein rPL34 mRNA, complete cds |
| 3253 | 16307 | 29231 | 3.14 | 9.2E-01 | BE622702.1 | EST_HUMAN | 601441338T1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916184 3' |
| 5808 | 18886 | | 1.73 | 9.2E-01 | 7108410 | NT | Mus musculus solute carrier family 30 (zinc transporter), member 4 (Slc30a4), mRNA |
| 8101 | 18180 | 32399 | 4.04 | 9.2E-01 | BF037586.1 | EST_HUMAN | 601461153F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3864661 5' |
| 6789 | 18843 | 33127 | 0.51 | 9.2E-01 | M64703.1 | NT | N.crassa valyl-tRNA synthetase (cyt-20/un-3) gene |
| 10018 | 22945 | 36412 | 0.77 | 9.2E-01 | AL161565.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65 |
| 10105 | 23031 | 36509 | 1.21 | 9.2E-01 | 6671677 | NT | Mus musculus carbonic anhydrase 4 (Car4), mRNA |
| 10628 | 23550 | 37050 | 3.42 | 9.2E-01 | 11430963 | NT | Homo sapiens lysosomal apyrase-like protein 1 (LALP1), mRNA |
| 10780 | 23701 | 37199 | 1.84 | 9.2E-01 | BF599251.1 | EST_HUMAN | 7c58e06LX1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3578219 3' similar to SW:NU5M_TRYBB |
| 12031 | 24907 | 38501 | 1.54 | 9.2E-01 | BF132402.1 | EST_HUMAN | P04540 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5; |
| 1629 | 14882 | 27638 | 2.31 | 9.1E-01 | T96875.1 | EST_HUMAN | 601820312F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052018 5' |
| 2134 | 15151 | | 2.06 | 9.1E-01 | 8923056 | NT | ye5201.s1 Soares fetal liver spleen tNFLS Homo sapiens cDNA clone IMAGE:121369 3' similar to contains |
| 2582 | 15583 | 28602 | 1.12 | 9.1E-01 | AF062919.1 | NT | Alu repetitive element; |
| 3218 | 16273 | 29195 | 1.11 | 9.1E-01 | T26418.1 | EST_HUMAN | Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA |
| 3218 | 16273 | 29196 | 1.11 | 9.1E-01 | T26418.1 | EST_HUMAN | Pseudomonas fluorescens DNA polymerase III (dnaE) gene, complete cds |
| 6291 | 19363 | 32802 | 1.68 | 9.1E-01 | L36033.1 | NT | AB200G8R Infant brain, LLNL array of Dr. M. Soares tNIB Homo sapiens cDNA clone LLAB200G8 5' |
| 6555 | 19712 | 32989 | 2.94 | 9.1E-01 | Q61704 | SWISSPROT | AB200G8R Infant brain, LLNL array of Dr. M. Soares tNIB Homo sapiens cDNA clone LLAB200G8 5' |
| 7827 | 20775 | 34152 | 16.4 | 9.1E-01 | AA806623.1 | EST_HUMAN | Human pte-B cell stimulating factor homologue (SDF1b) mRNA, complete cds |
| 8011 | 20949 | 34342 | 2.58 | 9.1E-01 | U72995.1 | NT | INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY CHAIN H3) |
| 10536 | 23458 | 36955 | 0.45 | 9.1E-01 | P38432 | SWISSPROT | ab71g08.s1 NCL CGAP_G081 Homo sapiens cDNA clone IMAGE:1338862 3' |
| 12580 | 25867 | | 10.31 | 9.1E-01 | AF050113.1 | NT | Rattus norvegicus Rab3 GDP/GTP exchange protein mRNA, complete cds |
| 4408 | 17434 | 30319 | 1.77 | 9.0E-01 | AF098810.1 | NT | P80-COILIN |
| 7622 | 20582 | 33946 | 0.65 | 9.0E-01 | L42547.1 | NT | Homo sapiens uncoupling protein-3 (UCP3) gene, complete cds |
| 7652 | 20612 | | 1.32 | 9.0E-01 | D38621.1 | NT | Homo sapiens neuroligin II-alpha gene, partial cds |
| 9704 | 22657 | 36112 | 0.55 | 9.0E-01 | AF086761.1 | NT | Homo sapiens neuroligin II-alpha gene, partial cds |
| 10189 | 23114 | 36598 | 0.44 | 9.0E-01 | U39702.1 | NT | Dentio retro LIM class homeodomain protein (lim5) mRNA, complete cds |
| | | | | | | | Xenopus laevis gene for aldolase, complete cds |
| | | | | | | | Dentio retro semaphorin 21a mRNA, complete cds |
| | | | | | | | Mycoplasma genitalium section 24 of 51 of the complete genome |
| 5781 | 18873 | 32054 | 2.37 | 8.9E-01 | AF028198.1 | NT | Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit> |
| 6377 | 19445 | | 1.28 | 8.9E-01 | X60996.1 | NT | Rabbit MHC fragment RLA-DF DNA |

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 6805 | 25683 | 32937 | 0.69 | 8.9E-01 | BF217939.1 | EST_HUMAN | 601882708F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4096216 5' |
| 6805 | 25683 | 32938 | 0.69 | 8.9E-01 | BF217939.1 | EST_HUMAN | 601882708F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4096216 5' |
| 7408 | 20375 | | 0.54 | 8.9E-01 | AB042297.1 | NT | Homo sapiens PTS gene for 6-pyruvoyl-tetrahydropterin synthase, complete cds |
| 8553 | 21521 | | 0.43 | 8.9E-01 | AF260225.1 | NT | Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced |
| 8769 | 21736 | 35167 | 1.09 | 8.9E-01 | AF259687.1 | NT | Chthona nana cytochrome-c oxidase subunit I (cod) gene, partial cds; mitochondrial gene for mitochondrial product |
| 12074 | 24948 | 38541 | 2.99 | 8.9E-01 | AE003944.1 | NT | Xylella fastidiosa, section 90 of 229 of the complete genome |
| 12420 | 25190 | | 5.46 | 8.9E-01 | AE002186.2 | NT | Chlamydia pneumoniae AR39, section 21 of 94 of the complete genome |
| 4573 | 17595 | 30489 | 1.58 | 8.8E-01 | O26350 | SWISSPROT | PUTATIVE F420-DEPENDENT NADP REDUCTASE |
| 5238 | 18246 | 31118 | 0.9 | 8.8E-01 | L41654.1 | NT | Trypanosoma brucei microtubule-associated protein (MAPP15) mRNA, 3' end of cds |
| 5447 | 18549 | 31462 | 0.7 | 8.8E-01 | AF310617.1 | NT | Pseudorabies virus Ea glycoprotein M gene, complete cds |
| 11418 | 24362 | 37897 | 2.31 | 8.8E-01 | Z28337.1 | NT | Maeruginosa (HUB 5-2-4) DNA from plasmid PMA1 |
| 12082 | 24954 | 38549 | 6.51 | 8.8E-01 | AA808055.1 | EST_HUMAN | cc38h11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1352037 3' similar to contains Alu repetitive element; contains element MER22 repetitive element ; |
| 12237 | 25952 | | 2.3 | 8.8E-01 | D90911.1 | NT | Synechocystis sp. PCC6803 complete genome, 13/27, 1576593-1719643 |
| 465 | 13538 | 26464 | 1.78 | 8.7E-01 | AF106953.2 | NT | Homo sapiens SOS1 (SOS1) gene, partial cds |
| 2411 | 15418 | 28442 | 0.91 | 8.7E-01 | 5901893 | NT | Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA |
| 2885 | 15944 | 28859 | 5.42 | 8.7E-01 | AA595863.1 | EST_HUMAN | nn05f11.s1 NCI_CGAP_P4.1 Homo sapiens cDNA clone IMAGE:1076877 |
| | | | | | | | Pseudomonas aeruginosa topoisomerase (top), putative transcriptional regulatory protein OhbR (ohbR), ortho-halobenzoate 1,2-dioxygenase beta-ISP protein OhbA (ohbA), OhbC (ohbC), ortho-halobenzoate 1,2-dioxygenase alpha-ISP protein OhbB (ohbB), and put> |
| 5043 | 18056 | | 2.78 | 8.7E-01 | AF121970.1 | NT | halobenzoate 1,2-dioxygenase (top), putative transcriptional regulatory protein OhbR (ohbR), ortho-halobenzoate 1,2-dioxygenase alpha-ISP protein OhbB (ohbB), and put> |
| 5247 | 18255 | 31125 | 0.97 | 8.7E-01 | BF219308.1 | EST_HUMAN | 601883175F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4096378 5' |
| 8374 | 21343 | 34754 | 0.65 | 8.7E-01 | AW897335.1 | EST_HUMAN | RC4-NN0057-120500-013-c07 NN0057 Homo sapiens cDNA |
| 9282 | 22248 | 35677 | 0.71 | 8.7E-01 | A1239456.1 | EST_HUMAN | qt39e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1846786 3' |
| 9282 | 22248 | 35678 | 0.71 | 8.7E-01 | A1239456.1 | EST_HUMAN | qt39e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1846786 3' |
| 10095 | 23021 | 36496 | 1.32 | 8.7E-01 | AE004963.1 | NT | Pseudomonas aeruginosa PA01, section 524 of 529 of the complete genome |
| 11181 | 24137 | 37669 | 4.56 | 8.7E-01 | BF363970.1 | EST_HUMAN | QV0-NN1021-100800-337-c03 NN1021 Homo sapiens cDNA |
| 12042 | 24917 | 38512 | 3.97 | 8.7E-01 | BF107694.1 | EST_HUMAN | 601823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3' |
| 12042 | 24917 | 38513 | 3.97 | 8.7E-01 | BF107694.1 | EST_HUMAN | 601823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3' |
| 475 | 13547 | | 2.65 | 8.6E-01 | X17012.1 | NT | Rat IGFI gene for insulin-like growth factor II |
| 859 | 13915 | 26874 | 4.32 | 8.6E-01 | W69089.1 | EST_HUMAN | zd44e03.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:343516 5' |
| | | | 1 | 8.6E-01 | 4503210 | NT | Homo sapiens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA |
| 2278 | 15291 | 28316 | | | | | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65 |
| 3635 | 16878 | 29592 | 0.87 | 8.6E-01 | AL161565.2 | NT | |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 3813 | 18853 | 28760 | 1.38 | 8.6E-01 | U49724.1 | NT | Drosophila melanogaster merlin (Dmerlin) mRNA, complete cds |
| 5207 | 18216 | 31081 | 2.6 | 8.6E-01 | BE147609.1 | EST_HUMAN | RC1-HT0228-160300-019-c05 HT0229 Homo sapiens cDNA |
| 6001 | 19084 | 32283 | 7.79 | 8.6E-01 | X00547.1 | NT | Chicken lipoprotein lipase gene |
| 6001 | 19084 | 32284 | 7.79 | 8.6E-01 | X60547.1 | NT | Chicken lipoprotein lipase gene |
| 6515 | 25661 | 32835 | 0.54 | 8.6E-01 | S76772.1 | NT | polyprotein [Coxsackie B4 virus CB4, host=mice, E2, originally derived from Edwards CB4 human strain, Genomic RNA Complete, 7397 nt] |
| 6887 | 19920 | 33215 | 1.7 | 8.6E-01 | AF143732.1 | NT | Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds |
| 6887 | 19920 | 33216 | 1.7 | 8.6E-01 | AF143732.1 | NT | Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds |
| 7770 | 20723 | | 0.81 | 8.6E-01 | AE000591.1 | NT | Helicobacter pylori 26695 section 69 of 134 of the complete genome |
| 8260 | 21229 | | 1.29 | 8.6E-01 | AP001518.1 | NT | Bacillus halodurans genomic DNA, section 12/14 |
| 8377 | 21346 | 34757 | 0.51 | 8.6E-01 | AF077837.1 | NT | Drosophila melanogaster collapsin response mediator protein (CRMP) mRNA, complete cds |
| 10044 | 22971 | | 0.49 | 8.6E-01 | AE000979.1 | NT | Archaeoglobus fulgidus section 128 of 172 of the complete genome |
| 12798 | 25717 | | 1.44 | 8.6E-01 | AL112162.1 | NT | Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation |
| 6888 | 19940 | 33235 | 1.5 | 8.5E-01 | AF165214.1 | NT | Bacteriophage D3, complete genome |
| 7768 | 20721 | 34093 | 2.49 | 8.5E-01 | BE542612.1 | EST_HUMAN | 601067107F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453505 5' |
| 8323 | 21292 | 34708 | 0.42 | 8.5E-01 | AL161572.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68 |
| 8761 | 21728 | 35150 | 0.93 | 8.5E-01 | P06601 | SWISSPROT | SEGMENTATION PROTEIN PAIRED |
| 8761 | 21728 | 35151 | 0.93 | 8.5E-01 | P06601 | SWISSPROT | SEGMENTATION PROTEIN PAIRED |
| 8849 | 21816 | 35236 | 0.57 | 8.5E-01 | AJ243213.1 | NT | Homo sapiens partial 6-HT4 receptor gene, exons 2 to 5 |
| 10715 | 23637 | 37129 | 1.35 | 8.5E-01 | AB006799.1 | NT | Cyanidium caldarium gene for SigC, complete cds |
| 10715 | 23637 | 37130 | 1.35 | 8.5E-01 | AB006799.1 | NT | Cyanidium caldarium gene for SigC, complete cds |
| 12565 | 25869 | | 2.25 | 8.5E-01 | 11418543 | NT | Homo sapiens human immunodeficiency virus type 1 enhancer-binding protein 1 (HIVEP1), mRNA |
| 12572 | 25283 | | 1.37 | 8.5E-01 | 9507008 | NT | Rattus norvegicus protein tyrosine phosphatase, non-receptor type 5 (Ptpn6), mRNA |
| 4782 | 17802 | 30893 | 0.85 | 8.4E-01 | AF083975.2 | NT | Fowl adenovirus 8, complete genome |
| 5571 | 25641 | 31627 | 2.68 | 8.4E-01 | L78726.1 | NT | Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7 |
| 5571 | 25641 | 31628 | 2.68 | 8.4E-01 | L78726.1 | NT | Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7 |
| 8107 | 21044 | 34443 | 0.51 | 8.4E-01 | AF051142.1 | NT | Mamestra brassicae pheromone binding protein 2 precursor (PBP2) mRNA, complete cds |
| 10317 | 23241 | | 3.25 | 8.4E-01 | AJ248287.1 | NT | Pyrococcus abyssi complete genome; segment 5/8 |
| 12005 | 24882 | 38478 | 1.54 | 8.4E-01 | M55584.1 | NT | Human collagenase type IV (CLG4) gene, exon 4 |
| 743 | 13804 | 26743 | 3.01 | 8.3E-01 | MP8437.1 | NT | Thermus thermophilus cytochrome c-552 (cycB) and CycB (cycB) genes, complete cds |
| 3111 | 16168 | 29078 | 3.15 | 8.3E-01 | AL161506.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18 |
| 3823 | 16863 | 29767 | 0.83 | 8.3E-01 | AB010879.1 | NT | Nicotiana tabacum mRNA for chloroplast ribosomal protein L10, complete cds |
| 4040 | 17078 | 28978 | 3.15 | 8.3E-01 | Y19177.1 | NT | Streptomyces antibioticus polyketide biosynthetic gene cluster |
| 5341 | 18446 | 31199 | 2.42 | 8.3E-01 | AL161540.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40 |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 10028 | 22955 | | 4.53 | 8.3E-01 | AI791952.1 | EST_HUMAN | nr01f12.y5 NCI CGAP_Co9 Homo sapiens cDNA clone IMAGE:1076495 5' similar to contains THR.t1 THR repetitive element; |
| 10489 | 23391 | 36886 | 1.1 | 8.3E-01 | AF098070.1 | NT | Drosophila melanogaster Lis1 homolog mRNA, complete cds |
| 10579 | 23501 | 36993 | 3.97 | 8.3E-01 | AF108133.1 | NT | Mus musculus neuro-d4 gene, exons 3 through 12 and partial cds |
| 11033 | 23997 | 37524 | 2.97 | 8.3E-01 | AE000903.1 | NT | Methanobacterium thermoautotrophicum from bases 1270510 to 1283409 (section 109 of 148) of the complete genome |
| 11050 | 24013 | | 1.92 | 8.3E-01 | 7212472 | NT | Phytophthora infestans mitochondrion, complete genome |
| 11634 | 24571 | 38136 | 2.22 | 8.3E-01 | AF020503.1 | NT | Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5 |
| 2068 | 15085 | 28103 | 2.24 | 8.2E-01 | AB000489.1 | NT | Rattus norvegicus mRNA for RPHO-1, complete cds |
| 2101 | 15118 | | 1.08 | 8.2E-01 | AF145589.1 | NT | Mus musculus trophinin (Tnn) gene, complete cds |
| 2688 | 15684 | | 1.06 | 8.2E-01 | AW376990.1 | EST_HUMAN | IL3-CT0219-161199-031-C08 CT0219 Homo sapiens cDNA |
| 3918 | 16988 | 28871 | 0.75 | 8.2E-01 | AB014574.1 | NT | Homo sapiens mRNA for KIAA0674 protein, partial cds |
| 3940 | 16980 | 28895 | 0.92 | 8.2E-01 | AF063417.1 | NT | Tanystylum orbiculare elongation factor 1-alpha mRNA, partial cds |
| 6800 | 19854 | 33139 | 0.57 | 8.2E-01 | X95283.1 | NT | G.gallus mRNA for C-Serrat-1 protein |
| 6800 | 19854 | 33140 | 0.57 | 8.2E-01 | X95283.1 | NT | G.gallus mRNA for C-Serrat-1 protein |
| 6941 | 20165 | 33498 | 0.85 | 8.2E-01 | AJ010142.1 | NT | Amanita muscaria mRNA for SCII25 protein |
| 7082 | 20103 | 33414 | 3.69 | 8.2E-01 | AW379433.1 | EST_HUMAN | CM4-H10243-081199-037-e01 HT0243 Homo sapiens cDNA |
| 7484 | 25682 | 33807 | 4.38 | 8.2E-01 | Z12126.1 | NT | S.cerevisiae MET, LEU4, and POL1 genes encoding MET4 protein, alpha-isopropylmalate (alpha-IPM) synthetase (partial), and DNA polymerase alpha (partial) |
| 8787 | 21784 | 35176 | 0.58 | 8.2E-01 | BE263145.1 | EST_HUMAN | 601144885F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160412 5' |
| 10385 | 23307 | 36785 | 0.66 | 8.2E-01 | AB014530.1 | NT | Homo sapiens mRNA for KIAA0630 protein, partial cds |
| 10419 | 23341 | 36827 | 1.59 | 8.2E-01 | AF032699.1 | NT | Homo sapiens thioredoxin-related protein mRNA, complete cds |
| 10583 | 23505 | 36998 | 0.59 | 8.2E-01 | AF223888.1 | NT | Oncorhynchus tshawytscha isolate T-20 somatolactin precursor gene, exon 1 |
| 10583 | 23505 | 36999 | 0.59 | 8.2E-01 | AF223888.1 | NT | Oncorhynchus tshawytscha isolate T-20 somatolactin precursor gene, exon 1 |
| 10751 | 23673 | 37169 | 3.84 | 8.2E-01 | Q9J170 | SWISSPROT | MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN |
| 10751 | 23673 | 37170 | 3.84 | 8.2E-01 | Q9J170 | SWISSPROT | MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN |
| 11957 | 24836 | 38432 | 2.97 | 8.2E-01 | L10127.1 | NT | Mollusca contagiosum virus type 1 ORF1 and ORF2 DNA |
| 12038 | 24913 | 38507 | 4.82 | 8.2E-01 | P10383 | SWISSPROT | OVARIAN TUMOR LOCUS PROTEIN |
| 12043 | 24918 | 38514 | 6.1 | 8.2E-01 | H87398.1 | EST_HUMAN | yw14d02.r1 Soares_placenta_8t69weeks_2NHP8t69W Homo sapiens cDNA clone IMAGE:262195 5' similar to gb:M36072 60S RIBOSOMAL PROTEIN L7A (HUMAN); |
| 12586 | 25290 | -31781 | 2.98 | 8.2E-01 | AJ001261.1 | NT | Mus musculus mRNA for NIPSNAP2 protein |
| 2769 | 15761 | | 1.48 | 8.1E-01 | AF191839.1 | NT | Mus musculus TANK binding kinase TBK1 (Tbkt) mRNA, complete cds |
| 3472 | 16518 | 29439 | 3.67 | 8.1E-01 | AF055066.1 | NT | Homo sapiens MHC class 1 region |

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| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 3472 | 16518 | 29440 | 3.67 | 8.1E-01 | AF05086.1 | NT | Homo sapiens MHC class 1 region |
| 5792 | 18884 | 32068 | 0.51 | 8.1E-01 | Q01727 | SWISSPROT | MELANOCYTE STIMULATING HORMONE RECEPTOR (MSH-R) (MELANOTROPIN RECEPTOR) |
| 6448 | 19513 | 32763 | 0.84 | 8.1E-01 | U16790.1 | NT | (MELANOCORTIN-1 RECEPTOR) (MC1-R) |
| 6777 | 19832 | 33114 | 2.47 | 8.1E-01 | Q13491 | SWISSPROT | Mus musculus putative collagen alpha-2(XI) chain (COL11A2) gene, partial cds |
| 6777 | 19832 | 33115 | 2.47 | 8.1E-01 | Q13491 | SWISSPROT | NEURONAL MEMBRANE GLYCOPROTEIN M6-B |
| 7755 | 20708 | 34077 | 0.55 | 8.1E-01 | O47477 | SWISSPROT | NEURONAL MEMBRANE GLYCOPROTEIN M6-B |
| | | | | | | | CYTCHROME B |
| 8243 | 21212 | 34818 | 1.12 | 8.1E-01 | AF022713.2 | NT | Drosophila melanogaster putative inorganic phosphate cotransporter (Picot) gene, partial cds; putative sodium channel (Nach) and putative amylase-related protein (Amyrel) genes, complete cds; and putative serine-enriched protein (gprs) gene, partial cds |
| 8243 | 21212 | 34819 | 1.12 | 8.1E-01 | AF022713.2 | NT | Drosophila melanogaster putative inorganic phosphate cotransporter (Picot) gene, partial cds; putative sodium channel (Nach) and putative amylase-related protein (Amyrel) genes, complete cds; and putative serine-enriched protein (gprs) gene, partial cds |
| 8956 | 21922 | 35348 | 0.91 | 8.1E-01 | AP001517.1 | NT | enriched protein (gprs) gene, partial cds |
| 8956 | 21922 | 35350 | 0.91 | 8.1E-01 | AP001517.1 | NT | Bacillus halodurans genomic DNA, section 11/14 |
| | | | | | | | Bacillus halodurans genomic DNA, section 11/14 |
| 9122 | 22088 | 35516 | 1.13 | 8.1E-01 | AW242647.1 | EST_HUMAN | xn01h03.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2682469 3' similar to SW:LYAR_MOUSE |
| 10484 | 23406 | 36902 | 0.64 | 8.1E-01 | P06425 | SWISSPROT | Q06288 CELL GROWTH REGULATING NUCLEOLAR PROTEIN; contains MER22.b1 PTR5 repetitive element; |
| | | | | | | | PROBABLE E4 PROTEIN |
| 10776 | 23697 | 37195 | 0.42 | 8.1E-01 | N84541.1 | EST_HUMAN | KK9872F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone KK9872 5' similar to |
| 11812 | 24697 | 38277 | 4.05 | 8.1E-01 | BE938558.1 | EST_HUMAN | EST(CLONE C-OPE11) |
| 11812 | 24697 | 38278 | 4.05 | 8.1E-01 | BE938558.1 | EST_HUMAN | RC0-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA |
| 12298 | 25109 | 31839 | 1.73 | 8.1E-01 | AE001711.1 | NT | RC0-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA |
| 178 | 13279 | | 3.32 | 8.0E-01 | AJ271510.1 | NT | Thermotoga maritima section 23 of 136 of the complete genome |
| 288 | 13383 | 26310 | 5.97 | 8.0E-01 | AJ132772.1 | NT | Staphylococcus aureus partial pla gene for phosphate acetyltransferase allele 15 |
| 2051 | 15070 | | 1.72 | 8.0E-01 | BF530962.1 | EST_HUMAN | Staphylococcus aureus partial pla gene for phosphate acetyltransferase allele 15 |
| 3093 | 16151 | 29065 | 1.41 | 8.0E-01 | AF127897.1 | NT | Bos taurus tub and rif genes |
| 3324 | 16375 | 29296 | 1.3 | 8.0E-01 | AB008183.1 | NT | 602072473F1 NCL_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:421509 5' |
| 3717 | 16760 | | 2.36 | 8.0E-01 | AL162758.2 | NT | 602072473F1 NCL_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:421509 5' |
| 4563 | 17586 | 30478 | 6.45 | 8.0E-01 | X83739.2 | NT | Saimiri boliviensis olfactory receptor (SBO27) gene, partial cds |
| 8322 | 21291 | | 2.31 | 8.0E-01 | AW901489.1 | EST_HUMAN | Mus musculus gene for olfactory glycoprotein, complete cds |
| 8870 | 21837 | 35259 | 1.05 | 8.0E-01 | Y11095.1 | NT | Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 717 |
| | | | | | | | G.gallus mRNA for nicotinic acetylcholine receptor (nAChR) beta 3 subunit |
| 11303 | 24253 | 37779 | 1.58 | 8.0E-01 | Q92793 | SWISSPROT | RC0-NN1012-270300-021-h06 NN1012 Homo sapiens cDNA |
| | | | | | | | Rice stripe virus RNA 3 |
| | | | | | | | CREB-BINDING PROTEIN |

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|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 454 | 13527 | 26457 | 0.78 | 7.9E-01 | D11476.1 | NT | Lymantria dispar nuclear polyhedrosis virus gene for DNA polymerase, complete cds |
| 716 | 13778 | | 0.78 | 7.9E-01 | AE002130.1 | NT | Ureaplasma urealyticum section 31 of 59 of the complete genome |
| 1609 | 14641 | | 23.05 | 7.9E-01 | AB040885.1 | NT | Homo sapiens mRNA for KIAA1452 protein, partial cds |
| 1663 | 14695 | | 1.28 | 7.9E-01 | U32739.1 | NT | Haemophilus influenzae Rd section 54 of 163 of the complete genome |
| 2272 | 15285 | 28311 | 7.38 | 7.9E-01 | AB004816.1 | NT | Oryctolagus cuniculus mRNA for mitsugumin28, complete cds |
| 2273 | 15286 | 28312 | 2.36 | 7.9E-01 | AF130459.1 | NT | Danio rerio Tap4-associated protein Tap1A (tap1A) mRNA, complete cds |
| 3528 | 16574 | 28497 | 3 | 7.9E-01 | AF228664.1 | NT | Gallus gallus SOXB transcription factor (SOXB) mRNA, complete cds |
| 4330 | 17358 | | 0.88 | 7.9E-01 | BE263612.1 | EST_HUMAN | 601192033F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535785 5' |
| 4642 | 17663 | 30551 | 1.15 | 7.9E-01 | 6753745 | NT | Mus musculus embigin (Emb), mRNA |
| 4642 | 17663 | 30552 | 1.15 | 7.9E-01 | 6753745 | NT | Mus musculus embigin (Emb), mRNA |
| 5244 | 18252 | 31123 | 1.03 | 7.9E-01 | AF229943.1 | NT | Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene |
| 6478 | 19544 | 32792 | 0.76 | 7.9E-01 | D38145.1 | NT | Human mRNA for prostacyclin synthase, complete cds |
| 8446 | 21415 | 34828 | 3.37 | 7.9E-01 | X90996.1 | NT | P. sativum GR gene |
| 8905 | 22857 | 36319 | 4.3 | 7.9E-01 | U01912.1 | NT | Giardia lamblia variant-specific surface protein G3M-B (vspG3M-B) mRNA, partial cds |
| 10409 | 23331 | 36816 | 4.3 | 7.9E-01 | P19719 | SWISSPROT | SMALL HYDROPHOBIC PROTEIN |
| 10451 | 23373 | 36864 | 0.82 | 7.9E-01 | AV700860.1 | EST_HUMAN | AV700860 GKC Homo sapiens cDNA clone GKCDRE12 3' |
| 10877 | 23787 | 37298 | 0.82 | 7.9E-01 | AB000631.1 | NT | Streptococcus mutans DNA for sigma 42 protein, dTDP-4-keto-L-rhamnose reductase, complete cds |
| 11350 | 24300 | | 2.81 | 7.9E-01 | 7662471 | NT | Homo sapiens KIAA1072 protein (KIAA1072), mRNA |
| 11546 | 24487 | 38041 | 2.22 | 7.9E-01 | P19022 | SWISSPROT | NEURAL-CADHERIN PRECURSOR (N-CADHERIN) |
| 877 | 13932 | | 1.96 | 7.8E-01 | Z43785.1 | EST_HUMAN | HSC1KH041 normalized infant brain cDNA Homo sapiens cDNA clone c-1kh04 |
| 2283 | 15296 | 28320 | 6.12 | 7.8E-01 | AW959567.1 | EST_HUMAN | EST371637 MAGE resequences, MAGF Homo sapiens cDNA |
| 4730 | 17750 | 30642 | 1.33 | 7.8E-01 | U87305.1 | NT | Rattus norvegicus transmembrane receptor Unc5H1 mRNA, complete cds |
| 5075 | 18085 | | 0.8 | 7.8E-01 | AW753353.1 | EST_HUMAN | RC3-C10254-130100-023-c02 C10254 Homo sapiens cDNA |
| 6187 | 19262 | 32498 | 2.5 | 7.8E-01 | AF115856.1 | NT | Sphenodon punctatus alpha endase mRNA, partial cds |
| 6344 | 19413 | 32655 | 1.04 | 7.8E-01 | P05231 | SWISSPROT | INTERLEUKIN-6 PRECURSOR (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2) (INTERFERON BETA-2) (HYBRIDOMA GROWTH FACTOR) |
| 6806 | 19694 | 32839 | 0.72 | 7.8E-01 | AL445066.1 | NT | Thermoplasma acidophilum complete genome, segment 4/5 |
| 8836 | 21803 | 35221 | 1.29 | 7.8E-01 | BF108927.1 | EST_HUMAN | 7154d05.x1 Soares NSF_FB_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525178 3' |
| 9589 | 22551 | 36002 | 1.34 | 7.8E-01 | Y10159.1 | NT | D. discoideum racGAP gene |
| 9687 | 22640 | 36097 | 0.52 | 7.8E-01 | 4826873 | NT | Homo sapiens nucleoporin 214kD (CAIN) (NUP214), mRNA |
| 10483 | 23405 | | 1.01 | 7.8E-01 | Q25452 | SWISSPROT | MUSCLE CALCIUM CHANNEL ALPHA-1 SUBUNIT (MDL-ALPHA1) |

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|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 12559 | 25948 | | 2.32 | 7.8E-01 | L28280.1 | NT | Arabidopsis thaliana 1-amino-1-cyclopropanecarboxylate synthase (ACS5) gene, complete cds |
| 145 | 13248 | 26177 | 6.69 | 7.7E-01 | AF184345.1 | NT | Lycopersicon hirsutum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds |
| 727 | 13788 | | 3.26 | 7.7E-01 | AF050157.1 | NT | Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (Aa1pha) and major histocompatibility protein class II beta chain (Ib2eta) genes, complete cds; butyrophilin-like (NG9), butyrophilin-1² |
| 2724 | 15718 | 28736 | 2 | 7.7E-01 | O33915 | SWISSPROT | CITRATE SYNTHASE |
| 3368 | 18418 | | 0.76 | 7.7E-01 | 8393408 | NT | Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GALNAc-T7) (GALNAC-T7), mRNA |
| 3614 | 16658 | 29576 | 3.83 | 7.7E-01 | AF118085.1 | NT | Homo sapiens PRO1975 mRNA, complete cds |
| 4425 | 17452 | 30343 | 3.04 | 7.7E-01 | AF199488.1 | NT | Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds |
| 4425 | 17452 | 30344 | 3.04 | 7.7E-01 | AF199488.1 | NT | Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds |
| 5640 | 18736 | 31899 | 1.25 | 7.7E-01 | P16553 | SWISSPROT | RAFFINOSE INVERTASE (INVERTASE) |
| 5640 | 18736 | 31900 | 1.25 | 7.7E-01 | P16553 | SWISSPROT | RAFFINOSE INVERTASE (INVERTASE) |
| 6066 | 19147 | 32359 | 0.53 | 7.7E-01 | R08600.1 | EST_HUMAN | yf24b02.s1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127755 3' |
| 10204 | 23129 | 36616 | 0.72 | 7.7E-01 | AB021134.1 | NT | Daphnia magna hemoglobin gene cluster (dhb3, dhb1 and dhb2 genes), complete cds |
| 12447 | 25207 | | 5.53 | 7.7E-01 | 11497621 | NT | Archaeoglobus fulgidus, complete genome |
| 6218 | 19282 | 32525 | 4.49 | 7.6E-01 | AF059510.1 | NT | Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds |
| 6218 | 19282 | 32526 | 4.49 | 7.6E-01 | AF059510.1 | NT | Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds |
| 6667 | 19724 | 32999 | 0.65 | 7.6E-01 | P37938 | SWISSPROT | MATING-TYPE PROTEIN A-ALPHA Z4 |
| 7029 | 18361 | 31248 | 0.98 | 7.6E-01 | A1253399.1 | EST_HUMAN | aq14b12.x1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030879 |
| 7029 | 18361 | 31282 | 0.98 | 7.6E-01 | A1253399.1 | EST_HUMAN | aq14b12.x1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030879 |
| 7252 | 19987 | 33295 | 0.89 | 7.6E-01 | U72487.1 | NT | Rattus norvegicus calcium-independent alpha-lactalbumin receptor mRNA, complete cds |
| 8400 | 21369 | 34778 | 1.33 | 7.6E-01 | AF146793.2 | NT | Mus musculus neuromedin U precursor (Nmu) gene, partial cds; iPLP (Tphlp) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (Pft27) gene, complete cds; and H5AR (H5ar) gene, complete cds |
| 8464 | 21433 | 34849 | 1.92 | 7.6E-01 | 8857752 | NT | Mus musculus advinin (Advin-pending), mRNA |
| 8464 | 21433 | 34850 | 1.92 | 7.6E-01 | 8857752 | NT | Mus musculus advinin (Advin-pending), mRNA |
| 8668 | 21636 | 35058 | 0.43 | 7.6E-01 | Q01098 | SWISSPROT | GLUTAMATE (NMDA) RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C) |
| 8668 | 21636 | 35059 | 0.43 | 7.6E-01 | Q01098 | SWISSPROT | GLUTAMATE (NMDA) RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C) |

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| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 9318 | 22263 | 35714 | 1.01 | 7.6E-01 | 6753577 | NT | Mus musculus cytochrome P450, 2b9, phenobarbital inducible, type a (Cyp2b9), mRNA |
| 9634 | 22578 | 36026 | 5.25 | 7.6E-01 | P30372 | SWISSPROT | MUSCARINIC ACETYLCHOLINE RECEPTOR M2 |
| 9634 | 22578 | 36029 | 5.25 | 7.6E-01 | P30372 | SWISSPROT | MUSCARINIC ACETYLCHOLINE RECEPTOR M2 |
| 11685 | 24651 | 38229 | 2.09 | 7.6E-01 | X86347.1 | NT | H. aspersa mRNA for neurofilament NF70 |
| 11685 | 24651 | 38230 | 2.09 | 7.6E-01 | X86347.1 | NT | H. aspersa mRNA for neurofilament NF70 |
| 12020 | 24897 | | 3.05 | 7.6E-01 | AL161592.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 88 |
| 12203 | 25045 | | 3.8 | 7.6E-01 | AB020702.1 | NT | Homo sapiens mRNA for KIAA0895 protein, partial cds |
| 514 | 13585 | | 1.67 | 7.5E-01 | AL163301.2 | NT | Homo sapiens chromosome 21 segment HS21C101 |
| 586 | 13654 | 26568 | 1.01 | 7.5E-01 | AF020503.1 | NT | Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5 |
| 7764 | 20717 | 34090 | 0.78 | 7.5E-01 | AF052730.1 | NT | Drosophila melanogaster tyrosine kinase receptor protein (eph) mRNA, complete cds |
| 12516 | 25247 | | 4.53 | 7.5E-01 | AF163151.2 | NT | Homo sapiens dentin sialophosphoprotein precursor (DSPP) gene, complete cds |
| 13027 | 25575 | 31697 | 1.57 | 7.5E-01 | AE000823.1 | NT | Methanobacterium thermoautotrophicum from bases 317350 to 328792 (section 29 of 148) of the complete genome |
| 1132 | 14175 | 27124 | 1.35 | 7.4E-01 | AI598146.1 | EST_HUMAN | h14b09.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167577 3' similar to contains Alu repetitive element; contains element MIR repetitive element; |
| 2350 | 15359 | 28381 | 0.93 | 7.4E-01 | AB011106.1 | NT | Homo sapiens mRNA for KIAA0534 protein, partial cds |
| 3739 | 16781 | 29693 | 18.81 | 7.4E-01 | AF112538.1 | NT | Malva pusilla actin (Act1) mRNA, complete cds |
| 3919 | 16959 | 29872 | 2.01 | 7.4E-01 | AF133310.1 | NT | Vibrio cholerae phage CTXphi Calcutta-rsR-a (rsR-a) and Calcutta-rsR-b (rsR-b) genes, complete cds |
| 4340 | 17367 | 30250 | 6.99 | 7.4E-01 | AL163246.2 | NT | Homo sapiens chromosome 21 segment HS21C046 |
| 8176 | 21146 | 34553 | 1.04 | 7.4E-01 | AL161551.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51 |
| 8176 | 21146 | 34554 | 1.04 | 7.4E-01 | AL161551.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51 |
| 8980 | 21946 | 35370 | 0.78 | 7.4E-01 | BF346266.1 | EST_HUMAN | 602018456F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4154340 5' |
| 9063 | 22029 | | 0.64 | 7.4E-01 | U87980.1 | NT | Rattus norvegicus leukocyte common antigen receptor (LAR) gene, trans-spliced alternative untranslated exon |
| 9452 | 22416 | 35854 | 7.09 | 7.4E-01 | BE747503.1 | EST_HUMAN | 601573026F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834174 5' |
| 9511 | 22474 | 35918 | 1.14 | 7.4E-01 | AA187986.1 | EST_HUMAN | zp67h01.s1 Stratiogene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:625297 3' similar to SW:TCPO_MOUSE_P42932 T-COMPLEX PROTEIN 1, THE TA SUBUNIT ; |
| 10767 | 23688 | 37185 | 0.74 | 7.4E-01 | 11424933 | NT | Homo sapiens NY-REN-45 antigen (LOC51133), mRNA |
| 12171 | 25021 | | 4.46 | 7.4E-01 | 6753217 | NT | Mus musculus complement component 1 inhibitor (C1inh), mRNA |
| 12284 | 25101 | | 1.54 | 7.4E-01 | AI472641.1 | EST_HUMAN | ta13h01.x1 NCI_CGAP_Lym5 Homo sapiens cDNA clone IMAGE:2043985 3' |
| 3999 | 17038 | | 0.64 | 7.3E-01 | AP000062.1 | NT | Aeropyrum pernix genomic DNA, section 5/7 |
| 4647 | 17668 | 30555 | 0.97 | 7.3E-01 | AE001166.1 | NT | Borrelia burgdorferi (section 52 of 70) of the complete genome |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 4729 | 17749 | 30641 | 4.57 | 7.3E-01 | AF225421.1 | NT | Homo sapiens HT017 mRNA, complete cds |
| 5135 | 18144 | 31024 | 1.18 | 7.3E-01 | O43103 | SWISSPROT | FERRICHRONE SIDEROPHORE PEPTIDE SYNTHETASE |
| 6761 | 19815 | 33094 | 6.03 | 7.3E-01 | L35772.1 | NT | Mus musculus antigen (CD72) gene |
| 6761 | 19815 | 33095 | 6.03 | 7.3E-01 | L35772.1 | NT | Mus musculus antigen (CD72) gene |
| 7301 | 26879 | 33608 | 0.92 | 7.3E-01 | AJ011418.1 | NT | Lycopodium esculentum mRNA for ubiquitin activating enzyme |
| 7692 | 20650 | 34014 | 0.53 | 7.3E-01 | Z14133.1 | NT | D.melanogaster Chc mRNA for clathrin heavy chain |
| 7794 | 20746 | 34119 | 7.46 | 7.3E-01 | M26511.1 | NT | V.alginolyticus sucrose (scrB) gene, complete cds |
| 7794 | 20746 | 34120 | 7.46 | 7.3E-01 | M26511.1 | NT | V.alginolyticus sucrose (scrB) gene, complete cds |
| 8115 | 21052 | 34450 | 0.51 | 7.3E-01 | U34631.1 | NT | Mus musculus alpha-4 integrin gene, exon 7 |
| 11759 | 24687 | 38287 | 3.11 | 7.3E-01 | AA678019.1 | EST_HUMAN | 225b08.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:431799.3 |
| 11759 | 24687 | 38268 | 3.11 | 7.3E-01 | AA678019.1 | EST_HUMAN | 225b08.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:431799.3 |
| 832 | 13889 | | 2.03 | 7.2E-01 | L29281.1 | NT | Rattus norvegicus initiation factor-2 kinase (eIF-2a) mRNA, complete cds |
| 1974 | 14995 | 27997 | 3.23 | 7.2E-01 | X79140.1 | NT | N.tabacum Nelf-4A13 mRNA |
| 2488 | 15472 | 28495 | 1.91 | 7.2E-01 | AB009605.1 | NT | Gallus gallus gene for melanocortin 2-receptor, complete cds |
| 3080 | 18137 | 29048 | 1.47 | 7.2E-01 | AF198100.1 | NT | Fowlpox virus, complete genome |
| 3487 | 18513 | 29434 | 2.44 | 7.2E-01 | AF066606.1 | NT | Giardia intestinalis variant-specific surface protein (vsp417-6) gene, vsp417-6(A-1 allele, complete cds |
| 4803 | 17820 | 30714 | 2.99 | 7.2E-01 | D90314.1 | NT | L.mesenteroides gene for sucrose phosphorylase (EC 2.4.1.7) |
| 5159 | 18168 | 31046 | 1.57 | 7.2E-01 | AF196779.1 | NT | Homo sapiens transcription factor IGHM enhancer 3, JIM11 protein, JIM4 protein, JIM5 protein, T54 protein, JIM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 8, and synaptophysin genes, complete cds; and L-type calcium channel a2 |
| 5159 | 18168 | 31047 | 1.57 | 7.2E-01 | AF196779.1 | NT | Homo sapiens transcription factor IGHM enhancer 3, JIM11 protein, JIM4 protein, JIM5 protein, T54 protein, JIM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 8, and synaptophysin genes, complete cds; and L-type calcium channel a2 |
| 7421 | 20388 | 33739 | 0.78 | 7.2E-01 | U98633.1 | NT | Solanum tuberosum cold-stress inducible protein (C17) gene, complete cds |
| 8797 | 21764 | 35186 | 1.24 | 7.2E-01 | AF236061.1 | NT | Oryctolagus cuniculus RING-finger binding protein mRNA, partial cds |
| 9314 | 22279 | | 0.52 | 7.2E-01 | AV743773.1 | EST_HUMAN | AV743773 CB Homo sapiens cDNA clone CBMAFD06.5 |
| 10705 | 23627 | 37123 | 2.59 | 7.2E-01 | BF670061.1 | EST_HUMAN | 602118381 F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4275381.5 |
| 11091 | 24051 | 37574 | 3.38 | 7.2E-01 | U82623.1 | NT | Rattus norvegicus cytochrome mRNA, complete cds |
| 12523 | 18343 | 31291 | 1.43 | 7.2E-01 | U02568.1 | NT | Dictyocaulus viviparus nematode polyprotein antigen precursor (Dva) mRNA, complete cds |
| 12700 | 25360 | | 5.56 | 7.2E-01 | AF000063.1 | NT | Aeropyrum pernix genomic DNA, section 6/7 |
| 693 | 13755 | 26885 | 13.3 | 7.1E-01 | D21070.1 | NT | Rana catesbeiana mRNA for bullfrog skeletal muscle calcium release channel (ryanodine receptor) alpha isoform(RYR1), complete cds |
| 3075 | 18132 | 28045 | 13.21 | 7.1E-01 | AJ270777.1 | NT | Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 15-16 |

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| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 4236 | 17265 | 30151 | 3.29 | 7.1E-01 | 7305360 | NT | Mus musculus obogelin (Otog), mRNA |
| 4236 | 17265 | 30152 | 3.29 | 7.1E-01 | 7305360 | NT | Mus musculus obogelin (Otog), mRNA |
| 6058 | 19139 | 32350 | 1.55 | 7.1E-01 | BF681034.1 | EST_HUMAN | 602155438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296344 5' |
| 6058 | 19139 | 32351 | 1.55 | 7.1E-01 | BF681034.1 | EST_HUMAN | 602155438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296344 5' |
| 7137 | 20113 | 33426 | 6.92 | 7.1E-01 | U36232.1 | NT | Drosophila melanogaster 8-pyruvoyltetrahydropterin synthase (pr) gene, complete cds |
| 8533 | 21501 | 34918 | 0.48 | 7.1E-01 | H54244.1 | EST_HUMAN | y98d09.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:202961 3' |
| 9088 | 22054 | 35477 | 0.85 | 7.1E-01 | BE074185.1 | EST_HUMAN | RC1-BT0567-301299-011-409 BT0567 Homo sapiens cDNA |
| 9088 | 22054 | 35478 | 0.85 | 7.1E-01 | BE074185.1 | EST_HUMAN | RC1-BT0567-301299-011-409 BT0567 Homo sapiens cDNA |
| 10214 | 23139 | 36628 | 1.28 | 7.1E-01 | BE604405.1 | EST_HUMAN | 601496330F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898495 5' |
| 10774 | 23695 | 37193 | 1.13 | 7.1E-01 | M12961.1 | NT | Human T-cell receptor gamma-chain J2 gene |
| 12499 | 25773 | | 2.34 | 7.1E-01 | AA421492.1 | EST_HUMAN | zu08n11.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:731109 3' |
| 1233 | 14270 | 27229 | 1.13 | 7.0E-01 | AB014514.1 | NT | Homo sapiens mRNA for KIAA0614 protein, partial cds |
| 1233 | 14270 | 27230 | 1.13 | 7.0E-01 | AB014514.1 | NT | Homo sapiens mRNA for KIAA0614 protein, partial cds |
| 2455 | 15460 | 28482 | 1.09 | 7.0E-01 | N62412.1 | EST_HUMAN | y273e07.s1 Soares multiple sclerosis_2NbhMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element; |
| 2455 | 15460 | 28483 | 1.09 | 7.0E-01 | N62412.1 | EST_HUMAN | y273e07.s1 Soares multiple sclerosis_2NbhMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element; |
| 5096 | 18106 | | 2.11 | 7.0E-01 | AL163301.2 | NT | Homo sapiens chromosome 21 segment HS21C101 |
| 6062 | 19143 | | 0.95 | 7.0E-01 | AB021316.1 | NT | Arabidopsis thaliana mRNA for chlorophyll b synthase, complete cds |
| 8721 | 21689 | | 8.51 | 7.0E-01 | AE000253.1 | NT | Escherichia coli K-12 MG1655 section 143 of 400 of the complete genome |
| 9871 | 22824 | 35077 | 0.52 | 7.0E-01 | U53868.1 | NT | Clostridium acetabutylicum mannitol-specific phosphotransferase system (PTS) system, mtaA, mtiR, mtiF, and mtiD genes, complete cds |
| 9871 | 22824 | 35078 | 0.52 | 7.0E-01 | U53868.1 | NT | Clostridium acetabutylicum mannitol-specific phosphotransferase system (PTS) system, mtaA, mtiR, mtiF, and mtiD genes, complete cds |
| 11454 | 24397 | 37943 | 1.71 | 7.0E-01 | AV763842.1 | EST_HUMAN | AV763842 MDS Homo sapiens cDNA clone MDSCH04 5' |
| 11454 | 24397 | 37944 | 1.71 | 7.0E-01 | AV763842.1 | EST_HUMAN | AV763842 MDS Homo sapiens cDNA clone MDSCH04 5' |
| 13035 | 25811 | 31528 | 1.35 | 7.0E-01 | 9630464 | NT | Bacteriophage N15 virion, complete genome |
| 971 | 14023 | 26976 | 12.59 | 6.9E-01 | U59674.1 | NT | Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds |
| 971 | 14023 | 26977 | 12.59 | 6.9E-01 | U59674.1 | NT | Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds |
| 1313 | 14349 | 27315 | 2.22 | 6.9E-01 | AA593530.1 | EST_HUMAN | m28a09.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1085176 3' |
| 3233 | 16298 | 29210 | 1.8 | 6.9E-01 | AE002271.2 | NT | Chlamydia muridarum, section 3 of 85 of the complete genome |
| 5249 | 18257 | 31126 | 0.92 | 6.9E-01 | AV714502.1 | EST_HUMAN | AV714502 DCB Homo sapiens cDNA clone DCBATA12 5' |

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|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 5878 | 18967 | 32158 | 0.8 | 6.9E-01 | AB035682.1 | NT | Branchiostoma belcheri BbNA3 mRNA for melochord actin, complete cds |
| 6104 | 19183 | 32402 | 0.55 | 6.9E-01 | Y18278.1 | NT | Drosophila melanogaster mRNA for A-kinase anchor protein DAKAP550, partial |
| 6508 | 19570 | 32822 | 1.5 | 6.9E-01 | BE296188.1 | EST_HUMAN | 601177333F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532328 5' |
| 8312 | 21281 | 34692 | 3.39 | 6.9E-01 | AL161573.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69 |
| 8312 | 21281 | 34693 | 3.39 | 6.9E-01 | AL161573.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69 |
| 9526 | 22489 | | 0.73 | 6.9E-01 | AF118046.1 | NT | Entamoeba dispar cation transporting ATPase (atpase) gene, partial cds |
| 10053 | 22980 | 36447 | 0.55 | 6.9E-01 | AF208319.1 | NT | Musa acuminata pectate lyase 1 (PL1) mRNA, complete cds |
| 10053 | 22980 | 36448 | 0.55 | 6.9E-01 | AF208319.1 | NT | Musa acuminata pectate lyase 1 (PL1) mRNA, complete cds |
| 11587 | 24525 | 38081 | 2.03 | 6.9E-01 | D89013.1 | NT | Homo sapiens DAN gene, complete cds |
| 11587 | 24525 | 38082 | 2.03 | 6.9E-01 | D89013.1 | NT | Homo sapiens DAN gene, complete cds |
| 12145 | 25766 | | 3.91 | 6.9E-01 | Q99958 | SWISSPROT | FORKHEAD BOX PROTEIN C2 (FORKHEAD-RELATED PROTEIN FKHL14) (MESENCHYME FORK HEAD PROTEIN 1) (MFH-1 PROTEIN) (TRANSCRIPTION FACTOR FKHL14) |
| 958 | 14011 | 26964 | 1.52 | 6.8E-01 | AF017784.1 | NT | Giardia intestinalis carbamate kinase gene, complete cds |
| 2682 | 15678 | | 1.26 | 6.8E-01 | D90917.1 | NT | Synechocystis sp. PCC6803 complete genome, 27/27, 3418852-3573470 |
| 2840 | 14651 | 27627 | 1.5 | 6.8E-01 | AA854475.1 | EST_HUMAN | aj75605.st Soares, parathyroid_tumor_Nb-HPA Homo sapiens cDNA clone IMAGE:1402256 3' similar to |
| 4602 | 17623 | 30516 | 1.75 | 6.8E-01 | J00762.1 | NT | gb:X56411.mat ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (HUMAN); |
| 9996 | 22923 | 36388 | 1.67 | 6.8E-01 | AB037766.1 | NT | Rat(hooded) prolactin gene : exon iii and flanks |
| 11424 | 24368 | 37903 | 1.77 | 6.8E-01 | AJ276675.1 | NT | Homo sapiens mRNA for KIAA1345 protein, partial cds |
| 11424 | 24368 | 37904 | 1.77 | 6.8E-01 | AJ276675.1 | NT | Stagonospora avenae bg11 gene for beta-glucosidase, exons 1-4 |
| 11450 | 24393 | 37938 | 1.82 | 6.8E-01 | AF038939.1 | NT | Stagonospora avenae bg11 gene for beta-glucosidase, exons 1-4 |
| 11450 | 24393 | 37939 | 1.82 | 6.8E-01 | AF038939.1 | NT | Mus musculus zinc finger protein (Peg3) mRNA, complete cds |
| | | | | | | NT | Mus musculus zinc finger protein (Peg3) mRNA, complete cds |
| | | | | | | NT | Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG28, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial> |
| 11931 | 24812 | 38407 | 1.49 | 6.8E-01 | AF110520.1 | NT | Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG28, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial> |
| 11931 | 24812 | 38408 | 1.49 | 6.8E-01 | AF110520.1 | NT | Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG28, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial> |
| 298 | 13392 | 26320 | 25.45 | 6.7E-01 | AF213884.1 | NT | Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds |
| 339 | 13428 | 26350 | 28.03 | 6.7E-01 | AF213884.1 | NT | Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds |
| 1927 | 14951 | | 1.07 | 6.7E-01 | M12192.1 | NT | Quali fast skeletal muscle troponin I gene, complete cds |

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| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 2157 | 15173 | 28192 | 1.79 | 6.7E-01 | AA451864.1 | EST_HUMAN | z12g12.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786310 3' similar to contains element TAR1 repetitive element ; |
| 2176 | 15886 | 28213 | 2.65 | 6.7E-01 | AF189073.1 | NT | Drosophila melanogaster Ns185C gene, complete cds; NMDMC isoform (Nmdmc) gene, complete cds, alternatively spliced; and transcription factor (Relish) gene, complete cds, alternatively spliced |
| 3009 | 16087 | 28987 | 3.96 | 6.7E-01 | 6878580 | NT | Mus musculus Wiskott-Aldrich syndrome protein (Wasp), mRNA |
| 4481 | 17506 | 30395 | 0.78 | 6.7E-01 | X74421.1 | NT | S.tuberosum mRNA for glucose-6-phosphate dehydrogenase |
| 5002 | 18016 | 30903 | 0.97 | 6.7E-01 | AW079110.1 | EST_HUMAN | xa95g12.x1 NCLCGAP_Cot17 Homo sapiens cDNA clone IMAGE:2574598 3' |
| 5587 | 18883 | 31651 | 0.7 | 6.7E-01 | J04836.1 | NT | M.barkeri ATPase alpha and beta subunit (atpA and atpB) genes, complete cds |
| 5587 | 18883 | 31652 | 0.7 | 6.7E-01 | J04836.1 | NT | M.barkeri ATPase alpha and beta subunit (atpA and atpB) genes, complete cds |
| 6073 | 19154 | 32366 | 0.93 | 6.7E-01 | AE001486.1 | NT | Helicobacter pylori, strain J99 section 47 of 132 of the complete genome |
| 6458 | 19821 | 32771 | 1.26 | 6.7E-01 | 9635035 | NT | Gallid herpesvirus 2, complete genome |
| 6456 | 19521 | 32772 | 1.26 | 6.7E-01 | 9635035 | NT | Gallid herpesvirus 2, complete genome |
| 7537 | 20500 | | 4.57 | 6.7E-01 | AE004606.1 | NT | Pseudomonas aeruginosa PA01, section 167 of 529 of the complete genome |
| 7563 | 20526 | 33984 | 0.98 | 6.7E-01 | AE001486.1 | NT | Helicobacter pylori, strain J99 section 47 of 132 of the complete genome |
| 10503 | 23425 | | 0.82 | 6.7E-01 | M3046.1 | NT | Human placental protein 14 (PP14) gene, complete cds |
| 11300 | 24250 | 37776 | 2.62 | 6.7E-01 | BF354649.1 | EST_HUMAN | CM3-HT0769-010600-197-03 HT0769 Homo sapiens cDNA |
| 11787 | 23942 | 37464 | 3.23 | 6.7E-01 | O14357 | SWISSPROT | N-ACETYLGLUCOSAMINYL-PHOSPHATIDYLINOSITOL BIOSYNTHETIC PROTEIN GPI |
| 11989 | 24847 | 38444 | 1.62 | 6.7E-01 | AA342521.1 | EST_HUMAN | EST48065 Fetal spleen Homo sapiens cDNA 3' and |
| 2509 | 15512 | 28538 | 1.82 | 6.8E-01 | AF075240.1 | NT | Homo sapiens SLIT1 protein (SLIT2) mRNA, partial cds |
| 2711 | 15705 | 28721 | 1.4 | 6.8E-01 | AF189339.1 | NT | Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds |
| 3501 | 16548 | 29474 | 1.41 | 6.8E-01 | 4506880 | NT | Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA |
| 3670 | 16713 | 29628 | 4.37 | 6.8E-01 | Y07669.1 | NT | Calbicans random DNA marker, 282bp |
| 4136 | 17168 | | | | | | Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds |
| 5258 | 18266 | 31134 | 1.13 | 6.8E-01 | AL161572.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68 |
| 5282 | 18288 | 31150 | 0.95 | 6.8E-01 | Z82002.1 | NT | S.pneumoniae pcpB and pcpC genes |
| 5282 | 18288 | 31151 | 0.95 | 6.8E-01 | Z82002.1 | NT | S.pneumoniae pcpB and pcpC genes |
| 6466 | 19531 | 32779 | 3.83 | 6.8E-01 | 6880577 | NT | Mus musculus Khesin light chain 2 (Kic2), mRNA |
| 7949 | 20890 | 34281 | 3.57 | 6.8E-01 | AV680506.1 | EST_HUMAN | AV680506 GLC Homo sapiens cDNA clone GLCGID04 3' |
| 8912 | 21878 | 35304 | 0.58 | 6.8E-01 | AV704700.1 | EST_HUMAN | AV704700 ADB Homo sapiens cDNA clone ADBCAF11 5' |
| 10023 | 22950 | | 1.56 | 6.8E-01 | AL163278.2 | NT | Homo sapiens chromosome 21 segment HS21C078 |

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|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 12748 | 25395 | 31758 | 1.78 | 6.6E-01 | AE004382.1 | NT | Vibrio cholerae chromosome II, section 39 of 93 of the complete chromosome |
| 624 | 13689 | 26606 | 0.96 | 6.5E-01 | M75140.1 | NT | H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds |
| 624 | 13689 | 26607 | 0.96 | 6.5E-01 | M75140.1 | NT | H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds |
| 3448 | 18493 | 29412 | 4.63 | 6.5E-01 | AB041225.1 | NT | Mus musculus gene for Tbb2, complete cds |
| 4311 | 17340 | 30220 | 4.28 | 6.5E-01 | AJ27265.1 | NT | Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8 |
| 5102 | 18112 | 30884 | 3.71 | 6.5E-01 | U28021.1 | NT | Phaseolus vulgaris ATPase gamma subunit mRNA, nuclear gene encoding mitochondrial protein, partial cds |
| 5204 | 18213 | 31088 | 1.13 | 6.5E-01 | Z70628.1 | NT | H. sapiens mRNA for immunoglobulin heavy chain variable region (9D4-A6, VH4, 4-59/DP-71) |
| 5518 | 25640 | 31551 | 2.13 | 6.5E-01 | P18480 | SWISSPROT | TRANSCRIPTION REGULATORY PROTEIN SNF5 (SWI/SNF COMPLEX COMPONENT SNF5) |
| 5802 | 18894 | 32077 | 0.58 | 6.5E-01 | AL163249.2 | NT | Homo sapiens chromosome 21 segment HS21C049 |
| 6887 | 19939 | 33234 | 1.24 | 6.5E-01 | D88348.1 | NT | Chicken mRNA for 115-kDa melanosomal matrix protein, complete cds |
| 7841 | 20786 | 34163 | 0.84 | 6.5E-01 | X04769.1 | NT | Murine Ig-related lambda(50) gene (exon 1) transcribed selectively in pre-B lymphocytes |
| 7930 | 20873 | 34282 | 0.89 | 6.5E-01 | A179982.1 | EST_HUMAN | wc46a02.x1 NCL CGAP_P28 Homo sapiens cDNA clone IMAGE:2321842 3' |
| 10197 | 23122 | 37117 | 1.03 | 6.5E-01 | U78904.1 | EST_HUMAN | y21p04.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108847 3' |
| 10699 | 23621 | 37117 | 2.2 | 6.5E-01 | AF118676.1 | NT | Mus musculus small GTP-binding protein RAB25 (Rab25) gene, complete cds |
| 10997 | 23963 | 37487 | 2.19 | 6.5E-01 | H87583.1 | EST_HUMAN | yw17f06.r1 Soares_placenta_8to9weeks_2NbhP8b9w Homo sapiens cDNA clone IMAGE:252515 5' |
| 11045 | 24009 | 37635 | 2.88 | 6.5E-01 | AA601287.1 | EST_HUMAN | no15c07.s1 NCL CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100748 3' |
| 11143 | 24103 | | 3.43 | 6.5E-01 | AU138078.1 | EST_HUMAN | AU138078 PLACE1 Homo sapiens cDNA clone PLACE1007810 5' |
| 11925 | 24806 | 38399 | 2.3 | 6.5E-01 | AF014115.1 | NT | Plasmodium berghei cytochrome c oxidase subunit III, cytochrome c oxidase subunit I, and cytochrome b genes, mitochondrial genes encoding mitochondrial proteins, complete cds |
| | | | | | | | Fugu rubripes U2 small nuclear ribonucleoprotein auxiliary factor subunit-related protein (U2AF1-RS2), 19 kDa Golgi adaptor protein adaptin (AP19), and phosphorylase kinase alpha 2 subunit (PHKA2) genes, complete cds; kelch protein (KELCH1) and kelch p> |
| 11970 | 24848 | 38445 | 1.47 | 6.5E-01 | AF146687.1 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 76' |
| 12130 | 24899 | 38604 | 1.61 | 6.5E-01 | AL161580.2 | NT | h74a10.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3178130 3' |
| 12554 | 25276 | | 2.65 | 6.5E-01 | BE46050.1 | EST_HUMAN | Drosophila melanogaster 8kd dynein light chain mRNA, complete cds |
| 252 | 13349 | 26275 | 10.51 | 6.4E-01 | U48848.1 | NT | Mus musculus dystroglycan 1 (DAG1) gene, exons 1 and 2 and complete cds |
| 3470 | 18518 | 29437 | 3.26 | 6.4E-01 | U48854.2 | NT | Homo sapiens mRNA for KIAA1607 protein, partial cds |
| 3875 | 18914 | 29823 | 1.34 | 6.4E-01 | AB046827.1 | NT | M. musculus wtn gene |
| 4519 | 17544 | 30430 | 0.89 | 6.4E-01 | Y12488.1 | NT | M. musculus wtn gene |
| 4519 | 17544 | 30431 | 0.89 | 6.4E-01 | Y12488.1 | NT | M. musculus wtn gene |
| 5192 | 18201 | 31073 | 1 | 6.4E-01 | H85337.1 | EST_HUMAN | ys9c08.r1 Soares retina N2b5HR Homo sapiens cDNA clone IMAGE:222096 5' |
| 8960 | 21928 | 35953 | 1.57 | 6.4E-01 | AE001247.1 | NT | Treponema pallidum section 63 of 87 of the complete genome |

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Table 4
Single Exon Probes Expressed In Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 10449 | 23371 | 36863 | 6.94 | 6.4E-01 | U82828.1 | NT | Homo sapiens ataxia telangiectasia (ATM) gene, complete cds |
| 10464 | 23386 | 36879 | 1.18 | 6.4E-01 | BF670405.1 | EST_HUMAN | 602150289F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291126 5' |
| 12666 | 25342 | | 5.76 | 6.4E-01 | AV759212.1 | EST_HUMAN | AV759212 MDS Homo sapiens cDNA clone MDSGCG09 5' |
| 434 | 13508 | 26442 | 3.27 | 6.3E-01 | P08228 | SWISSPROT | HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III) |
| 536 | 13607 | 26525 | 2.19 | 6.3E-01 | U32689.1 | NT | Haemophilus influenzae Rd section 4 of 163 of the complete genome |
| 2171 | 15187 | 28208 | 3.4 | 6.3E-01 | U81136.1 | NT | Shigella flexneri multi-antibiotic resistance locus |
| 2583 | 15584 | 28603 | 2.72 | 6.3E-01 | U75331.1 | NT | Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds |
| 2583 | 15584 | 28604 | 2.72 | 6.3E-01 | U75331.1 | NT | Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds |
| 3029 | 16087 | | 0.8 | 6.3E-01 | Y17275.1 | NT | Lycopodium obscurum p89a gene, complete cds |
| 6182 | 19257 | 32490 | 0.87 | 6.3E-01 | BE093906.1 | EST_HUMAN | PMO-BT0757-010500-002-a05 BT0757 Homo sapiens cDNA |
| 6753 | 19807 | 33088 | 1.07 | 6.3E-01 | L27798.1 | NT | Streptococcus dysgalactiae (mag) gene, complete cds |
| 6753 | 19807 | 33089 | 1.07 | 6.3E-01 | L27798.1 | NT | Streptococcus dysgalactiae (mag) gene, complete cds |
| 8866 | 21833 | | 3.17 | 6.3E-01 | BE902044.1 | EST_HUMAN | 601676889F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959351 5' |
| 9238 | 22204 | 35636 | 0.8 | 6.3E-01 | S62927.1 | NT | glycoprotein IIIa (Alu 1 and 3 fusion junction) [human, Genomic Mutant, 300 nt] |
| 9575 | 22537 | 35989 | 0.74 | 6.3E-01 | BF216984.1 | EST_HUMAN | 601884050F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4102596 5' |
| 9775 | 22716 | 38171 | 2.86 | 6.3E-01 | 9627621 | NT | Varicella virus, complete genome |
| 9775 | 22716 | 38172 | 2.86 | 6.3E-01 | 9627621 | NT | Varicella virus, complete genome |
| 10298 | 23223 | | 0.63 | 6.3E-01 | AE002329.2 | NT | Chlamydia muridarum, section 59 of 85 of the complete genome |
| 10792 | 23713 | 37215 | 1.55 | 6.3E-01 | Z73003.1 | NT | S. cerevisiae chromosome VII reading frame ORF YGR218w |
| 10895 | 23815 | 37322 | 0.98 | 6.3E-01 | AE000313.1 | NT | Escherichia coli K-12 MG1655 section 203 of 400 of the complete genome |
| 11400 | 24345 | 37878 | 1.52 | 6.3E-01 | AA877715.1 | EST_HUMAN | nt09h06.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1161371 3' similar to TR:O02916 O02916 HLAR : |
| 11663 | 24599 | 38173 | 6.95 | 6.3E-01 | A1904160.1 | EST_HUMAN | CM-BT043-090299-046 BT043 Homo sapiens cDNA |
| 11754 | 24682 | 38261 | 1.79 | 6.3E-01 | P47003 | SWISSPROT | HYPOTHETICAL 13.7 KD PROTEIN IN INO1-IDS2 INTERGENIC REGION |
| 11915 | 24796 | 38387 | 2.09 | 6.3E-01 | P36073 | SWISSPROT | HYPOTHETICAL 15.3 KD PROTEIN IN VMA12-APN1 INTERGENIC REGION |
| 12258 | 25926 | 31306 | 5.44 | 6.3E-01 | 9910293 | NT | Mus musculus keratin complex 2, gene 8g (Krt2-8g), mRNA |
| 12359 | 25149 | | 1.81 | 6.3E-01 | AF105227.1 | NT | Homo sapiens 3'-phosphoadenosine 5'-phosphosulfate synthetase (PAPSS) mRNA, complete cds |
| 12570 | 25845 | | 3.19 | 6.3E-01 | X83528.1 | NT | C. limicola pscD gene |
| 5970 | 19055 | 32255 | 2.97 | 6.2E-01 | Q10135 | SWISSPROT | HYPOTHETICAL 1425 KD PROTEIN C23E2.02 IN CHROMOSOME 1 |
| 7737 | 20692 | | 2.75 | 6.2E-01 | AF022253.1 | NT | Mus musculus calcium-sensing receptor related protein 4 (Casr-rs4) mRNA, partial cds |
| 7791 | 25690 | 34117 | 1.12 | 6.2E-01 | AL021127.2 | NT | Mus musculus chromosome X contigA; putative Magea9 gene, Caltractin, NAD(P) ⁺ steroid dehydrogenase end Zinc finger protein 185 |
| 8644 | 21612 | 35034 | 5.41 | 6.2E-01 | H72255.1 | EST_HUMAN | ys01c08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213542 3' |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 9208 | 22174 | 35805 | 0.54 | 6.2E-01 | AF034411.1 | NT | Lycopodium esculentum cytosolic Cu,Zn superoxide dismutase (Sod) gene, partial cds, and dehydroquinata dehydratase/shikimate:NADP oxidoreductase gene, complete cds |
| 9804 | 21127 | 34531 | 1.87 | 6.2E-01 | BE562687.1 | EST_HUMAN | 601338146F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690010 5' |
| 9888 | 22804 | | 2.17 | 6.2E-01 | M24461.1 | NT | Human pulmonary surfactant-associated protein SP-B (SFTPB) mRNA, complete cds |
| 10438 | 23360 | 36849 | 7.04 | 6.2E-01 | AL161511.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23 |
| 10902 | 23822 | 37332 | 5.32 | 6.2E-01 | P27410 | SWISSPROT | NON-STRUCTURAL POLYPEPTIDE [CONTAINS: RNA-DIRECTED RNA POLYMERASE; THIOL PROTEASE P3C; HELICASE (2C LIKE PROTEIN); COAT PROTEIN] |
| 10902 | 23822 | 37333 | 5.32 | 6.2E-01 | P27410 | SWISSPROT | NON-STRUCTURAL POLYPEPTIDE [CONTAINS: RNA-DIRECTED RNA POLYMERASE; THIOL PROTEASE P3C; HELICASE (2C LIKE PROTEIN); COAT PROTEIN] |
| 2404 | 15411 | | 5.9 | 6.1E-01 | 6878076 | NT | Mus musculus secreted acidic cytochrome rich glycoprotein (Sparc), mRNA |
| 5914 | 18710 | 31868 | 1.3 | 6.1E-01 | M59940.1 | NT | Caenorhabditis elegans N2 CcmYdD (hlt-1) alternatively spliced genes, complete cds |
| 7053 | 20075 | 33382 | 3.54 | 6.1E-01 | M64733.1 | NT | Rat TRPM-2 gene, complete cds |
| 7053 | 20075 | 33383 | 3.54 | 6.1E-01 | M64733.1 | NT | Rat TRPM-2 gene, complete cds |
| 7218 | 20238 | 33572 | 0.7 | 6.1E-01 | AW105653.1 | EST_HUMAN | xd50h03.x1 NCL CGAG_Ov23 Homo sapiens cDNA clone IMAGE:2597237 3' similar to gb:X12671_ma1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN); |
| 7312 | 20283 | 33824 | 0.84 | 6.1E-01 | Q63769 | SWISSPROT | SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC) |
| 8575 | 21543 | 34953 | 3.68 | 6.1E-01 | AF033535.1 | NT | Arabidopsis thaliana putative zinc transporter (ZIP1) mRNA, complete cds |
| 9147 | 22113 | 35537 | 1.17 | 6.1E-01 | 11431085 | NT | Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA |
| 9147 | 22113 | 35538 | 1.17 | 6.1E-01 | 11431085 | NT | Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA |
| 9770 | 22711 | 36165 | 23.08 | 6.1E-01 | AF236117.1 | NT | Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds |
| 9770 | 22711 | 36166 | 23.08 | 6.1E-01 | AF236117.1 | NT | Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds |
| 10202 | 23127 | 36613 | 0.99 | 6.1E-01 | AE004452.1 | NT | Pseudomonas aeruginosa PA01, section 13 of 529 of the complete genome |
| 10408 | 23328 | 36812 | 1.53 | 6.1E-01 | AF119117.1 | NT | Homo sapiens dopamine transporter (SLC6A3) gene, complete cds |
| 11308 | 24256 | | 1.91 | 6.1E-01 | X74507.1 | NT | P. sativum mdh1 mRNA for chloroplast malate dehydrogenase (NADP+) |
| 12041 | 24916 | 38510 | 1.63 | 6.1E-01 | S83182.1 | NT | hyaluronan-binding protein=hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt] |
| 12041 | 24916 | 38511 | 1.63 | 6.1E-01 | S83182.1 | NT | hyaluronan-binding protein=hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt] |
| 12555 | 25731 | 31615 | 2.77 | 6.1E-01 | AB041350.1 | NT | Mus musculus Col4a5 mRNA for type IV collagen alpha 5 chain, complete cds |
| 495 | 13567 | 28490 | 1.41 | 6.0E-01 | D87675.1 | NT | Homo sapiens DNA for amyloid precursor protein, complete cds |
| 563 | 13933 | | 2.75 | 6.0E-01 | 5602999 | NT | Homo sapiens adaptor-related protein complex 3, mu 2 subunit (CLA20), mRNA |
| 1364 | 14398 | 27369 | 1.92 | 6.0E-01 | AF065253.1 | NT | Human respiratory syncytial virus strain CH93-535 attachment protein (G) gene, complete cds |
| 3628 | 18668 | 29770 | 0.9 | 6.0E-01 | AJ233396.1 | NT | Viral hemorrhagic septicemia virus N, P, M, G, Nv, L genes, French strain 07-71 |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 4217 | 17246 | | 1.61 | 6.0E-01 | AF058895.1 | NT | Homo sapiens Notch3 (NOTCH3) gene, exons 26, 27, and 28 |
| 4279 | 17308 | 30187 | 0.99 | 6.0E-01 | AB025319.1 | NT | Yaba monkey tumor virus DNA, BamH1 restriction fragment E, M and partial C, partial and complete cds |
| 5353 | 18458 | 31327 | 2.14 | 6.0E-01 | P20288 | SWISSPROT | D(2) DOPAMINE RECEPTOR |
| 5514 | 18614 | 31547 | 2.22 | 6.0E-01 | AW139713.1 | EST_HUMAN | UIH-B11-aeb-a-10-0-U1.s1 NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718619 3' |
| 6689 | 19746 | 33022 | 2.68 | 6.0E-01 | U38813.1 | NT | Musca domestica insecticide-susceptible strain voltage-sensitive sodium channel mRNA, complete cds |
| 6818 | 19872 | 33161 | 0.67 | 6.0E-01 | Q04912 | SWISSPROT | MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON) |
| 6988 | 20211 | 33539 | 0.78 | 6.0E-01 | L10234.1 | NT | Strongylocentrotus purpuratus kinesin light chain isoform 2 mRNA, complete cds |
| 6988 | 20211 | 33540 | 0.78 | 6.0E-01 | L10234.1 | NT | Strongylocentrotus purpuratus kinesin light chain isoform 2 mRNA, complete cds |
| 7577 | 20539 | 33898 | 5.51 | 6.0E-01 | AJ277661.1 | NT | Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1 |
| 8461 | 21430 | 34847 | 4.55 | 6.0E-01 | P02835 | SWISSPROT | SEGMENTATION PROTEIN FUSHI TARAZU |
| 8461 | 21430 | 34848 | 4.55 | 6.0E-01 | P02835 | SWISSPROT | SEGMENTATION PROTEIN FUSHI TARAZU |
| 10182 | 23107 | 36589 | 1.84 | 6.0E-01 | AB008193.1 | NT | Homo sapiens genes for leukotriene B4 receptor BLT2, leukotriene B4 receptor BLT1, complete cds |
| 10638 | 23558 | | 1.66 | 6.0E-01 | Q01497 | SWISSPROT | PEROXISOMAL MEMBRANE PROTEIN PER9 (PEROXIN-3) |
| 10749 | 23871 | | 0.46 | 6.0E-01 | BE837779.1 | EST_HUMAN | RC2-FN0094-190700-017-408 FN0094 Homo sapiens cDNA |
| 11878 | 24780 | 38345 | 2.79 | 6.0E-01 | AI420623.1 | EST_HUMAN | tt08f07.x1 NCL CGAP_P28 Homo sapiens cDNA clone IMAGE:2095621 3' |
| 12638 | 25322 | 31788 | 1.87 | 6.0E-01 | | NT | Homo sapiens nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), mRNA |
| 12731 | 25384 | | 2.78 | 6.0E-01 | AA706087.1 | EST_HUMAN | z98g05.s1 Soares fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462776 3' |
| 12918 | 25777 | 31522 | 4.71 | 6.0E-01 | 9055303 | NT | Mus musculus cGMP-inhibited phosphodiesterase (Pde3a), mRNA |
| 12947 | 25715 | | 3.4 | 6.0E-01 | BE157617.1 | EST_HUMAN | RC1-HT0375-030500-015-c03 HT0375 Homo sapiens cDNA |
| 1002 | 14053 | 27003 | 0.97 | 5.9E-01 | U32701.1 | NT | Haemophilus influenzae Rd section 16 of 163 of the complete genome |
| 3283 | 16337 | 29256 | 4.95 | 5.9E-01 | AL163267.2 | NT | Homo sapiens chromosome 21 segment HS21C087 |
| 3283 | 16337 | 29257 | 4.95 | 5.9E-01 | AL163267.2 | NT | Homo sapiens chromosome 21 segment HS21C087 |
| 4250 | 17279 | | 4.09 | 5.9E-01 | AF162756.1 | NT | Rattus norvegicus ceneidin 2 mRNA, partial cds |
| 6609 | 19667 | 32943 | 1.45 | 5.9E-01 | AF065440.2 | NT | Homo sapiens low density lipoprotein receptor-related protein II (LRP2) gene, exon 1 and partial cds |
| 7481 | 20447 | 33803 | 2.44 | 5.9E-01 | AB023486.1 | NT | Homo sapiens gene for histamine H2 receptor, promoter region and complete cds |
| 8332 | 21301 | 34718 | 0.46 | 5.9E-01 | D90911.1 | NT | Synechocystis sp. PCC6803 complete genome, 13/27, 1576593-1719643 |
| 8985 | 21951 | 35375 | 0.48 | 5.9E-01 | D12922.1 | NT | Legionella pneumophila gene for iron superoxide dismutase, complete cds |
| 9901 | 22853 | 36314 | 0.89 | 5.9E-01 | AF083204.2 | NT | Chlamydia trachomatis strain KUW31/Cx major outer membrane protein (omp1) gene, complete cds |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 10273 | 23198 | | 0.68 | 5.9E-01 | P06463 | SWISSPROT | EG PROTEIN |
| 10548 | 23470 | 36965 | 1.19 | 5.9E-01 | P55284 | SWISSPROT | VASCULAR ENDOTHELIAL-CADHERIN PRECURSOR (VE-CADHERIN) (CADHERIN-5) |
| 11031 | 23985 | 37523 | 2.46 | 5.9E-01 | Q9X0I3 | SWISSPROT | THYMIDYLATE KINASE (DTMP KINASE) |
| 11037 | 24001 | 37528 | 49.8 | 5.9E-01 | AF197944.1 | NT | Xenopus laevis receptor protein tyrosine phosphatase delta (XPTP-D) mRNA, complete cds |
| 11309 | 24259 | 37795 | 2.48 | 5.9E-01 | AW937175.1 | EST_HUMAN | PM1-DT0041-190100-002-h03 DT0041 Homo sapiens cDNA |
| 11526 | 24487 | 38021 | 1.53 | 5.9E-01 | AF064926.1 | NT | Mus spretus strain SPRET/IEI CD48 antigen (Cd48) gene, partial cds |
| 12297 | 25108 | 31838 | 2.43 | 5.9E-01 | L42320.1 | NT | Oryctolagus cuniculus alpha 1 anti-hypsin (alpha 1 AT) gene, promoter region |
| 12541 | 25264 | | 2.86 | 5.9E-01 | AB017705.1 | NT | Aspergillus oryzae pyrG gene for orotidine-5'-phosphate decarboxylase, complete cds |
| 12740 | 25390 | | 6.24 | 5.9E-01 | P34926 | SWISSPROT | MICROTUBULE-ASSOCIATED PROTEIN 1A (CONTAINS: MAP1 LIGHT CHAIN LC2) |
| 1924 | 14948 | 27044 | 1.28 | 5.9E-01 | P40472 | SWISSPROT | SIM1 PROTEIN |
| 2571 | 15572 | 28592 | 1 | 5.9E-01 | 7305230 | NT | Mus musculus low density lipoprotein B (Ldlb), mRNA |
| 4009 | 17048 | 28934 | 1 | 5.9E-01 | BF695738.1 | EST_HUMAN | 601852474F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076131 5' |
| 4542 | 17565 | 30452 | 4.23 | 5.9E-01 | AB009077.1 | NT | Vigna radiata mRNA for protein pyrophosphatase, complete cds |
| 5448 | 18550 | | 0.84 | 5.9E-01 | AE002152.1 | NT | Ureaplasma urealyticum section 53 of 59 of the complete genome |
| 5609 | 18705 | 31882 | 0.75 | 5.9E-01 | Q10699 | SWISSPROT | POTENTIAL 5'-3' EXONUCLEASE |
| 6308 | 19379 | 32618 | 1.82 | 5.9E-01 | D78659.1 | EST_HUMAN | HUM500E06B Human placenta polyA+ (TFujwara) Homo sapiens cDNA clone GEN-500E06 5' |
| 6445 | 19510 | 32760 | 0.73 | 5.9E-01 | D50601.1 | NT | Shigella sonnei DNA for 28 ORFs, complete cds |
| 6985 | 20208 | | 2.55 | 5.9E-01 | S65091.1 | NT | cyclic AMP-regulated phosphoprotein (rats, mRNA, 1030 nt) |
| 8219 | 21188 | | 2.63 | 5.9E-01 | H41571.1 | EST_HUMAN | yn91b03.s1 Soares adult brain N255HB55Y Homo sapiens cDNA clone IMAGE:175757 3' similar to |
| 8423 | 21392 | 34802 | 0.59 | 5.9E-01 | A1280051.1 | EST_HUMAN | gb:S78187 M-PHASE INDUCER PHOSPHATASE 2 (HUMAN); |
| 8423 | 21392 | 34803 | 0.59 | 5.9E-01 | A1280051.1 | EST_HUMAN | qh85d10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1853779 3' |
| 8532 | 21500 | 34916 | 2.57 | 5.9E-01 | P14328 | SWISSPROT | SPORE COAT PROTEIN SP96 |
| 8532 | 21500 | 34917 | 2.57 | 5.9E-01 | P14328 | SWISSPROT | SPORE COAT PROTEIN SP96 |
| 9243 | 22209 | 35640 | 9.77 | 5.9E-01 | AJ270774.1 | NT | Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 6-11 |
| 9323 | 22288 | 35718 | 1.02 | 5.9E-01 | Q27368 | SWISSPROT | TRANSCRIPTION FACTOR E2F |
| 9324 | 22289 | 35719 | 0.46 | 5.9E-01 | Q20471 | SWISSPROT | PUTATIVE CASEIN KINASE I F46F2.2 IN CHROMOSOME X |
| 9954 | 22981 | | 0.81 | 5.9E-01 | BF031606.1 | EST_HUMAN | 60155774F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827288 5' |
| 11334 | 24284 | 37808 | 6.9 | 5.9E-01 | AJ243213.1 | NT | Homo sapiens partial 6-HT4 receptor gene, exons 2 to 5 |
| 11373 | 24320 | | 2.69 | 5.9E-01 | BF700092.1 | EST_HUMAN | 602127577F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284403 5' |
| 11476 | 24419 | | 1.61 | 5.9E-01 | BF700092.1 | EST_HUMAN | 602127577F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284403 5' |
| 1492 | 14525 | 27498 | 1.11 | 5.7E-01 | P08727 | SWISSPROT | APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV) |
| 1492 | 14525 | 27497 | 1.11 | 5.7E-01 | P08727 | SWISSPROT | APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV) |
| 3056 | 16113 | | 0.77 | 5.7E-01 | 8755253 | NT | Mus musculus plasmacytoma variant translocation 1 (Pv1), mRNA |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 3237 | 16282 | 28214 | 1.38 | 5.7E-01 | Q8WTJ2 | SWISSPROT | POTATIVE TRANSCRIPTION FACTOR OVO-LIKE 1 (MOVO1) (MOVO1A) |
| 3515 | 16561 | | 2.79 | 5.7E-01 | AB033503.1 | NT | Populus euphratica peacs-2 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds |
| 3922 | 16982 | 28875 | 1.05 | 5.7E-01 | AF011591.1 | NT | Homo sapiens T cell receptor beta chain (BV6S7-2BJTS1) mRNA, partial cds |
| 5213 | 18222 | 31097 | 1.22 | 5.7E-01 | 4505050 | NT | Homo sapiens lymphocyte antigen 8 complex, locus H (LY8H) mRNA |
| 6490 | 19555 | 32805 | 4.36 | 5.7E-01 | BF035413.1 | EST_HUMAN | 601454982F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3858590 5' |
| 6869 | 19922 | 33218 | 0.82 | 5.7E-01 | AA194201.1 | EST_HUMAN | z38c06.r1 Soares, NHMPU, S1 Homo sapiens cDNA clone IMAGE:665674 5' |
| 7042 | 18374 | 31262 | 1.3 | 5.7E-01 | AL111440.1 | NT | Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation |
| 8041 | 20978 | 34374 | 2.13 | 5.7E-01 | P00373 | SWISSPROT | PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR) (P5C REDUCTASE) |
| 8303 | 21272 | | 0.51 | 5.7E-01 | AJ251835.1 | NT | Mus musculus Kong1, Ltrpc5, Mash2, Tapa-1, Tssc4 and Tssc8 genes, alternative transcripts |
| 8723 | 21691 | | 0.52 | 5.7E-01 | AI065061.1 | EST_HUMAN | HA0895 Human fetal liver cDNA library Homo sapiens cDNA |
| 10159 | 23084 | 36560 | 1.22 | 5.7E-01 | AL161532.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32 |
| 10159 | 23084 | 36561 | 1.22 | 5.7E-01 | AL161532.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32 |
| 10940 | 23660 | 37376 | 0.75 | 5.7E-01 | BF540962.1 | EST_HUMAN | 602067712F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4066610 5' |
| 12252 | 25078 | | 1.49 | 5.7E-01 | BE715051.1 | EST_HUMAN | MR3-HT0736-180700-003-a02 HT0736 Homo sapiens cDNA |
| 1889 | 14914 | 27907 | 1.6 | 5.6E-01 | AF087732.1 | NT | Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds |
| 1889 | 14914 | 27908 | 1.6 | 5.6E-01 | AF087732.1 | NT | Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds |
| 3376 | 16426 | 29351 | 1.53 | 5.6E-01 | AB018283.2 | NT | Homo sapiens mRNA for KIAA0740 protein, partial cds |
| 3376 | 16426 | 29352 | 1.53 | 5.6E-01 | AB018283.2 | NT | Homo sapiens mRNA for KIAA0740 protein, partial cds |
| 4268 | 17297 | 30174 | 0.77 | 5.6E-01 | D83135.1 | NT | Chicken TBP gene, exon8, complete cds |
| 5205 | 18214 | 31089 | 0.93 | 5.6E-01 | BF032377.1 | EST_HUMAN | 601452855F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3856717 5' |
| 9155 | 22121 | 35550 | 14.66 | 5.6E-01 | AF694703.1 | EST_HUMAN | AV684703 GKc Homo sapiens cDNA clone GKCF5F05 5' |
| 9155 | 22121 | 35551 | 14.66 | 5.6E-01 | AF694703.1 | EST_HUMAN | AV684703 GKc Homo sapiens cDNA clone GKCF5F05 5' |
| 9730 | 22758 | 36211 | 1.23 | 5.6E-01 | AB038782.1 | NT | Homo sapiens MUC3A gene for intestinal mucin, partial cds |
| 12153 | 25011 | | 3.4 | 5.6E-01 | BE888280.1 | EST_HUMAN | 601514007F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915457 5' |
| 12270 | 25092 | 36178 | 1.73 | 5.6E-01 | AA493535.1 | EST_HUMAN | ng75g10.s1 NCL CGAP_P16 Homo sapiens cDNA clone IMAGE:940674 similar to contains element PTR7 repetitive element |
| 12636 | 18341 | 31280 | 1.51 | 5.6E-01 | AL191501.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13 |
| 12682 | 25340 | | 3.05 | 5.6E-01 | P50505 | SWISSPROT | HIGH AFFINITY POTASSIUM TRANSPORTER |
| 13080 | 25596 | | 4.95 | 5.6E-01 | BF573828.1 | EST_HUMAN | 602132029F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271334 5' |
| 13110 | 26630 | | 1.33 | 5.6E-01 | AA663881.1 | EST_HUMAN | ae74804.s1 Strabagene schizo brain S11 Homo sapiens cDNA clone IMAGE:969871 3' |
| 1216 | 14254 | 27212 | 0.82 | 5.5E-01 | 8393912 | NT | Rattus norvegicus Propionyl Coenzyme A carboxylase, beta polypeptide (Pccb), mRNA |
| 2712 | 15706 | 28722 | 5.31 | 5.5E-01 | P03341 | SWISSPROT | GAG POLYPEPTIDE [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10] |

Table 4

Single Exon Probes Expressed In Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 2712 | 15706 | 28723 | 5.31 | 5.5E-01 | P03341 | SWISSPROT | GAG POLYPEPTIDE [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10] |
| 2929 | 15987 | 28908 | 0.78 | 5.5E-01 | 5902085 | NT | Homo sapiens superkiller viralicidic activity 2 (S. cerevisiae homolog)-like (SKIV2L), mRNA |
| 3079 | 16136 | | 1.48 | 5.5E-01 | H46219.1 | EST_HUMAN | yo18a10.s1 Soares adult brain N266HB55Y Homo sapiens cDNA clone IMAGE:178266 3' |
| 3248 | 16303 | 29227 | 4.75 | 5.5E-01 | AF227240.1 | NT | Rabbit oral papillomavirus, complete genome |
| 3704 | 16747 | 29661 | 2.24 | 5.5E-01 | P48765 | SWISSPROT | FOS-RELATED ANTIGEN-1 |
| 5209 | 18218 | 31094 | 1.06 | 5.5E-01 | U69097.1 | NT | Bos taurus MHC class II beta-chain BcLA-DIB1 gene, partial cds |
| 7467 | 20433 | 33789 | 0.58 | 5.5E-01 | AF030001.1 | NT | Mus musculus major histocompatibility locus class III region:butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complete |
| 7467 | 20433 | 33790 | 0.58 | 5.5E-01 | AF030001.1 | NT | Mus musculus major histocompatibility locus class III region:butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complete |
| 7504 | 20469 | | 0.67 | 5.5E-01 | AB015596.1 | NT | Carassius auratus gene for gonadotropin II beta subunit, complete cds |
| 8792 | 21759 | 35181 | 0.66 | 5.5E-01 | A1791766.1 | EST_HUMAN | α82c01.y6 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1602339 5' |
| 10125 | 23051 | | 0.69 | 5.5E-01 | U88415.1 | NT | Crimean-Congo hemorrhagic fever virus strain SPU 415/85 nucleoprotein gene, complete cds |
| 10743 | 23665 | 37160 | 0.87 | 5.5E-01 | T05047.1 | EST_HUMAN | EST02635 Fetal brain, Stragogene (cat#936206) Homo sapiens cDNA clone HIFBQC35 |
| 146 | 13249 | 26178 | 9.02 | 5.4E-01 | 7657266 | NT | Homo sapiens KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA |
| 148 | 13249 | 26179 | 9.02 | 5.4E-01 | 7657266 | NT | Homo sapiens KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA |
| 587 | 13655 | 26569 | 1.34 | 5.4E-01 | AF232006.1 | NT | Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and Gsta (gsta) genes, complete cds; and unknown genes |
| 587 | 13655 | 26570 | 1.34 | 5.4E-01 | AF232006.1 | NT | Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and Gsta (gsta) genes, complete cds; and unknown genes |
| 1278 | 14311 | 27272 | 2.99 | 5.4E-01 | AW896087.1 | EST_HUMAN | QVJ-NN0040-070400-160-c04 NN0040 Homo sapiens cDNA |
| 2116 | 15133 | | 2.81 | 5.4E-01 | AE002247.2 | NT | Chlamydia pneumoniae AR39, section 74 of 84 of the complete genome |
| 2265 | 15279 | 28304 | 2.26 | 5.4E-01 | AJ276682.1 | NT | Drosophila melanogaster mRNA for 15,15' beta carotene dioxygenase (beta-diox gene) |
| 5740 | 18834 | 32014 | 0.91 | 5.4E-01 | AW842327.1 | EST_HUMAN | PM2-CN0300-030200-003-c10 CN0300 Homo sapiens cDNA |
| 6315 | 18386 | 32628 | 0.8 | 5.4E-01 | AB025017.1 | NT | Rattus norvegicus gene for TIS11, complete cds |
| 7226 | 20248 | 33582 | 0.77 | 5.4E-01 | BE96592.2 | EST_HUMAN | 601660276R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906090 3' |
| 7558 | 20521 | 33877 | 0.76 | 5.4E-01 | Z21619.1 | NT | S.cerevisiae RIB3 gene encoding DBP synthase |
| 7558 | 20521 | 33878 | 0.76 | 5.4E-01 | Z21619.1 | NT | S.cerevisiae RIB3 gene encoding DBP synthase |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 7560 | 20523 | 33881 | 1.78 | 5.4E-01 | Q64428 | SWISSPROT | MITOCHONDRIAL TRIFUNCTIONAL ENZYME ALPHA SUBUNIT PRECURSOR (TP-ALPHA) [INCLUDES: LONG-CHAIN ENOYL-COA HYDRATASE ; LONG CHAIN 3-HYDROXYACYL-COA DEHYDROGENASE] |
| 10349 | 23273 | | 1.93 | 5.4E-01 | BF572536.1 | EST_HUMAN | 602078545F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243890 5' |
| 11414 | 24358 | 37893 | 2.19 | 5.4E-01 | P36858 | SWISSPROT | NITRATE REDUCTASE [NADPH] (NR) |
| 11652 | 24589 | 38159 | 1.82 | 5.4E-01 | AW373694.1 | EST_HUMAN | QV4-BT0536-271299-058-H04 BT0536 Homo sapiens cDNA |
| 11941 | 24821 | 38416 | 3.29 | 5.4E-01 | Q60675 | SWISSPROT | LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN) |
| 11941 | 24821 | 38417 | 3.29 | 5.4E-01 | Q60675 | SWISSPROT | LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN) |
| 12215 | 25054 | | 3.88 | 5.4E-01 | A1858398.1 | EST_HUMAN | w137g04.x1 NCI_CGAP_U1 Homo sapiens cDNA clone IMAGE:2427126 3' similar to gb:M13452 LAMIN A (HUMAN); |
| 517 | 13588 | 26508 | 1.86 | 5.3E-01 | AF019413.1 | NT | Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21- hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B (Bf), and complement component C2 (C2) genes.> |
| 2150 | 15166 | 28182 | 0.97 | 5.3E-01 | AF113919.1 | NT | Brassica oleracea var. capitata phospholipase D2 (PLD2) gene, complete cds |
| 2794 | 15786 | 28803 | 8.62 | 5.3E-01 | 4506328 | NT | Brassica oleracea var. capitata phospholipase D2 (PLD2) gene, complete cds |
| 2794 | 15786 | 28804 | 8.62 | 5.3E-01 | 4506328 | NT | Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA |
| 3257 | 16311 | 28232 | 3.25 | 5.3E-01 | AF087658.1 | NT | Homo sapiens secreted C-type lectin precursor (LIS1C) gene, complete cds |
| 4239 | 17268 | | 1.33 | 5.3E-01 | U39887.1 | NT | Myoplasma genitalium section 9 of 51 of the complete genome |
| 5533 | 18631 | 31569 | 2.06 | 5.3E-01 | A1820921.1 | EST_HUMAN | zu42h12.y5 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740711 5' |
| 5533 | 18631 | 31570 | 2.06 | 5.3E-01 | A1820921.1 | EST_HUMAN | zu42h12.y5 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740711 5' |
| 5633 | 18729 | 31890 | 0.76 | 5.3E-01 | AA193672.1 | EST_HUMAN | zu42g09.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:666112 5' |
| 5633 | 18729 | 31891 | 0.76 | 5.3E-01 | AA193672.1 | EST_HUMAN | zu42g09.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:666112 5' |
| 5729 | 18823 | 32003 | 2 | 5.3E-01 | BE645620.1 | EST_HUMAN | 7e73c12.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783 |
| 5729 | 18823 | 32004 | 2 | 5.3E-01 | BE645620.1 | EST_HUMAN | 7e73c12.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783 |
| 9255 | 22221 | | 1.94 | 5.3E-01 | L01950.2 | NT | Protein DISULFIDE ISOMERASE PRECURSOR (HUMAN); Roridula gorgonias ribulose 1,5-bisphosphate carboxylase (bcl.) gene, partial cds; chloroplast gene for chloroplast product |
| 9307 | 22272 | 35703 | 0.76 | 5.3E-01 | BF433956.1 | EST_HUMAN | 7q71c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3' similar to contains element MER29 repetitive element ; |
| 9307 | 22272 | 35704 | 0.76 | 5.3E-01 | BF433956.1 | EST_HUMAN | 7q71c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3' similar to contains element MER29 repetitive element ; |

Table 4

Single Exon Probes Expressed In Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 10572 | 23494 | 36986 | 0.74 | 5.3E-01 | AI954210.1 | EST_HUMAN | vx94b02.x1 NCI_CGAP_Mat15 Homo sapiens cDNA clone IMAGE:2551275 3' similar to SW:COXA_HUMAN P20874 CYTOCHROME C OXIDASE POLYPEPTIDE VA PRECURSOR ; |
| 10977 | 23897 | 37410 | 0.7 | 5.3E-01 | 11428833 | NT | Homo sapiens nucleoporin 214KD (CAIN) (NUP214), mRNA |
| 11886 | 24767 | 38354 | 5.19 | 5.3E-01 | BE566291.1 | EST_HUMAN | 601339867F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682168 5' |
| 12144 | 25775 | | 4.97 | 5.3E-01 | AA916053.1 | EST_HUMAN | ag30e05.s1 NCI_CGAP_Br7 Homo sapiens cDNA clone IMAGE:1441376 3' similar to gb:J02611 |
| 817 | 13875 | 26823 | 16.24 | 5.2E-01 | L20770.1 | NT | APOLIPOPROTEIN D PRECURSOR (HUMAN); Drosophila melanogaster helix-loop-helix mRNA, complete cds |
| 1168 | 14209 | 27163 | 7.88 | 6.2E-01 | Q9WV30 | SWISSPROT | NUCLEAR FACTOR OF ACTIVATED T CELLS 5 (T CELL TRANSCRIPTION FACTOR NFAT5) (NF-AT5) (REL DOMAIN-CONTAINING TRANSCRIPTION FACTOR NFAT5) |
| 1195 | 14235 | 27190 | 3.01 | 5.2E-01 | AF224492.1 | NT | Homo sapiens phospholipid scramblase 1 gene, complete cds |
| 1903 | 14927 | | 3.19 | 5.2E-01 | AL163285.2 | NT | Homo sapiens chromosome 21 segment HS21C085 |
| 2156 | 15172 | 28191 | 2.36 | 5.2E-01 | AB018283.2 | NT | Homo sapiens mRNA for KIAA0740 protein, partial cds |
| 3136 | 16193 | 29102 | 1.57 | 5.2E-01 | U65942.1 | NT | Chlamydomonas abortus strain S2613 POM91A and POM90A precursor, genes, complete cds |
| 3251 | 16306 | | 1.14 | 5.2E-01 | D73443.1 | NT | Azotobacter vinelandii lcd gene for isocitrate dehydrogenase, complete cds |
| 3416 | 18464 | | 1.39 | 5.2E-01 | AL116780.1 | NT | Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation |
| 3458 | 16504 | 29424 | 2.72 | 5.2E-01 | AA984165.1 | EST_HUMAN | am77g05.s1 Striatagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1616504 3' |
| 3648 | 16691 | | 1 | 5.2E-01 | AF020269.1 | NT | Medicago sativa chloroplast malate dehydrogenase precursor (p1mdh) mRNA, nuclear gene encoding chloroplast protein, complete cds |
| 5180 | 18189 | | 1.04 | 5.2E-01 | AL163281.2 | NT | Homo sapiens chromosome 21 segment HS21C081 |
| 5736 | 18830 | 32008 | 1.02 | 5.2E-01 | AA284261.1 | EST_HUMAN | zc44d09.T7 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:325169 3' |
| 10088 | 25700 | 36489 | 0.84 | 5.2E-01 | X02218.1 | NT | Chicken duplicated genes for histone H2A, H4 and a histone H3 gene |
| 10088 | 25700 | 36490 | 0.84 | 5.2E-01 | X02218.1 | NT | Chicken duplicated genes for histone H2A, H4 and a histone H3 gene |
| 10292 | 23217 | 36701 | 0.52 | 5.2E-01 | AA194518.1 | EST_HUMAN | zp05b09.f1 Striatagene muscle 937209 Homo sapiens cDNA clone IMAGE:628793 5' |
| 10387 | 23309 | 36787 | 1.76 | 5.2E-01 | AF143952.2 | NT | Homo sapiens PELOTA (PELOTA) gene, complete cds |
| 13031 | 25578 | | 6.62 | 5.2E-01 | P18516 | SWISSPROT | RETINOIC ACID RECEPTOR GAMMA (RAR-GAMMA) (RETINOIC ACID RECEPTOR DELTA) (RAR-DELTA) |
| 819 | 13684 | 26602 | 2.34 | 5.1E-01 | M58509.1 | NT | Human adrenodoxin reductase gene, exons 3 to 12 |
| 649 | 13715 | 26636 | 3.53 | 5.1E-01 | AJ233944.1 | NT | Polyangium vitellinum (strain Pl vt1) 16S rRNA gene |
| 649 | 13715 | 26637 | 3.53 | 5.1E-01 | AJ233944.1 | NT | Polyangium vitellinum (strain Pl vt1) 16S rRNA gene |
| 1690 | 14692 | | 1.28 | 5.1E-01 | X87885.1 | NT | R.norvegicus mRNA for mammalian fusca protein |
| 4103 | 17137 | 30032 | 4.81 | 5.1E-01 | AI858495.1 | EST_HUMAN | mf39b12.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2427263 3' |
| 4216 | 17245 | 30130 | 2.99 | 5.1E-01 | P96380 | SWISSPROT | TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF) |
| 6348 | 19417 | 32658 | 0.57 | 5.1E-01 | BE541068.1 | EST_HUMAN | 601063808F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3450000 5' |
| 6407 | 19475 | | 0.83 | 5.1E-01 | AV712326.1 | EST_HUMAN | AV712326 DCA Homo sapiens cDNA clone DCAAU07 5' |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 7102 | 20036 | 33339 | 1.52 | 5.1E-01 | R08073.1 | EST_HUMAN | y94a09.s1 Soares placenta Nb2-HP Homo sapiens cDNA clone IMAGE:146872 3' |
| 8818 | 21884 | 35309 | 0.62 | 5.1E-01 | AW806881.1 | EST_HUMAN | QV4-ST0023-160400-172-a01 ST0023 Homo sapiens cDNA |
| 8918 | 21884 | 35310 | 0.62 | 5.1E-01 | AW806881.1 | EST_HUMAN | QV4-ST0023-160400-172-a01 ST0023 Homo sapiens cDNA |
| 10043 | 22970 | 36437 | 4.3 | 5.1E-01 | J05412.1 | NT | Human regenerating protein (reg) gene, complete cds |
| 10046 | 22973 | 36440 | 3.2 | 5.1E-01 | W22302.1 | EST_HUMAN | 65B1 Human retina cDNA Tsp509I-cleaved sublibrary Homo sapiens cDNA not directional |
| 10521 | 23443 | 36941 | 0.89 | 5.1E-01 | M94579.1 | NT | Human carboxyl ester lipase (CEL) gene, complete cds |
| 12264 | 25088 | 38174 | 2.09 | 5.1E-01 | BF540777.1 | EST_HUMAN | 602067471F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4066744 5' |
| 12368 | 25709 | | 2.47 | 5.1E-01 | BF030207.1 | EST_HUMAN | 601556863F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826767 5' |
| 12611 | 25310 | | 3.62 | 5.1E-01 | BF439882.1 | EST_HUMAN | nac51110.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3406218 3' similar to contains element |
| 2144 | 15161 | 28176 | 0.97 | 5.0E-01 | 4885552 | NT | TAR1 repetitive element; |
| 2144 | 15161 | 28177 | 0.97 | 5.0E-01 | 4885552 | NT | Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA |
| 2154 | 15170 | 28187 | 2.39 | 5.0E-01 | AF008210.1 | NT | Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA |
| 2154 | 15170 | 28188 | 2.39 | 5.0E-01 | AF008210.1 | NT | Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEB), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene> |
| 2172 | 15188 | | 0.91 | 5.0E-01 | AL161533.2 | NT | Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEB), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene> |
| 3761 | 16802 | 29714 | 0.8 | 5.0E-01 | U55574.1 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 33 |
| 3842 | 16882 | 29796 | 1 | 5.0E-01 | L39483.1 | NT | Mus musculus anti-DNA immunoglobulin light chain IgM mRNA, antibody 363p.138, partial cds |
| 3887 | 16927 | 29835 | 2.74 | 5.0E-01 | AB033010.1 | NT | Rattus norvegicus jagged protein mRNA, complete cds |
| 6801 | 18855 | | 0.64 | 5.0E-01 | BF576199.1 | EST_HUMAN | Homo sapiens mRNA for KIAA1184 protein, partial cds |
| 7926 | 20869 | 34256 | 0.68 | 5.0E-01 | AL161549.2 | NT | 602132642F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271939 5' |
| 7926 | 20869 | 34257 | 0.66 | 5.0E-01 | AL161549.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 49 |
| 8875 | 21842 | | 1.87 | 5.0E-01 | M92304.1 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 49 |
| 9018 | 21884 | 35404 | 0.59 | 5.0E-01 | BF107948.1 | EST_HUMAN | Xenopus laevis smooth muscle beta-tropomyosin mRNA, complete cds |
| 9813 | 21136 | 34538 | 3.16 | 5.0E-01 | BF171212.1 | EST_HUMAN | 601823850R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043485 3' |
| | | | | | | | 601903871F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4136632 5' |
| | | | | | | | GLYCOTEN DEBRANCHING ENZYME (GLYCOTEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)] |
| 9983 | 22910 | 36375 | 1.31 | 5.0E-01 | P35573 | SWISSPROT | GLYCOTEN DEBRANCHING ENZYME (GLYCOTEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)] |
| 9983 | 22910 | 36376 | 1.31 | 5.0E-01 | P35573 | SWISSPROT | GLYCOTEN DEBRANCHING ENZYME (GLYCOTEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)] |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 10756 | 23678 | | 1.38 | 5.0E-01 | BE869218.1 | EST_HUMAN | 601445024F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849436 5' |
| 12302 | 25113 | | 6.28 | 5.0E-01 | AF029215.1 | NT | Mus musculus MRC OX-2 antigen homolog gene, exons 2-6, and complete cds |
| 13004 | 25558 | | 2.21 | 5.0E-01 | AL163302.2 | NT | Homo sapiens chromosome 21 segment HS21C102 |
| 13011 | 25563 | | 5.8 | 5.0E-01 | O13961 | SWISSPROT | NUCLEAR ENVELOPE PROTEIN CUT11 |
| 790 | 13849 | 26796 | 2.03 | 4.9E-01 | BF571462.1 | EST_HUMAN | 602076649F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243860 5' |
| 1668 | 14700 | 27675 | 2.37 | 4.9E-01 | AJ243955.1 | NT | Xenopus laevis mRNA for c-Jun protein, 1978 BP |
| 1921 | 14945 | 27941 | 0.99 | 4.9E-01 | U40893.1 | NT | Cavia porcellus pulmonary surfactant protein A (SP-a) mRNA, complete cds |
| 5480 | 18580 | 31491 | 1.43 | 4.9E-01 | Q61554 | SWISSPROT | FIBRILLIN 1 PRECURSOR |
| 6153 | 19228 | 32457 | 2.67 | 4.9E-01 | AF020931.1 | NT | Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10 |
| 6153 | 19228 | 32458 | 2.67 | 4.9E-01 | AF020931.1 | NT | Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10 |
| 7685 | 20643 | 34007 | 1.69 | 4.9E-01 | AB040051.1 | NT | Oryza sativa subsp. japonica mEF-G mRNA for mitochondrial elongation factor G, complete cds |
| 7972 | 20911 | 34301 | 0.7 | 4.9E-01 | Q10606 | SWISSPROT | PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N-ACETYLGLUCOSAMINYLTRANSFERASE |
| 7972 | 20911 | 34302 | 0.7 | 4.9E-01 | Q10606 | SWISSPROT | PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N-ACETYLGLUCOSAMINYLTRANSFERASE |
| 9341 | 22306 | | 1.77 | 4.9E-01 | BF209791.1 | EST_HUMAN | 601874964F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4102503 5' |
| 9542 | 22505 | 35954 | 0.99 | 4.9E-01 | AW339905.1 | EST_HUMAN | hc90c02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2907266 3' similar to TR:O85714 |
| 9651 | 26009 | | 2.64 | 4.9E-01 | 10946863 | NT | O85714 HERC2 ; |
| 10681 | 23603 | 37097 | 0.86 | 4.9E-01 | AF053980.1 | NT | Mus musculus unc13 homolog (C. elegans) 1 (Unc13h1), mRNA |
| 10888 | 23808 | 37314 | 0.57 | 4.9E-01 | X90000.1 | NT | Mus musculus adenyl cyclase 1 (Adcy1) cDNA, partial cds |
| 12196 | 25041 | | 1.41 | 4.9E-01 | AF176912.1 | NT | H. sapiens DNA for BCL7A gene and BCL7A/IGH locus fusion |
| 12997 | 25963 | | 6.43 | 4.9E-01 | AA613662.1 | EST_HUMAN | Homo sapiens neurotrophin-1/B-cell stimulating factor-3 gene, complete cds |
| 5585 | 18681 | 31649 | 8.83 | 4.8E-01 | J02987.1 | NT | mq22e11.s1 NCL_CGAP_Cor10 Homo sapiens cDNA clone IMAGE:1144652 3' |
| 5836 | 18889 | 33184 | 0.69 | 4.8E-01 | U92882.1 | NT | Saccharomyces cerevisiae sporulation protein (SPO11) gene required for meiotic recombination, complete cds |
| 6846 | 18899 | | 3.82 | 4.8E-01 | AA659878.1 | EST_HUMAN | Mus musculus slow skeletal muscle tropomyosin T (Tmt1) gene, complete cds |
| 7538 | 20501 | | 1.98 | 4.8E-01 | 5031660 | NT | nu8f09.a1 NCL_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1217513 |
| 7929 | 20872 | 34261 | 0.78 | 4.8E-01 | AL163209.2 | NT | Homo sapiens reproduction 8 (D8S2298E) mRNA |
| 8037 | 20974 | 34369 | 3.56 | 4.8E-01 | AL161492.2 | NT | Homo sapiens chromosome 21 segment HS21C009 |
| 8037 | 20974 | 34370 | 3.56 | 4.8E-01 | AL161492.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4 |
| 8237 | 21206 | 34611 | 0.98 | 4.8E-01 | A1820744.1 | EST_HUMAN | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4 |
| 9600 | 22604 | | 0.87 | 4.8E-01 | BE155148.1 | EST_HUMAN | y7710.y5 Soares breast 2NbtHbt Homo sapiens cDNA clone IMAGE:154795 5' similar to contains element MER8 repetitive element ; |
| 10368 | 23291 | | 0.56 | 4.8E-01 | BF568633.1 | EST_HUMAN | PM1-HT0350-201299-004-b04 HT0350 Homo sapiens cDNA |
| 11081 | 24043 | | 1.75 | 4.8E-01 | X83502.1 | NT | 602184267F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300048 5' |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 12277 | 25098 | | 1.65 | 4.8E-01 | AL163227.2 | NT | Homo sapiens chromosome 21 segment HS21C027 |
| 12503 | 25737 | | 3.32 | 4.8E-01 | AF227565.1 | NT | Trypanosoma cruzi transposon VIP II SIRE repeat region |
| 13088 | 25786 | | 1.49 | 4.8E-01 | AJ132984.1 | NT | Chlamydomonas reinhardtii cop gene, exons 1-8 |
| 6664 | 19721 | 32896 | 8.88 | 4.7E-01 | BF217173.1 | EST_HUMAN | 601883380F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4096387 5' |
| 7241 | 19976 | 33273 | 0.92 | 4.7E-01 | AI204374.1 | EST_HUMAN | q772a09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755544 3' |
| 8197 | 21167 | 34577 | 0.59 | 4.7E-01 | T11414.1 | EST_HUMAN | hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811 5'end |
| 8197 | 21167 | 34578 | 0.59 | 4.7E-01 | T11414.1 | EST_HUMAN | hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811 5'end |
| 9430 | 22394 | 35834 | 0.57 | 4.7E-01 | 6981501 | NT | Rattus norvegicus Spermathe binding protein (Sbp), mRNA |
| 11193 | 24148 | | 4.76 | 4.7E-01 | AF102873.1 | NT | Influenza A virus isolate HK51697 hemagglutinin (HA) gene, partial cds |
| 11422 | 24366 | 37901 | 1.78 | 4.7E-01 | U41069.1 | NT | Human collagen alpha2(X) (COL11A2) gene, exons 6 through 16, and partial cds |
| 11613 | 24551 | 38111 | 1.74 | 4.7E-01 | BF529658.1 | EST_HUMAN | 602043889F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4181303 5' |
| 11704 | 24659 | 38246 | 1.49 | 4.7E-01 | AW889448.1 | EST_HUMAN | RC8-NT0028-240400-011-E08 NT0029 Homo sapiens cDNA |
| 12399 | 25173 | | 1.53 | 4.7E-01 | BE887763.1 | EST_HUMAN | 601511333F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912488 5' |
| 12929 | 25513 | | 1.38 | 4.7E-01 | BF79515.1 | EST_HUMAN | 602153926F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294974 5' |
| 3756 | 16798 | 29709 | 1.53 | 4.6E-01 | BF693300.1 | EST_HUMAN | 602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5' |
| 3756 | 16798 | 29710 | 1.53 | 4.6E-01 | BF693300.1 | EST_HUMAN | 602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5' |
| 5190 | 18198 | | 0.93 | 4.6E-01 | M11267.1 | NT | Bovine steroid 21-hydroxylase gene (P-450-c21) gene, complete cds |
| 5493 | 18593 | 31503 | 1 | 4.6E-01 | BF313593.1 | EST_HUMAN | 601900234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129472 5' |
| 5493 | 18593 | 31504 | 1 | 4.6E-01 | BF313593.1 | EST_HUMAN | 601900234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129472 5' |
| 5548 | 18645 | 31586 | 3.33 | 4.6E-01 | Q90843 | SWISSPROT | INTERFERON REGULATORY FACTOR 3 (IRF-3) |
| 5548 | 18645 | 31587 | 3.33 | 4.6E-01 | Q90843 | SWISSPROT | INTERFERON REGULATORY FACTOR 3 (IRF-3) |
| 5625 | 18721 | 31880 | 1.95 | 4.6E-01 | BE734781.1 | EST_HUMAN | 601568755F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843637 5' |
| 5639 | 18735 | 31897 | 3.12 | 4.6E-01 | AI247679.1 | EST_HUMAN | qh59h02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to |
| 5639 | 18735 | 31898 | | | | | TR:O15338 O15338 BUTYROPHILIN.; |
| 5647 | 18743 | 31909 | 3.12 | 4.6E-01 | AI247679.1 | EST_HUMAN | qh59h02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to |
| 5730 | 18824 | | 1.46 | 4.6E-01 | P20050 | SWISSPROT | TR:O15338 O15338 BUTYROPHILIN.; |
| 5821 | 18911 | | 0.85 | 4.6E-01 | AF212124.1 | NT | MEIOSIS SPECIFIC PROTEIN HOP1 |
| 6002 | 19085 | 32285 | 0.78 | 4.6E-01 | BE817247.1 | EST_HUMAN | Anolis schwartzi cytochrome b gene, partial cds; mitochondrial gene for mitochondrial product |
| | | | 0.51 | 4.6E-01 | D26215.1 | NT | PMO-BN0260-120600-001-F07 BN0260 Homo sapiens cDNA |
| | | | | | | | Unidentified soil bacteria 16S rRNA gene encoding 16S ribosomal RNA |
| | | | | | | | Methanobacterium thermoautotrophicum from bases 1165751 to 1176238 (section 100 of 148) of the complete genome |
| 6388 | 19454 | 32699 | 0.92 | 4.6E-01 | AE000894.1 | NT | Bacillus subtilis Bbma (bbma) gene, complete cds |
| 6881 | 19933 | 33231 | 0.52 | 4.6E-01 | AF115340.1 | NT | |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 6932 | 20158 | 33474 | 1.43 | 4.8E-01 | U62332.1 | NT | Emricella nidulans NEMPA (nemPA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds |
| 6932 | 20158 | 33475 | 1.43 | 4.8E-01 | U62332.1 | NT | Emricella nidulans NEMPA (nemPA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds |
| 7441 | 25981 | 33759 | 0.53 | 4.8E-01 | L07320.1 | NT | Murine cytomegalovirus $\alpha 1$ protein gene, complete cds |
| 8001 | 20940 | 34333 | 0.78 | 4.8E-01 | AA493577.1 | EST_HUMAN | h04h05.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943353 similar to contains Alu repetitive element; contains element L1 repetitive element; |
| 8083 | 21029 | | 0.53 | 4.8E-01 | AE004031.1 | NT | Xylella fastidiosa, section 177 of 229 of the complete genome |
| 8863 | 21831 | 35052 | 13.28 | 4.8E-01 | BF697399.1 | EST_HUMAN | 802130953F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4287828 5' |
| 9089 | 22065 | 35490 | 0.47 | 4.8E-01 | AA832237.1 | EST_HUMAN | 0076b08.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1572087 3' similar to gb:M36341 ADP-RIBOSYLATION FACTOR 4 (HUMAN); |
| 9099 | 22065 | 35491 | 0.47 | 4.8E-01 | AA832237.1 | EST_HUMAN | 0076b08.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1572087 3' similar to gb:M36341 ADP-RIBOSYLATION FACTOR 4 (HUMAN); |
| 9656 | 22599 | 36048 | 0.99 | 4.8E-01 | P55202 | SWISSPROT | ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE) |
| 9656 | 22599 | 36049 | 0.99 | 4.8E-01 | P55202 | SWISSPROT | ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE) |
| 10024 | 22951 | 36418 | 0.89 | 4.8E-01 | AF162283.1 | NT | Glycine max acetyl-CoA carboxylase (accB-1) gene, complete cds; nuclear gene for chloroplast product |
| 10024 | 22951 | 36419 | 0.89 | 4.8E-01 | AF162283.1 | NT | Glycine max acetyl-CoA carboxylase (accB-1) gene, complete cds; nuclear gene for chloroplast product |
| 10335 | 23259 | 36736 | 1.62 | 4.8E-01 | A1915634.1 | EST_HUMAN | wg73e12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370786 3' |
| 10335 | 23259 | 36737 | 1.62 | 4.8E-01 | A1915634.1 | EST_HUMAN | wg73e12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370786 3' |
| 11335 | 24285 | | 2.28 | 4.8E-01 | P98163 | SWISSPROT | PUTATIVE VITELLOGENIN RECEPTOR PRECURSOR (YL) |
| 11343 | 24283 | 37818 | 4.94 | 4.8E-01 | BE185449.1 | EST_HUMAN | IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA |
| 11343 | 24283 | 37819 | 4.94 | 4.8E-01 | BE185449.1 | EST_HUMAN | IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA |
| 11445 | 24388 | 37930 | 3.88 | 4.8E-01 | BE272325.1 | EST_HUMAN | 601126068F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2989865 5' |
| 11789 | 23954 | 37476 | 4.41 | 4.8E-01 | AF019369.1 | NT | Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds |
| 11789 | 23954 | 37477 | 4.41 | 4.8E-01 | AF019369.1 | NT | Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds |
| 12449 | 25208 | | 1.69 | 4.8E-01 | D53316.1 | EST_HUMAN | HUM105F03B Clontech human fetal brain polyA+ mRNA (#6635) Homo sapiens cDNA clone GEN-105F03 5' |
| 1718 | 14748 | | 0.92 | 4.5E-01 | BE311420.1 | EST_HUMAN | 601142105F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3505993 5' |
| 1926 | 14950 | 27946 | 1.34 | 4.5E-01 | AE001931.1 | NT | Deinococcus radiodurans R1 section 88 of 229 of the complete chromosome 1 |
| 1926 | 14950 | 27947 | 1.34 | 4.5E-01 | AE001931.1 | NT | Deinococcus radiodurans R1 section 88 of 229 of the complete chromosome 1 |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 2881 | 15940 | 28857 | 5.36 | 4.5E-01 | AA677086.1 | EST_HUMAN | z55d02.s1 Soares fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:454179 3' |
| 3328 | 16379 | 29300 | 3.85 | 4.5E-01 | Q05763 | SWISSPROT | BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN |
| 3389 | 16438 | 29364 | 1.62 | 4.5E-01 | AF126378.1 | NT | PRECURSOR (HSPG) (PERLECAN) (PLC) |
| 4060 | 17096 | | 1.23 | 4.5E-01 | Q28247 | SWISSPROT | Mus musculus DNA polymerase epsilon catalytic subunit (Pole) gene, exons 2 through 12 |
| 4101 | 17135 | 30030 | 1.12 | 4.5E-01 | A1708908.1 | EST_HUMAN | COLLAGEN ALPHA 5(V) CHAIN |
| 4205 | 18325 | | 4.08 | 4.5E-01 | AW873495.1 | EST_HUMAN | as96d09.x1 Barslead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2353480 3' |
| 4980 | 17895 | 30884 | 1.09 | 4.5E-01 | BE963445.2 | EST_HUMAN | hs60g02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3041810 3' |
| 5628 | 18724 | 31885 | 1.3 | 4.5E-01 | AW608814.1 | EST_HUMAN | 601687225R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866023 3' |
| 6760 | 19814 | | 1.74 | 4.5E-01 | Q00956 | SWISSPROT | QV2-PT0012-140100-031-c09 PT0012 Homo sapiens cDNA |
| 7644 | 20604 | 33969 | 0.93 | 4.5E-01 | M37036.1 | NT | COAT PROTEIN |
| 7867 | 20811 | 34183 | 2.64 | 4.5E-01 | A1858849.1 | EST_HUMAN | Rat nucleolar proteins B23.1 and B23.2 |
| 7991 | 20930 | 34325 | 0.51 | 4.5E-01 | P50070 | SWISSPROT | w32d02.x1 NCL_CGAP_U1 Homo sapiens cDNA clone IMAGE:2426618 3' similar to TR:Q92923 Q92923 |
| 8650 | 21618 | | 0.87 | 4.5E-01 | M32661.1 | NT | SWISNF COMPLEX 170 KDA SUBUNIT. ; |
| 8746 | 21714 | 35137 | 3.86 | 4.5E-01 | A1848596.1 | EST_HUMAN | D.melanogaster Shw2 protein mRNA, complete cds |
| | | | | | | | ts56g11.x1 NCL_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2282644 3' |
| 8905 | 21871 | 35297 | 0.74 | 4.5E-01 | Q52728 | SWISSPROT | POLY-BETA-HYDROXYBUTYRATE POLYMERASE (POLY(3-HYDROXYBUTYRATE) POLYMERASE) |
| 9133 | 22099 | | 1.72 | 4.5E-01 | 11444786 | NT | (PHB POLYMERASE) (PHB SYNTHASE) (POLY(3-HYDROXYALKANOATE) POLYMERASE) (PHA |
| 9351 | 22316 | 35742 | 0.78 | 4.5E-01 | AE000218.1 | NT | POLYMERASE) (PHA SYNTHASE) (POLYHYDROXYALKANOIC ACID SYNTHASE) |
| 10300 | 23225 | | 0.89 | 4.5E-01 | 9630816 | NT | Homo sapiens hypothetical protein DKFZp547G183 (DKFZp547G183), mRNA |
| 10861 | 23781 | 37281 | 26.2 | 4.5E-01 | M86006.1 | EST_HUMAN | Escherichia coli K-12 MG1655 section 108 of 400 of the complete genome |
| 10861 | 23781 | 37282 | 26.2 | 4.5E-01 | M86006.1 | EST_HUMAN | Bombyx mori nuclear polyhedrosis virus, complete genome |
| 11212 | 24165 | 37695 | 2.3 | 4.5E-01 | AW591271.1 | EST_HUMAN | EST02531 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCY17 |
| 12165 | 25955 | | 5.3 | 4.5E-01 | BE871461.1 | EST_HUMAN | EST02531 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCY17 |
| 12349 | 25144 | | 1.48 | 4.5E-01 | O18638 | SWISSPROT | EST02531 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCY17 |
| 12452 | 25211 | | 1.54 | 4.5E-01 | AJ132045.1 | NT | xo14h01.x1 NCL_CGAP_U13 Homo sapiens cDNA clone IMAGE:2703985 3' similar to SW:INT8_MOUSE |
| 12891 | 25478 | | 8.22 | 4.5E-01 | 11422099 | NT | Q64252 VIRAL INTEGRATION SITE PROTEIN INT-6. [1]; |
| 2052 | 15071 | | 2.23 | 4.4E-01 | 6680503 | NT | 601449201F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852961 5' |
| | | | | | | | OUT AT FIRST PROTEIN |
| | | | | | | | Theileria annulata shAT2 gene |
| | | | | | | | Homo sapiens testis-specific kinase 2 (TESK2), mRNA |
| | | | | | | | Mus musculus integral membrane-associated protein 1 (limap1), mRNA |
| 2398 | 15405 | 28430 | 7.02 | 4.4E-01 | P49765 | SWISSPROT | VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED FACTOR) |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 3328 | 16377 | 29298 | 1.36 | 4.4E-01 | AF058790.1 | NT | Rattus norvegicus SynGAP-b mRNA, complete cds |
| 3328 | 16377 | 29299 | 1.36 | 4.4E-01 | AF058790.1 | NT | Rattus norvegicus SynGAP-b mRNA, complete cds |
| 3330 | 16381 | 29302 | 1.9 | 4.4E-01 | BF056726.1 | EST_HUMAN | 7197402.y1 NCL_CGAP_B116 Homo sapiens cDNA clone IMAGE:3383795 5' |
| 4262 | 17291 | | 1.75 | 4.4E-01 | BE378707.1 | EST_HUMAN | 601237139F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:360393 5' |
| 5494 | 18594 | 31505 | 1.63 | 4.4E-01 | P04929 | SWISSPROT | HISTIDINE-RICH GLYCOPROTEIN PRECURSOR |
| 5494 | 18594 | 31506 | 1.63 | 4.4E-01 | P04929 | SWISSPROT | HISTIDINE-RICH GLYCOPROTEIN PRECURSOR |
| 5772 | 18864 | 32045 | 1.77 | 4.4E-01 | S66019.1 | NT | much [rats, Sprague-Dawley, sulfur-dioxide-treated tracheal epithelium, mRNA Partial, 390 nt] |
| 5790 | 18862 | 32064 | 1.82 | 4.4E-01 | AV720408.1 | EST_HUMAN | AV720408 GLC Homo sapiens cDNA clone GLCSC12 5' |
| 6064 | 19145 | 32356 | 1.42 | 4.4E-01 | A1198413.1 | EST_HUMAN | q182h11.x1 NCL_CGAP_B1m25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR:Q29168 Q29168 |
| 6064 | 19145 | 32357 | 1.42 | 4.4E-01 | A1198413.1 | EST_HUMAN | q182h11.x1 NCL_CGAP_B1m25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR:Q29168 Q29168 |
| 6368 | 19436 | 32680 | 1.9 | 4.4E-01 | AW080795.1 | EST_HUMAN | xc27e08.x1 NCL_CGAP_C018 Homo sapiens cDNA clone IMAGE:2585510 3' similar to TR:O95154 O95154 |
| 6462 | 19527 | | 1.17 | 4.4E-01 | AA776132.1 | EST_HUMAN | AF140311.s1 Striatagene schizo brain S11 Homo sapiens cDNA clone IMAGE:509836 3' |
| 7627 | 20587 | 33950 | 0.95 | 4.4E-01 | AE000571.1 | NT | TYROSINE-PROTEIN KINASE LYN (HUMAN); |
| 8173 | 21143 | | 12.58 | 4.4E-01 | Z11679.1 | NT | Helicobacter pylori 26695 section 49 of 134 of the complete genome |
| 9115 | 22081 | 35509 | 0.74 | 4.4E-01 | AA056427.1 | EST_HUMAN | Siuberosum mRNA for induced siobin lip protein (partial) |
| 9506 | 22469 | 35913 | 0.72 | 4.4E-01 | AF112540.1 | NT | z68a03.s1 Striatagene cdon (#937204) Homo sapiens cDNA clone IMAGE:509836 3' |
| 9538 | 22501 | 35949 | 0.56 | 4.4E-01 | AW612578.1 | EST_HUMAN | HIV-1 isolate 08107v6 from USA, envelope glycoprotein (env) gene, partial cds |
| 9645 | 22589 | 36038 | 1.21 | 4.4E-01 | O62838 | SWISSPROT | h05008.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2954222 3' similar to SW:MSH6 HUMAN P52701 DNA MISMATCH REPAIR PROTEIN MSH6 ; |
| 10321 | 23245 | 36725 | 2.1 | 4.4E-01 | A1268650.1 | EST_HUMAN | ZINC FINGER X-CHROMOSOMAL PROTEIN |
| 10322 | 23246 | | 3.91 | 4.4E-01 | P28922 | SWISSPROT | q33909.x1 NCL_CGAP_Lj15 Homo sapiens cDNA clone IMAGE:1910921 3' |
| 10457 | 23379 | 36872 | 5.07 | 4.4E-01 | P35590 | SWISSPROT | GLYCOPROTEIN B PRECURSOR (GLYCOPROTEIN 14) |
| 10740 | 23662 | 37158 | 1.27 | 4.4E-01 | S78404.1 | NT | TYROSINE-PROTEIN KINASE RECEPTOR TIE-1 PRECURSOR |
| 10740 | 23662 | 37157 | 1.27 | 4.4E-01 | S78404.1 | NT | beta-HKA=H-K-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2] |
| 12432 | 25198 | 31824 | 5.76 | 4.4E-01 | 6877874 | NT | beta-HKA=H-K-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2] |
| 12861 | 25465 | 31727 | 2.83 | 4.4E-01 | 9627742 | NT | Mus musculus sodium channel, type X, alpha polypeptide (Scn10a), mRNA |
| 12867 | 25535 | | 1.45 | 4.4E-01 | P54725 | SWISSPROT | Autographa californica nucleopolydnavirus, complete genome |
| 411 | 13484 | 26419 | 2.49 | 4.3E-01 | AF155218.1 | NT | UV EXCISION REPAIR PROTEIN PROTEIN RAD23 HOMOLOG A (HHR23A) |
| 411 | 13484 | 26420 | 2.49 | 4.3E-01 | AF155218.1 | NT | Callitrix jacchus MW/LW opsin gene, upstream flanking region |
| 1607 | 14639 | 27616 | 0.96 | 4.3E-01 | AW866550.1 | EST_HUMAN | Callitrix jacchus MW/LW opsin gene, upstream flanking region |

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Table 4
Single Exon Probes Expressed In Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 2883 | 16942 | | 1.83 | 4.3E-01 | AW935269.1 | EST_HUMAN | CM2-DT0003-010200-077-c01 DT0003 Homo sapiens cDNA |
| 3073 | 16130 | 29042 | 0.94 | 4.3E-01 | AW999477.1 | EST_HUMAN | MRO-BN0070-270300-008-g04 BN0070 Homo sapiens cDNA |
| 4178 | 17209 | 30085 | 1.32 | 4.3E-01 | J00306.1 | NT | Human somatostatin 1 gene and flanks |
| 4435 | 13484 | 26419 | 1.63 | 4.3E-01 | AF155218.1 | NT | Calitritix jacchus MW/LW opsin gene, upstream flanking region |
| 4435 | 13484 | 26420 | 1.63 | 4.3E-01 | AF155218.1 | NT | Calitritix jacchus MW/LW opsin gene, upstream flanking region |
| 5154 | 18164 | | 1.17 | 4.3E-01 | 9635250 | NT | Xestia c-nigrum granulovirus, complete genome |
| 5291 | 18296 | 31157 | 1.16 | 4.3E-01 | BE780162.1 | EST_HUMAN | 801468030F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3871255 5' |
| 5438 | 18540 | 31449 | 0.89 | 4.3E-01 | P48634 | SWISSPROT | LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2) |
| 5438 | 18540 | 31450 | 0.89 | 4.3E-01 | P48634 | SWISSPROT | LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2) |
| 5990 | 19075 | 32273 | 1.5 | 4.3E-01 | BE181655.1 | EST_HUMAN | QV1-HT0638-070500-191-d08 HT0638 Homo sapiens cDNA |
| 6010 | 19093 | 32293 | 1.93 | 4.3E-01 | AF179825.1 | NT | Salinix sclerous difactory receptor (SSC186) gene, partial cds |
| 6866 | 19919 | 33214 | 4 | 4.3E-01 | AJ001678.1 | NT | Coturnix coturnix japonica linc gene |
| 7049 | 20071 | | 0.86 | 4.3E-01 | O33367 | SWISSPROT | DNA GYRASE SUBUNIT B |
| 7662 | 20622 | | 1.83 | 4.3E-01 | BF348001.1 | EST_HUMAN | 602023134F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4158296 5' |
| 8116 | 21053 | | 0.62 | 4.3E-01 | M58643.1 | NT | Human lipoprotein associated coagulation inhibitor (LACI) gene, exon 2 |
| 8770 | 21737 | | 2.56 | 4.3E-01 | U97040.1 | NT | Methanococcus voltae flagella-related protein C-1 (flaC-fla) genes, complete cds |
| 9610 | 22614 | 36066 | 1.04 | 4.3E-01 | Y14604.1 | NT | Erwinia amylovora rcsV gene |
| 10084 | 23011 | 36483 | 1.88 | 4.3E-01 | AW630048.1 | EST_HUMAN | h174e10.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968554 5' |
| 10084 | 23011 | 36484 | 1.88 | 4.3E-01 | AW630048.1 | EST_HUMAN | h174e10.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968554 5' |
| 10589 | 23511 | 37005 | 0.85 | 4.3E-01 | AW170559.1 | EST_HUMAN | nr63e05.x1 Soares_NHCeC_cervical_tumor Homo sapiens cDNA clone IMAGE:2698400 3' similar to TR:000169 O00189 MU-ADAPTIN-RELATED PROTEIN 2 ; |
| 10879 | 23799 | 37301 | 0.48 | 4.3E-01 | H65292.1 | EST_HUMAN | y45605.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:208209 3' |
| 11277 | 20178 | 33603 | 1.55 | 4.3E-01 | AF075629.1 | NT | Equus caballus microsatellite LEX027 |
| 11539 | 24480 | 38031 | 1.77 | 4.3E-01 | AW993658.1 | EST_HUMAN | RC3-BN0034-290200-013-c12 BN0034 Homo sapiens cDNA |
| 11539 | 24480 | 38032 | 1.77 | 4.3E-01 | AW993658.1 | EST_HUMAN | RC3-BN0034-290200-013-c12 BN0034 Homo sapiens cDNA |
| 13055 | 25592 | | 2.24 | 4.3E-01 | AJ003022.1 | NT | Streptomyces coelicolor whiH gene |
| 1360 | 18685 | 27365 | 1.77 | 4.2E-01 | Q39102 | SWISSPROT | CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR |
| 3623 | 16666 | 29580 | 4.43 | 4.2E-01 | AE003947.1 | NT | Xylella fastidiosa, section 93 of 229 of the complete genome |
| 3651 | 16694 | 29609 | 1.04 | 4.2E-01 | AI280338.1 | EST_HUMAN | q94b01.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1879945 3' |
| 3724 | 18324 | | 1.22 | 4.2E-01 | N81203.1 | EST_HUMAN | 768E1 fetal brain cDNA Homo sapiens cDNA clone 768E1-K similar to R07879, Z40498 |
| 3893 | 18933 | 29843 | 0.69 | 4.2E-01 | AW835527.1 | EST_HUMAN | QV0-L T0015-180200-127-h01 LT0015 Homo sapiens cDNA |
| 4007 | 17048 | 29953 | 1.72 | 4.2E-01 | Q04886 | SWISSPROT | SOX-8 PROTEIN |
| 4726 | 17746 | 30637 | 4.9 | 4.2E-01 | AA534093.1 | EST_HUMAN | np68h01.s1 NCI_CGAP_P10 Homo sapiens cDNA clone IMAGE:997777 similar to gb:M33600 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-1 BETA CHAIN (HUMAN); |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 4820 | 17837 | 30735 | 3.62 | 4.2E-01 | R13467.1 | EST_HUMAN | y77601.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:28278 5' |
| 5801 | 18893 | 32076 | 1.38 | 4.2E-01 | BF242055.1 | EST_HUMAN | 601879721F1 NIH_MGC_35 Homo sapiens cDNA clone IMAGE:4108493 5' |
| 5876 | 18965 | 32156 | 1.23 | 4.2E-01 | AW854162.1 | EST_HUMAN | RC3-C10254-060400-023-g04 CT0254 Homo sapiens cDNA |
| 6329 | 19399 | 32641 | 0.91 | 4.2E-01 | AL163247.2 | NT | Homo sapiens chromosome 21 segment HS21C047 |
| 7139 | 20115 | 33428 | 9.39 | 4.2E-01 | AU158472.1 | EST_HUMAN | AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3' |
| 7139 | 20115 | 33428 | 9.39 | 4.2E-01 | AU158472.1 | EST_HUMAN | AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3' |
| 7207 | 25877 | 33563 | 5.51 | 4.2E-01 | S82504.1 | NT | Breast-breast cancer gene (rats, WF, spleen, Genomic, 419 nt, segment 2 of 2) |
| 7300 | 20272 | 33607 | 5.9 | 4.2E-01 | AL161547.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 47 |
| 7822 | 20770 | 34149 | 0.52 | 4.2E-01 | AL163252.2 | NT | Homo sapiens chromosome 21 segment HS21C052 |
| 8325 | 21294 | 34708 | 2.56 | 4.2E-01 | AW857448.1 | EST_HUMAN | EST369413 MAGI resequences, MAGE Homo sapiens cDNA |
| 8325 | 21294 | 34709 | 2.56 | 4.2E-01 | AW857448.1 | EST_HUMAN | EST369413 MAGI resequences, MAGE Homo sapiens cDNA |
| 8548 | 21516 | 34934 | 0.49 | 4.2E-01 | 4758039 | NT | Homo sapiens cytochrome c oxidase subunit VIc (COX6C), nuclear gene encoding mitochondrial protein, mRNA |
| 10329 | 23253 | | 0.72 | 4.2E-01 | AA705007.1 | EST_HUMAN | 265101.s1 Soares fetal liver spleen_1N1FLS_S1 Homo sapiens cDNA clone IMAGE:482849 3' |
| 10541 | 23493 | 36958 | 0.43 | 4.2E-01 | AF181854.1 | NT | Lassa virus strain 803213 glycoprotein precursor and nucleoprotein genes, complete cds |
| 10862 | 23782 | 37283 | 1.53 | 4.2E-01 | AW863666.1 | EST_HUMAN | MR3-SN0010-280300-103-h07 SN0010 Homo sapiens cDNA |
| 11382 | 24329 | 37858 | 2.39 | 4.2E-01 | AB023489.1 | NT | Oryzias latipes OIGC7 mRNA for membrane guanylyl cyclase, complete cds |
| 11723 | 24609 | 38185 | 1.77 | 4.2E-01 | BE068485.2 | EST_HUMAN | 601660352R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906085 3' |
| 13090 | 25618 | | 1.4 | 4.2E-01 | AI392837.1 | EST_HUMAN | tg10c05.x1 NCL CGAP CLL1 Homo sapiens cDNA clone IMAGE:2108360 3' |
| 1096 | 14140 | 27090 | 1.98 | 4.1E-01 | AI905481.1 | EST_HUMAN | RC-B1091-210189-142 BT091 Homo sapiens cDNA |
| 1105 | 14149 | 27099 | 1.33 | 4.1E-01 | AV705243.1 | EST_HUMAN | AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5' |
| 1105 | 14149 | 27100 | 1.33 | 4.1E-01 | AV705243.1 | EST_HUMAN | AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5' |
| 2722 | 15716 | 28734 | 1.43 | 4.1E-01 | 7705283 | NT | Homo sapiens anaphase-promoting complex subunit 7 (APC7), mRNA |
| 2951 | 16008 | 28932 | 2.07 | 4.1E-01 | AL161536.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36 |
| 2951 | 16008 | 28933 | 2.07 | 4.1E-01 | AL161536.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36 |
| 3314 | 16387 | 29287 | 0.69 | 4.1E-01 | AA906344.1 | EST_HUMAN | g94b08.s1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1505943 3' |
| 4303 | 17332 | 30212 | 2.54 | 4.1E-01 | AJ249207.1 | NT | Rhodococcus sp. AD45 isoG, isoH, isoI, isoA, isoB, isoC, isoD, isoE and isoF genes |
| 4334 | 17382 | | 0.84 | 4.1E-01 | AA909257.1 | EST_HUMAN | om33402.s1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1542819 3' |
| 4694 | 17715 | 30610 | 1.71 | 4.1E-01 | AV747980.1 | EST_HUMAN | AV747980 NPC Homo sapiens cDNA clone NPC9DF10 5' |
| 6103 | 19182 | 32401 | 4.57 | 4.1E-01 | BF681393.1 | EST_HUMAN | 602156590F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297319 5' |
| 6877 | 19930 | 33227 | 0.58 | 4.1E-01 | U02298.1 | NT | Mus musculus NIH 3T3 chemokine rantes (Scys5) gene, complete cds |
| 7666 | 20625 | 33989 | 2.96 | 4.1E-01 | U07535.1 | NT | Methanococcus jannaschii section 77 of 150 of the complete genome |
| 8370 | 21339 | 34750 | 1.16 | 4.1E-01 | BF574604.1 | EST_HUMAN | 602133261F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4289238 5' |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 9445 | 22409 | 35846 | 1.45 | 4.1E-01 | 6755521 | NT | Mus musculus signaling intermediate in Toll pathway-evolutionarily conserved (Sitpec-pending), mRNA |
| 9923 | 22807 | | 0.58 | 4.1E-01 | AF160597.1 | NT | Voelavo gymnocauidus Vgym560 cytochrome b (cytb) gene, complete cds; mitochondrial gene for |
| 10626 | 23548 | | 1.18 | 4.1E-01 | AL139076.2 | NT | mitochondrial product |
| 10775 | 23696 | 37194 | 1.1 | 4.1E-01 | AV649579.1 | EST_HUMAN | Campylobacter jejuni NCTC11168 complete genome; segment 3/6 |
| 10873 | 23793 | 37294 | 0.51 | 4.1E-01 | P18584 | SWISSPROT | AV649579 GLC Homo sapiens cDNA clone GLCBVD12 3' |
| 10873 | 23793 | 37295 | 0.51 | 4.1E-01 | P18584 | SWISSPROT | PROBABLE SERINE PROTEASE DO-LIKE PRECURSOR (59 KDA IMMUNOGENIC PROTEIN) (SK59) |
| 10943 | 23863 | | 2.1 | 4.1E-01 | BF349382.1 | EST_HUMAN | PROBABLE SERINE PROTEASE DO-LIKE PRECURSOR (59 KDA IMMUNOGENIC PROTEIN) (SK59) |
| 11188 | 24144 | 37677 | 39.55 | 4.1E-01 | X58700.1 | NT | CM2-HT0137-200989-010-e08 HT0137 Homo sapiens cDNA |
| 12751 | 25931 | | 3 | 4.1E-01 | D87675.1 | NT | Zea mays ZMPMS2 gene for 19 kDa zein protein |
| 142 | 15833 | | 0.65 | 4.0E-01 | AW847123.1 | EST_HUMAN | Homo sapiens DNA for amyloid precursor protein, complete cds |
| 1040 | 14085 | 27038 | 0.71 | 4.0E-01 | 8404656 | NT | RC2-CT0201-280989-012-d10 CT0201 Homo sapiens cDNA |
| 1342 | 14377 | 27346 | 1.17 | 4.0E-01 | AF203478.1 | NT | Laqueus rubellus mitochondrion, complete genome |
| 1481 | 14514 | | 5.11 | 4.0E-01 | 6679258 | NT | Drosophila melanogaster Dalmatian (dmt) mRNA, complete cds |
| 2022 | 16883 | 28054 | 1.12 | 4.0E-01 | Z96933.1 | NT | Mus musculus platelet derived growth factor receptor, beta polypeptide (Pdgfrb), mRNA |
| 2022 | 16883 | 28055 | 1.12 | 4.0E-01 | Z95933.1 | NT | Ascololus imnerus masc2 gene |
| 2167 | 15183 | 28203 | 1.09 | 4.0E-01 | AE001931.1 | NT | Ascololus imnerus masc2 gene |
| 2167 | 15183 | 28204 | 1.09 | 4.0E-01 | AE001931.1 | NT | Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1 |
| 2816 | 13246 | 26176 | 1.27 | 4.0E-01 | 6678480 | NT | Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1 |
| 2979 | 19037 | 28959 | 1.34 | 4.0E-01 | AL163280.2 | NT | Mus musculus ubiquitin-protein ligase e3 component n-recogin (Ubr1), mRNA |
| 2979 | 19037 | 28960 | 1.34 | 4.0E-01 | AL163280.2 | NT | Homo sapiens chromosome 21 segment HS21C080 |
| | | | | | | | Homo sapiens chromosome 21 segment HS21C080 |
| | | | | | | | Streptococcus pneumoniae Y1C (Y1C), Y1D (Y1D), penicillin-binding protein 2x (pbp2x), and undecaprenyl-phosphate-UDP-MurNAc-pentapeptide phospho-MurNAc-pentapeptide transferase (mraY) genes, complete cds |
| 3709 | 16752 | 29668 | 2.32 | 4.0E-01 | AF068903.1 | NT | Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1 |
| 3840 | 16880 | 29783 | 3.28 | 4.0E-01 | AJ277511.1 | NT | Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1 |
| 3840 | 16880 | 29784 | 3.28 | 4.0E-01 | AJ277511.1 | NT | NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 5, CHLOROPLAST |
| 4855 | 17872 | | 9.36 | 4.0E-01 | Q31849 | SWISSPROT | EST382691 MAGE resequences, MAGE Homo sapiens cDNA |
| 6015 | 19088 | 32299 | 1.14 | 4.0E-01 | AW970610.1 | EST_HUMAN | EST382691 MAGE resequences, MAGE Homo sapiens cDNA |
| 6226 | 19300 | 32533 | 0.51 | 4.0E-01 | BF243741.1 | EST_HUMAN | 601877833F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106221 5' |
| | | | | | | | STRUCTURAL POLYPEPTIDE (P130) [CONTAINS: COAT PROTEIN C; SPIKE GLYCOPROTEINS E3, E2 AND E1; 6 KD PEPTIDE] |
| 6578 | 19638 | 32904 | 0.92 | 4.0E-01 | P27285 | SWISSPROT | Homo sapiens OCTN2 gene, complete cds |
| 8345 | 21314 | 34729 | 0.8 | 4.0E-01 | AB016625.1 | NT | Homo sapiens OCTN2 gene, complete cds |
| 8360 | 22325 | 35753 | 0.98 | 4.0E-01 | AA323289.1 | EST_HUMAN | EST26086 Cerebellum II Homo sapiens cDNA 5' end similar to EST containing Alu repeat |

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Table 4
Single Exon Probes Expressed In Bone Marrow

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 11895 | 24776 | | 2 | 4.0E-01 | BF030262.1 | EST_HUMAN | 601558283F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3828092 5' |
| 12030 | 24908 | | 1.75 | 4.0E-01 | L76080.1 | NT | Synechocystis sp. PCC 9413 transposase gene, complete cds |
| 12448 | 25793 | | 3.03 | 4.0E-01 | AL163300.2 | NT | Homo sapiens chromosome 21 segment HS21C100 |
| 12968 | 25536 | | 1.6 | 4.0E-01 | P36049 | SWISSPROT | HYPOTHETICAL 49.7 KD PROTEIN IN GIN2-STE3 INTERGENIC REGION |
| 1378 | 14412 | 27383 | 1.95 | 3.9E-01 | AF206618.1 | NT | Gorilla gorilla carboxyl-ester lipase (CEL) gene, complete cds |
| 2650 | 15647 | 28670 | 3.62 | 3.9E-01 | AB033019.1 | NT | Homo sapiens mRNA for KIAA1183 protein, partial cds |
| 2716 | 15710 | 28726 | 4.26 | 3.9E-01 | X82032.1 | NT | H. sapiens B-myb gene |
| 2716 | 15710 | 28727 | 4.26 | 3.9E-01 | X82032.1 | NT | H. sapiens B-myb gene |
| 3113 | 16170 | 29080 | 4.56 | 3.9E-01 | AJ225896.1 | NT | Sinorhizobium meliloti egl, syrB2, cya3 genes and orf3 |
| 4105 | 17140 | 30035 | 1.25 | 3.9E-01 | BF592611.1 | EST_HUMAN | 761d01.x1 NCI_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3339169 3' |
| 5027 | 18041 | 30924 | 1.74 | 3.9E-01 | BE728667.1 | EST_HUMAN | 601563948F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3633699 5' |
| 6042 | 19124 | 32329 | 5.95 | 3.9E-01 | BF208036.1 | EST_HUMAN | 601862362F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4082055 5' |
| 6411 | 19479 | 32726 | 0.66 | 3.9E-01 | U82695.2 | NT | Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds |
| 8286 | 21255 | 34664 | 0.8 | 3.9E-01 | U79415.1 | NT | Homo sapiens prepro dipeptidyl peptidase I (DPP-I) gene, complete cds |
| 9213 | 22179 | 35610 | 0.73 | 3.9E-01 | AW177011.1 | EST_HUMAN | CM3-CT0105-170898-004-b08 CT0105 Homo sapiens cDNA |
| 9222 | 22188 | | 0.88 | 3.9E-01 | BF348634.1 | EST_HUMAN | 602019944F1 NCI_CGAP_Brn87 Homo sapiens cDNA clone IMAGE:4155322 5' |
| 9590 | 22552 | 36003 | 1.41 | 3.9E-01 | AW185888.1 | EST_HUMAN | xn86404.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701351 3' similar to TR:094821 |
| 9903 | 22855 | 36316 | 1.83 | 3.9E-01 | A1937337.1 | EST_HUMAN | wp76d02.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2467658 3' similar to |
| 10237 | 23162 | 36550 | 2.99 | 3.9E-01 | M19879.1 | NT | SW:RFX5 HUMAN P48382 BINDING REGULATORY FACTOR. ; |
| 10305 | 23230 | | 0.46 | 3.9E-01 | 11465620 | NT | Human clabindin 27 gene, exons 10 and 11, and L1 and Alu repeats |
| 10527 | 23449 | 36947 | 0.62 | 3.9E-01 | D86722.1 | NT | Porphyrin purpurea mitochondrion, complete genome |
| 10865 | 23885 | 37397 | 0.48 | 3.9E-01 | M18440.1 | NT | Nicotiana tabacum mRNA for TATA binding protein (TBP), complete cds |
| 12219 | 25868 | | 4.08 | 3.9E-01 | AF304354.1 | NT | Human beta-92-crystallin (B2-1) gene, exon 4, partial cds |
| 12344 | 25142 | | 2.01 | 3.9E-01 | Q61670 | SWISSPROT | Homo sapiens proteoglycan 3 (PRG3) gene, complete cds |
| 12840 | 25452 | | 1.49 | 3.9E-01 | 11433335 | NT | HOMEOBOX PROTEIN HLX1 |
| 161 | 13284 | | 9.02 | 3.8E-01 | 7019488 | NT | Homo sapiens hypothetical protein FLJ10583 (FLJ10583), mRNA |
| 506 | 13577 | | 0.8 | 3.8E-01 | AB029291.1 | NT | Homo sapiens protein kinase PKNbeta (pknbeta), mRNA |
| 1886 | 14911 | | 1.19 | 3.8E-01 | AE003870.1 | NT | Mus musculus pom-1 mRNA for pericentriolar material-1, complete cds |
| 2465 | 15469 | 28493 | 1.24 | 3.8E-01 | U41946.1 | NT | Xylella fastidiosa, section 16 of 229 of the complete genome |
| 2577 | 15578 | 28597 | 2.26 | 3.8E-01 | AF214117.1 | NT | Ceanothus abditus briggase acetylcholinesterase (ace-1) gene, complete cds |
| | | | | | | | Arabidopsis thaliana putative c-myc-like transcription factor (MYB3R-3) mRNA, complete cds |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 2640 | 15900 | 28662 | 4.89 | 3.8E-01 | 6878002 | NT | Mus musculus solute carrier family 1, member 6 (Slc1a6), mRNA |
| 3015 | 16073 | | 0.88 | 3.8E-01 | AJ251057.1 | NT | Human immunodeficiency virus type 1 complete genome (isolate 98SE-MP1213) |
| 3061 | 16118 | 29033 | 2.11 | 3.8E-01 | AF043383.1 | NT | Pleuroctes americanus aminopeptidase N (ampN) gene, partial cds |
| 3495 | 16542 | 29466 | 9.24 | 3.8E-01 | AL191618.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 30 |
| 3549 | 16595 | | 0.75 | 3.8E-01 | AI807219.1 | EST_HUMAN | wf38b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3' |
| 3566 | 16595 | | 0.97 | 3.8E-01 | AI807219.1 | EST_HUMAN | wf38b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3' |
| 3769 | 16811 | 29720 | 0.99 | 3.8E-01 | BE154080.1 | EST_HUMAN | PMO-HT0339-200400-010-G01 HT0339 Homo sapiens cDNA |
| 5691 | 18796 | 31967 | 1.08 | 3.8E-01 | Q04988 | SWISSPROT | TRANSCRIPTION FACTOR SOX-10 |
| 6473 | 19538 | | 0.6 | 3.8E-01 | S46825.1 | NT | prion protein [mink, Genomic, 2448 nt] |
| 6779 | 19834 | 33117 | 5.49 | 3.8E-01 | BE072399.1 | EST_HUMAN | QV3-BT0537-271299-049-e02 BT0537 Homo sapiens cDNA |
| 6924 | 20148 | 33468 | 4.76 | 3.8E-01 | AI374601.1 | EST_HUMAN | ta54f11.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2047817 3' similar to contains Alu repetitive element; |
| 7126 | 20059 | 33365 | 1.24 | 3.8E-01 | AL161513.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 25 |
| 7743 | 20697 | 34063 | 0.51 | 3.8E-01 | AA626274.1 | EST_HUMAN | zu88c05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745064 3' |
| 7759 | 20712 | | 4.27 | 3.8E-01 | X61597.1 | NT | M.musculus gene for kallikrein-binding protein |
| 7998 | 20937 | 34331 | 0.49 | 3.8E-01 | V00983.1 | NT | Yeast mitochondrial gene for ATPase (genes oli-2 and oli-4) |
| 8640 | 21608 | 35031 | 0.45 | 3.8E-01 | M81385.1 | NT | Mouse liver receptor homologous protein (LRH-1) mRNA, complete cds |
| 8903 | 21869 | 35294 | 2.04 | 3.8E-01 | AB046851.1 | NT | Homo sapiens mRNA for KIAA1631 protein, partial cds |
| 8972 | 21938 | 35363 | 0.79 | 3.8E-01 | 11441264 | NT | Homo sapiens FOS-like antigen-1 (FOSL1), mRNA |
| 9169 | 22135 | 35561 | 1.47 | 3.8E-01 | AL163279.2 | NT | Homo sapiens chromosome 21 segment HS21C079 |
| 9919 | 22740 | | 6.02 | 3.8E-01 | T95413.1 | EST_HUMAN | y643h06.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120539 5' similar to contains Alu repetitive element; contains PTR5 repetitive element ; |
| 11862 | 24744 | | 3.41 | 3.8E-01 | BE719219.1 | EST_HUMAN | RC0-HT0841-040800-032-b12 HT0841 Homo sapiens cDNA |
| 12000 | 24877 | 38473 | 2.61 | 3.8E-01 | R42550.1 | EST_HUMAN | y92h11.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:30289 3' |
| 12000 | 24877 | 38474 | 2.61 | 3.8E-01 | R42550.1 | EST_HUMAN | y92h11.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:30289 3' |
| 12433 | 25199 | | 4.23 | 3.8E-01 | AE001124.1 | NT | Borrelia burgdorferi (section 10 of 70) of the complete genome |
| 12557 | 25889 | | 2.63 | 3.8E-01 | U94788.1 | NT | Human p53 (TP53) gene, complete cds |
| 12667 | 26343 | | 2.84 | 3.8E-01 | BE829256.1 | EST_HUMAN | QV3-ET0063-190700-271-a05 ET0063 Homo sapiens cDNA |
| 13056 | 25864 | | 2.03 | 3.8E-01 | AF291483.1 | NT | Mus musculus vomeronasal receptor V1RA4 (V1ra4) gene, complete cds |
| 13063 | 25905 | 31422 | 1.4 | 3.8E-01 | T54787.1 | EST_HUMAN | y642b11.s1 Stragatene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:73821 3' similar to similar to gb:A06977 SERUM ALBUMIN PRECURSOR (HUMAN) |
| 13080 | 25611 | 31690 | 1.57 | 3.8E-01 | AF194972.1 | NT | Mus musculus developmental control protein mRNA, partial cds |
| 2490 | 15493 | 28518 | 12.56 | 3.7E-01 | AB037831.1 | NT | Homo sapiens mRNA for KIAA1410 protein, partial cds |
| 3474 | 16520 | 29442 | 11.71 | 3.7E-01 | AF056336.1 | NT | Danio rerio bone morphogenetic protein 4 precursor (BMP-4) gene, complete cds |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 3884 | 16924 | 28833 | 0.7 | 3.7E-01 | AA318482.1 | EST_HUMAN | EST121715 Adrenal gland tumor Homo sapiens cDNA 5' end |
| 4257 | 17286 | 30168 | 6.92 | 3.7E-01 | AJ218707.1 | EST_HUMAN | ok39c07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1510188 3' |
| 4348 | 17375 | 30255 | 1.64 | 3.7E-01 | AW878037.1 | EST_HUMAN | MR3-OT0007-080300-T04-602 OT0007 Homo sapiens cDNA |
| 4416 | 17443 | 30334 | 3 | 3.7E-01 | AE002408.1 | NT | Neisseria meningitidis serogroup B strain MC58 section 50 of 206 of the complete genome |
| 5857 | 18947 | 32132 | 1.16 | 3.7E-01 | AF135187.1 | NT | Homo sapiens interferon-induced protein p78 (MX1) gene, complete cds |
| 6060 | 19141 | 32353 | 1.35 | 3.7E-01 | AL163278.2 | NT | Homo sapiens chromosome 21 segment HS21C078 |
| 6659 | 19716 | 32963 | 0.66 | 3.7E-01 | M10806.1 | NT | Chicken (White leghorn) delta-1 and delta-2 crystallin genes, complete cds |
| 6690 | 19737 | | 0.77 | 3.7E-01 | L10353.1 | NT | Mus saxicola hemoglobin mRNA, complete cds |
| 7350 | 20320 | 33667 | 3.48 | 3.7E-01 | 11525843 | NT | Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA |
| 7658 | 20618 | 33983 | 0.65 | 3.7E-01 | BE873743.1 | EST_HUMAN | 601483887F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886652 5' |
| 7658 | 20618 | 33984 | 0.65 | 3.7E-01 | BE873743.1 | EST_HUMAN | 601483887F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886652 5' |
| 8089 | 21006 | 34404 | 0.71 | 3.7E-01 | T68802.1 | EST_HUMAN | y50a07.f3 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:66324 5' |
| 8672 | 21640 | 35064 | 1.93 | 3.7E-01 | 11436739 | NT | Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA |
| 8672 | 21640 | 35065 | 1.93 | 3.7E-01 | 11436739 | NT | Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA |
| 8708 | 21678 | 35101 | 0.69 | 3.7E-01 | AA902912.1 | EST_HUMAN | ok43b11.s1 NCL_CGAP_Leid2 Homo sapiens cDNA clone IMAGE:1516701 3' |
| 9556 | 22518 | | 3.78 | 3.7E-01 | AJ271386.1 | NT | Gallus gallus mRNA for beta-carotene 15,15'-dioxygenase (BCDO gene) |
| 10530 | 23432 | | 0.52 | 3.7E-01 | K00691.1 | NT | mouse Ig germline alpha membrane exons region |
| 10570 | 23492 | 36984 | 3.65 | 3.7E-01 | AJ336411.1 | EST_HUMAN | qt46b07.x1 Soares_fetal_lung_NbH-L19W Homo sapiens cDNA clone IMAGE:1950987 3' |
| 11205 | 24159 | 37689 | 1.9 | 3.7E-01 | X05958.1 | NT | Rabbit mRNA for fast skeletal muscle myosin heavy chain (MHC) |
| 11369 | 24316 | 37842 | 2.81 | 3.7E-01 | AJ297357.1 | NT | Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene |
| 11369 | 24316 | 37843 | 2.81 | 3.7E-01 | AJ297357.1 | NT | Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene |
| 11794 | 23949 | 37470 | 2.34 | 3.7E-01 | X04122.1 | NT | Bovine mRNA for terminal deoxynucleotidyltransferase (TdT) (EC 2.7.7.31) |
| 12014 | 24891 | | 1.53 | 3.7E-01 | AA973540.1 | EST_HUMAN | oc46d03.s1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1569221 3' similar to gb:M77698 |
| 12060 | 24933 | | 3.22 | 3.7E-01 | 6877678 | NT | TRANSCRIPTIONAL REPRESSOR PROTEIN YY1 (HUMAN); |
| 12136 | 25501 | | 2.6 | 3.7E-01 | J04982.1 | NT | Mus musculus retinoblastoma 1 (Rb1), mRNA |
| 12309 | 25117 | | 4.23 | 3.7E-01 | AJ243525.1 | NT | Human heart/skeletal muscle ATP/ADP translocator (ANT1) gene, complete cds |
| 12764 | 25406 | | 1.86 | 3.7E-01 | AL121154.1 | EST_HUMAN | Chlamydomonas reinhardtii partial omp1 gene for outer membrane protein 1 |
| 12829 | 25447 | 31722 | 2.71 | 3.7E-01 | Y18000.1 | NT | DKFZp762K075_r1 762 (synonym: hme2) Homo sapiens cDNA clone DKFZp762K075 5' |
| 997 | 14048 | | 11.36 | 3.6E-01 | U89241.1 | NT | Homo sapiens NF2 gene |
| 1317 | 14352 | 27320 | 2.66 | 3.6E-01 | T80255.1 | EST_HUMAN | Human mbp gene, partial cds |
| 1317 | 14352 | 27321 | 2.66 | 3.6E-01 | T80255.1 | EST_HUMAN | y03a05.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:24443 5' |
| 1931 | 14955 | 27951 | 6.09 | 3.6E-01 | AW590184.1 | EST_HUMAN | y03a05.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:24443 5' |
| 1931 | 14955 | 27952 | 6.09 | 3.6E-01 | AW590184.1 | EST_HUMAN | hg33f02.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2947419 3' |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 1988 | 14989 | 27992 | 6.4 | 3.6E-01 | AF216207.1 | NT | Mus musculus ribosomal protein S19 (Rps19) gene, complete cds |
| 2399 | 16406 | | 3.58 | 3.6E-01 | X76725.1 | NT | P. irregularis (P3804) gene for actin |
| 2483 | 15487 | 28510 | 1.29 | 3.6E-01 | U05435.1 | NT | Rattus norvegicus synaptic vesicle protein (SV2) mRNA, complete cds |
| 2483 | 15487 | 28511 | 1.29 | 3.6E-01 | U05435.1 | NT | Rattus norvegicus synaptic vesicle protein (SV2) mRNA, complete cds |
| 2495 | 15498 | 28524 | 1.63 | 3.6E-01 | AW812033.1 | EST_HUMAN | RCS-ST0171-181099-011-g07 ST0171 Homo sapiens cDNA |
| | | | | | | | PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE) |
| 2638 | 15637 | 28660 | 1.23 | 3.6E-01 | P24206 | SWISSPROT | Drosophila melanogaster sugar transporter 3 (sut3) mRNA, complete cds |
| 2910 | 18322 | | 5.89 | 3.6E-01 | AF199485.1 | NT | H. sapiens serobinin transporter gene, exons 9 and 10 |
| 3483 | 16529 | 29453 | 2.01 | 3.6E-01 | X76758.1 | NT | H. sapiens serobinin transporter gene, exons 9 and 10 |
| 3483 | 16529 | 29454 | 2.01 | 3.6E-01 | X76758.1 | NT | H. sapiens serobinin transporter gene, exons 9 and 10 |
| 4438 | 17482 | 30351 | 1.14 | 3.6E-01 | BE707883.1 | EST_HUMAN | RC1-HT0545-150600-014-b12 HT0545 Homo sapiens cDNA |
| 4787 | 17805 | 30697 | 0.72 | 3.6E-01 | Y11526.1 | NT | Z. mays mRNA for casein kinase II alpha subunit |
| 5045 | 18058 | 30937 | 2.61 | 3.6E-01 | AW339393.1 | EST_HUMAN | ha02g04.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:28725666 3' |
| 5136 | 18145 | 31025 | 0.65 | 3.6E-01 | BE067698.1 | EST_HUMAN | MR4-BT0358-270300-005-c10 BT0358 Homo sapiens cDNA |
| 5274 | 18280 | 31143 | 0.91 | 3.6E-01 | AF067959.1 | NT | Gallus gallus homeodomain protein HOXD-3 mRNA, complete cds |
| 5274 | 18280 | 31144 | 0.91 | 3.6E-01 | AF067959.1 | NT | Gallus gallus homeodomain protein HOXD-3 mRNA, complete cds |
| 5456 | 19558 | 31469 | 0.71 | 3.6E-01 | A1006565.1 | NT | Homo sapiens lipo gene intron 5 |
| 6205 | 19279 | 32512 | 1.1 | 3.6E-01 | P16431 | SWISSPROT | FORMATE HYDROGENLYASE SUBUNIT 5 PRECURSOR (PHL SUBUNIT 5) (HYDROGENASE-3 COMPONENT E) |
| 6623 | 19681 | 32958 | 1.8 | 3.6E-01 | Y10196.1 | NT | Homo sapiens PHEX gene |
| 7355 | 20325 | | 3.63 | 3.6E-01 | R94090.1 | EST_HUMAN | Y74a06.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:275987 5' |
| 7500 | 20465 | 33826 | 1.86 | 3.6E-01 | AW027174.1 | EST_HUMAN | w172c10.x1 Soares thymus NHFTh Homo sapiens cDNA clone IMAGE:2513010 3' similar to TR:O15117 |
| 8568 | 21534 | 34954 | 0.64 | 3.6E-01 | P98167 | SWISSPROT | O15117 FYN BINDING PROTEIN. [1]; |
| 8622 | 21590 | 35008 | 14.05 | 3.6E-01 | AL161583.2 | NT | SCO-SPONDIN |
| | | | | | | | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 79 |
| 9330 | 22285 | 35724 | 0.53 | 3.6E-01 | U91328.1 | NT | Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds |
| 9330 | 22295 | 35725 | 0.53 | 3.6E-01 | U91328.1 | NT | Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds |
| 9355 | 22320 | 35746 | 2.84 | 3.6E-01 | 4504956 | NT | Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 9355 | 22320 | 35747 | 2.84 | 3.6E-01 | 4504956 | NT | Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA |
| 9547 | 22510 | 35959 | 1.12 | 3.6E-01 | AL163204.2 | NT | Homo sapiens chromosome 21 segment HS21C004 |
| 9754 | 22695 | 36151 | 0.93 | 3.6E-01 | X17550.1 | NT | D. melanogaster singed gene, exons 3, 4, 5 & 6 |
| 9754 | 22695 | 36152 | 0.93 | 3.6E-01 | X17550.1 | NT | D. melanogaster singed gene, exons 3, 4, 5 & 6 |
| 9824 | 22873 | | 0.54 | 3.6E-01 | X62825.1 | NT | C. perfingens plc gene for phospholipase C upstream region containing bent DNA fragment |
| 10222 | 23147 | 36636 | 18.66 | 3.6E-01 | Q53194 | SWISSPROT | PROBABLE PEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN Y4TS |
| 10352 | 23276 | 36750 | 0.48 | 3.6E-01 | AW752801.1 | EST_HUMAN | MR2-CT0222-21099-002-b10 CT0222 Homo sapiens cDNA |
| 10352 | 23276 | 36751 | 0.48 | 3.6E-01 | AW752801.1 | EST_HUMAN | MR2-CT0222-21099-002-b10 CT0222 Homo sapiens cDNA |
| 11292 | 24242 | 37769 | 3.04 | 3.6E-01 | BE902390.1 | EST_HUMAN | 601676418F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958967 5' |
| 11442 | 24385 | 37925 | 3.26 | 3.6E-01 | AB004293.1 | NT | Arabidopsis thaliana mRNA for SigB, complete cds |
| 11772 | 25927 | 37448 | 5.83 | 3.6E-01 | AE000856.1 | NT | Methanobacterium thermoautotrophicum from bases 702375 to 714311 (section 62 of 148) of the complete genome |
| 12174 | 25989 | | 2.05 | 3.6E-01 | Y19210.1 | NT | Homo sapiens hHb5 gene for hair keratin, exons 1 to 9 |
| 12247 | 25076 | | 1.42 | 3.6E-01 | D90901.1 | NT | Synechocystis sp. PCC6803 complete genome, 3/27, 271600-402289 |
| 12257 | 25083 | | 6.35 | 3.6E-01 | AE000335.1 | NT | Escherichia coli K-12 MG1655 section 225 of 400 of the complete genome |
| 12417 | 25187 | | 6.26 | 3.6E-01 | U66888.1 | NT | Mus musculus Emv1 mRNA, complete cds |
| 12770 | 25410 | | 1.97 | 3.6E-01 | 11432598 | NT | Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog), translocated to, 10 (AF10), mRNA |
| 13033 | 25934 | | 3.33 | 3.6E-01 | AW190229.1 | EST_HUMAN | x80e11.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2679116 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN); |
| 115 | 13226 | 26150 | 1.42 | 3.5E-01 | AL161366.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36 |
| 210 | 13311 | 26238 | 3.29 | 3.5E-01 | 6678933 | NT | Mus musculus mannose receptor, C type 2 (Mrc2), mRNA |
| 726 | 13787 | 26722 | 1.48 | 3.5E-01 | 7706138 | NT | Homo sapiens GAP-like protein (LOC51306), mRNA |
| 726 | 13787 | 26723 | 1.48 | 3.5E-01 | 7706138 | NT | Homo sapiens GAP-like protein (LOC51306), mRNA |
| 780 | 13840 | 26785 | 4.95 | 3.5E-01 | BF128796.1 | EST_HUMAN | 601811060R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053951 3' |
| 1623 | 14656 | 27634 | 0.96 | 3.5E-01 | BF310688.1 | EST_HUMAN | 60189463F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124244 5' |
| 1646 | 14678 | 27651 | 2.57 | 3.5E-01 | U35776.1 | NT | Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds |
| 2291 | 15303 | 28328 | 1.28 | 3.5E-01 | P06768 | SWISSPROT | HOMEOBOX PROTEIN HOX-A4 (HOX-1.4) (MH-3) |
| 2613 | 15899 | 28636 | 1.13 | 3.5E-01 | AA223252.1 | EST_HUMAN | zr08a09.s1 StrataGene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650872 3' |
| 3818 | 16858 | | 7.27 | 3.5E-01 | AA642138.1 | EST_HUMAN | m60403.s1 NCI CGAP_Lym3 Homo sapiens cDNA clone IMAGE:1172357 3' |
| 4291 | 17320 | 30189 | 2.18 | 3.5E-01 | AF071253.1 | NT | Danio rerio homeobox protein (hox5b) gene, complete cds |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 4922 | 17939 | 30831 | 0.7 | 3.5E-01 | N81203.1 | EST_HUMAN | 788IE1 fetal brain cDNA Homo sapiens cDNA clone 788IE1-K similar to R07879, Z40498 |
| 4969 | 17984 | 30874 | 6.46 | 3.5E-01 | M18349.1 | NT | Rat leukocyte common antigen (L-CA) gene, exons 1 through 5 |
| 5407 | 18510 | 31387 | 0.84 | 3.5E-01 | Q96687 | SWISSPROT | EARLY E2A DNA-BINDING PROTEIN |
| 5407 | 18510 | 31388 | 0.84 | 3.5E-01 | Q96687 | SWISSPROT | EARLY E2A DNA-BINDING PROTEIN |
| 5629 | 18725 | 31886 | 1.36 | 3.5E-01 | J42045.1 | NT | Human mRNA for KIAA0086 gene, complete cds |
| 6365 | 19434 | | 0.77 | 3.5E-01 | AW863916.1 | EST_HUMAN | PM4-SN0012-030400-001-a11 SN0012 Homo sapiens cDNA |
| 6548 | 19609 | 32871 | 0.62 | 3.5E-01 | AA431833.1 | EST_HUMAN | zw78703.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782429 5' similar to TR:G1086935 |
| 6593 | 19653 | 32925 | 0.98 | 3.5E-01 | U37150.1 | NT | G1086935 F10F2.1 ; |
| 6821 | 19875 | 33164 | 0.92 | 3.5E-01 | Q24357 | SWISSPROT | Bos taurus peptide methionine sulfoxide reductase (msrA) mRNA, complete cds |
| 7257 | 19992 | | 3.65 | 3.5E-01 | X98505.1 | NT | GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHLOROPLAST PRECURSOR (G6PD) |
| 7789 | 20742 | 34115 | 0.81 | 3.5E-01 | P47281 | SWISSPROT | S. scrofa mRNA for CD31 protein (PECAM-1) |
| 7789 | 20742 | 34116 | 0.81 | 3.5E-01 | P47281 | SWISSPROT | HISTIDYL-TRNA SYNTHETASE (HISTIDINE-TRNA LIGASE) (HISRS) |
| 8023 | 20960 | 34356 | 0.7 | 3.5E-01 | X06091.1 | NT | HISTIDYL-TRNA SYNTHETASE (HISTIDINE-TRNA LIGASE) (HISRS) |
| 8406 | 21375 | | 2.17 | 3.5E-01 | 11448042 | NT | E. coli L-arabinose transport operon with genes araF, araG and araH |
| 8403 | 21378 | 34784 | 0.87 | 3.5E-01 | BF358871.1 | EST_HUMAN | Homo sapiens tumor protein p53-binding protein, 2 (TP53BP2), mRNA |
| 8810 | 21777 | | 0.58 | 3.5E-01 | AF061581.1 | NT | RC4-E70024-260600-014-d07 ET0024 Homo sapiens cDNA |
| 9279 | 22245 | 35874 | 1.14 | 3.5E-01 | 4507610 | NT | Rattus norvegicus Na-K-Cl cotransporter (Nkcc1) mRNA, complete cds |
| 10093 | 23019 | 36494 | 6.94 | 3.5E-01 | Q02294 | SWISSPROT | Homo sapiens tyrosine kinase non-receptor 1 (TNK1), mRNA |
| 10246 | 23171 | 36960 | 5.51 | 3.5E-01 | Z26825.1 | NT | VOLTAAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM CHANNEL, L |
| 10326 | 23250 | 36729 | 1.01 | 3.5E-01 | BE174794.1 | EST_HUMAN | TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 5) (BRAIN CALCIUM CHANNEL III) (BIII) |
| 11086 | 24047 | 37569 | 2.48 | 3.5E-01 | X61084.1 | NT | X.laavis gene for albumin including HP1 enhancer |
| 11362 | 24311 | 37838 | 1.68 | 3.5E-01 | AJ243178.1 | NT | QV2-HT0577-090400-128-c07 HT0577 Homo sapiens cDNA |
| 11362 | 24311 | 37839 | 1.88 | 3.5E-01 | AJ243178.1 | NT | C.griseus rhodopsin gene for opsin protein |
| 11919 | 24800 | 38391 | 1.87 | 3.5E-01 | N77597.1 | EST_HUMAN | Gallus gallus SPARC gene for osteonectin, promoter and exon 1 |
| 11940 | 24820 | | 1.77 | 3.5E-01 | M82885.1 | NT | Gallus gallus SPARC gene for osteonectin, promoter and exon 1 |
| 11991 | 24868 | 38463 | 1.6 | 3.5E-01 | L05145.1 | NT | yz80h12.r1 Soares_multiple_sclerosis_2NbhMSP Homo sapiens cDNA clone IMAGE:280375 5' |
| 12269 | 25991 | | 1.8 | 3.5E-01 | AF297468.1 | NT | Drosophila melanogaster dual bar protein (BarH2) gene, exon 1 |
| 12941 | 26139 | | 1.31 | 3.5E-01 | X64595.1 | NT | Human glucokinase (GCK) gene, repeat polymorphism |
| 12501 | 25240 | | 2.56 | 3.5E-01 | AE001774.1 | NT | Schistosoma mansoni strain NIMRI chromatin assembly factor 1 small subunit-like protein (RBAP48) mRNA, complete cds |
| 13085 | 25842 | 31430 | 3.37 | 3.5E-01 | H80814.1 | EST_HUMAN | B. taurus atpA1 gene for F(0)F(1) ATP synthase alpha-subunit |
| 13085 | 25842 | 31431 | 3.37 | 3.5E-01 | H80814.1 | EST_HUMAN | Thermotoga maritima section 86 of 136 of the complete genome |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 13108 | 26627 | | 1.57 | 3.5E-01 | 4758297 | NT | Homo sapiens v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neurofiblastoma derived oncogene homolog) (ERBB2), mRNA |
| 708 | 13770 | | 1.97 | 3.4E-01 | AJ242956.1 | NT | Homo sapiens partial N-myc (exon 3), HPV45 L2, HPV45 L1, HPV45 E6, HPV45 E7 and HPV45 E1 genes isolated from IC4 cervical carcinoma cell line |
| 977 | 14028 | 26982 | 9.08 | 3.4E-01 | Y09798.2 | NT | Pseudomonas fluorescens colR, cds genes, orf222 and partial hsaA gene |
| 1329 | 14384 | 27332 | 2.79 | 3.4E-01 | Y00554.1 | NT | Azotobacter vinelandii nifA gene for NifA protein (positive regulatory element) |
| 2410 | 15417 | 28441 | 2.01 | 3.4E-01 | D90909.1 | NT | Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418 |
| 3014 | 16072 | 28992 | 0.86 | 3.4E-01 | AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C010 |
| 3014 | 16072 | 28993 | 0.86 | 3.4E-01 | AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C010 |
| 3175 | 16230 | 29146 | 6.62 | 3.4E-01 | U83905.1 | NT | Canis familiaris rod photoreceptor cGMP-gated channel alpha-subunit (CNGC1) mRNA, complete cds |
| 3354 | 16405 | 29326 | 0.94 | 3.4E-01 | AF034862.1 | NT | Homo sapiens pulmonary surfactant protein D, promoter region and exon 1 |
| 3542 | 16588 | 29512 | 3.42 | 3.4E-01 | AF106835.1 | NT | Methylovorus sp. strain SS1 putative GrpE (grpE), DnaK (dnaK), and putative DnaJ (dnaJ) genes, complete cds |
| 3804 | 16844 | | 1.78 | 3.4E-01 | BF448010.1 | EST_HUMAN | 7n94e01.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3572232 3' similar to TR:Q8UJ15 |
| 4082 | 17116 | | 1.48 | 3.4E-01 | AA594196.1 | EST_HUMAN | Q9UJ15 DJ18C9.1 ; |
| 4674 | 17695 | 30582 | 1.72 | 3.4E-01 | BE069912.1 | EST_HUMAN | nc11b10.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100347 3' |
| 4989 | 18004 | | 4.71 | 3.4E-01 | AI240973.1 | EST_HUMAN | MR4-BT0403-230200-202-e01 BT0403 Homo sapiens cDNA |
| 5768 | 18860 | 32040 | 2.74 | 3.4E-01 | AL161594.2 | NT | q95c05.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1867208 3' similar to contains Alu repetitive element; |
| 5909 | 18995 | | 5.14 | 3.4E-01 | AA085313.1 | EST_HUMAN | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90 |
| 6122 | 18200 | | 1.74 | 3.4E-01 | U02971.1 | NT | zn12d11.s1 Strategene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:547221 3' |
| 6146 | 19221 | 32451 | 0.8 | 3.4E-01 | BE748912.1 | EST_HUMAN | Echovirus 22 1AB, 1C, 1D, 2A, 2B, 2C, 3A, 3B, 3C, 3D proteins RNA, complete mature peptides and cds |
| 6229 | 19303 | 32535 | 1.91 | 3.4E-01 | AW204505.1 | EST_HUMAN | 60157181T1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3838828 3' |
| 6362 | 19431 | 32674 | 1.78 | 3.4E-01 | AL120544.1 | EST_HUMAN | U1-H-B1-aei-e-12.0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2719582 3' |
| 6907 | 19859 | | 1.19 | 3.4E-01 | N95225.1 | EST_HUMAN | DKFZp761A249_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A249 5' |
| 7135 | 20111 | 33424 | 1.14 | 3.4E-01 | AI468082.1 | EST_HUMAN | zb53e12.s1 Soares_fetal_jung_NHL19W Homo sapiens cDNA clone IMAGE:307342 3' |
| 7261 | 19996 | 33293 | 0.61 | 3.4E-01 | BF678702.1 | EST_HUMAN | trf63g05.x1 NCI_CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2162840 3' similar to gb:S37431 LAMININ RECEPTOR (HUMAN); |
| 8238 | 21207 | | 0.54 | 3.4E-01 | AE000483.1 | NT | 602085283F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248365 5' |
| 8579 | 21547 | 34866 | 0.55 | 3.4E-01 | Y14930.1 | NT | Escherichia coli K-12 MG1655 section 383 of 400 of the complete genome |
| 8832 | 21799 | | 1.8 | 3.4E-01 | AA337063.1 | EST_HUMAN | Homo sapiens TCRAV28 gene, allele A4, partial |
| | | | | | | | EST41765 Endometrial tumor Homo sapiens cDNA 5' end |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 8909 | 21875 | 35301 | 0.84 | 3.4E-01 | L04690.1 | NT | Oribetulus griseus cholesterol 7-alpha-hydroxylase gene, complete cds |
| 9204 | 22170 | 35600 | 1.89 | 3.4E-01 | 9633624 | NT | Bovine enterovirus strain K2577, complete genome |
| 9567 | 22529 | 35978 | 4.43 | 3.4E-01 | P26013 | SWISSPROT | INTEGRIN BETA-3 PRECURSOR |
| 9567 | 22529 | 35979 | 4.43 | 3.4E-01 | P26013 | SWISSPROT | INTEGRIN BETA-8 PRECURSOR |
| 9776 | 22717 | | 0.49 | 3.4E-01 | AB017510.1 | NT | Ephydra fluvialis mRNA for PLC-gamma5, complete cds |
| 9801 | 21124 | 34527 | 6.03 | 3.4E-01 | U19492.1 | NT | Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds |
| 9801 | 21124 | 34528 | 6.03 | 3.4E-01 | U19492.1 | NT | Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds |
| 9855 | 22791 | 36243 | 0.43 | 3.4E-01 | AF183857.1 | NT | Dicystotellum discoideum putative C1M receptor GMFR1 mRNA, complete cds |
| 10054 | 22981 | 36449 | 1.09 | 3.4E-01 | U68783.1 | NT | Glycine max putative transcription factor SOOF-1 (soof-1) mRNA, complete cds |
| 10249 | 23174 | 36664 | 2.14 | 3.4E-01 | AJ225084.1 | NT | Homo sapiens FAA gene, exon 16, 17 and 18 |
| 10843 | 23763 | | 0.68 | 3.4E-01 | AE004096.1 | NT | Vibrio cholerae chromosome I, section 4 of 251 of the complete chromosome |
| 11357 | 24307 | | 3.51 | 3.4E-01 | AE000881.1 | NT | Methanobacterium thermoautotrophicum from bases 1018444 to 1029212 (section 87 of 148) of the complete genome |
| 11393 | 24339 | 37869 | 4.96 | 3.4E-01 | P06925 | SWISSPROT | PROBABLE E4 PROTEIN |
| 11427 | 24371 | 37909 | 1.67 | 3.4E-01 | AF045981.1 | NT | Rutillus arcasii cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds |
| 11828 | 24711 | 38295 | 1.58 | 3.4E-01 | AB035507.1 | NT | Rattus norvegicus mRNA for s-glycerin/MUC18, complete cds |
| 11856 | 24738 | 38323 | 3.3 | 3.4E-01 | AL161515.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27 |
| 12089 | 24970 | 38567 | 1.9 | 3.4E-01 | AJ559986.1 | EST_HUMAN | tg77g06.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2214874 3' similar to contains L1.b1 L1 repetitive element; |
| 12149 | 25008 | | 2.08 | 3.4E-01 | U93604.1 | NT | Citrus variegation virus putative replicase gene, partial cds |
| 12261 | 25085 | | 1.59 | 3.4E-01 | Z21621.1 | NT | S.cerevisiae RIB5 gene encoding Riboflavin synthase |
| 12485 | 25231 | | 13.04 | 3.4E-01 | L26339.1 | NT | Human autoantigen mRNA, complete cds |
| 12512 | 25761 | | 3.88 | 3.4E-01 | BE218652.1 | EST_HUMAN | hy42h08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176127 3' similar to contains PTR5.13 |
| 12567 | 25865 | | 2.19 | 3.4E-01 | 9838361 | NT | PTR5 repetitive element; |
| 12673 | 25845 | 31763 | 3.46 | 3.4E-01 | AJ297131.1 | NT | Beta vulgaris mitochondrion, complete genome |
| 12672 | 25538 | | 1.94 | 3.4E-01 | AF019413.1 | NT | Mus musculus SIL, MAP_17, CYP_a, SCL & CYP_b genes |
| 15 | 13135 | 26033 | 10.37 | 3.3E-01 | X07990.1 | NT | Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W), RD, complement factor B (Bf), and complement component C2 (C2) genes> |
| 108 | 13135 | 26033 | 4.34 | 3.3E-01 | X07990.1 | NT | Rhizobium leguminosarum sym plasmid pRL5.J1 nodX gene |
| 448 | 13521 | 26454 | 1.3 | 3.3E-01 | AL161545.2 | NT | Rhizobium leguminosarum sym plasmid pRL5.J1 nodX gene |
| 534 | 13700 | 26621 | 2.26 | 3.3E-01 | 7662485 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45 |
| | | | | | | | Homo sapiens KIAA1100 protein (KIAA1100), mRNA |

Table 4

Single Exon Probes Expressed In Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 1205 | 14244 | 27203 | 3.29 | 3.3E-01 | Q12446 | SWISSPROT | PROLINE-RICH PROTEIN LAS17 |
| 1310 | 14346 | 27312 | 2.44 | 3.3E-01 | BF568880.1 | EST_HUMAN | 602184016T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300251 3' |
| 1610 | 14642 | 27618 | 1.55 | 3.3E-01 | 6753685 | NT | Mus musculus disintegrin 5 (Dign5), mRNA |
| 1752 | 14781 | | 1.13 | 3.3E-01 | AA332734.1 | EST_HUMAN | EST367722 Embryo, 8 week 1 Homo sapiens cDNA 5' end |
| 2043 | 15062 | | 1.01 | 3.3E-01 | AF031148.1 | NT | Methylococcus capsulatus strain Bath outer membrane protein MopB (mopB) gene, complete cds |
| 2414 | 15421 | | 4.45 | 3.3E-01 | 4507834 | NT | Homo sapiens uridine monophosphate synthetase (rotate phosphoribosyl transferase and orokidine-5'-decarboxylase) (UMPS) mRNA |
| 2660 | 16018 | 28945 | 1.76 | 3.3E-01 | AJ251805.1 | NT | Bacteriophage phi-Yeo3-12 complete genome |
| 3028 | 16086 | | 0.8 | 3.3E-01 | O02743 | SWISSPROT | INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (IL-12A) (CYTOTOXIC LYMPHOCYTE MATURATION FACTOR 35 KD SUBUNIT) (CLMF P35) |
| 3068 | 16125 | 29038 | 0.91 | 3.3E-01 | AJ007832.2 | NT | Streptomyces argillaceus mithramycin biosynthetic genes |
| 3506 | 16553 | 29479 | 1.27 | 3.3E-01 | AB012922.1 | NT | Homo sapiens MTA1-L1 gene, complete cds |
| 3822 | 16862 | 29766 | 2.18 | 3.3E-01 | O84645 | SWISSPROT | EXODEOXYRIBONUCLEASE V BETA CHAIN |
| 3832 | 16872 | 29773 | 0.8 | 3.3E-01 | P22602 | SWISSPROT | GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER COMPONENT PROTEINASE (HC-PRO); PROTEIN P3] |
| 3989 | 17029 | 29809 | 1.54 | 3.3E-01 | AL161488.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10 |
| 4028 | 17064 | 29885 | 2.02 | 3.3E-01 | AF200446.1 | NT | Hypoxylon fragiforme chitin synthase gene, partial cds |
| 4395 | 17423 | | 1.51 | 3.3E-01 | D31662.1 | NT | Rattus norvegicus DNA for regucalcin, partial cds |
| 4715 | 17735 | | 1.41 | 3.3E-01 | AJ539114.1 | EST_HUMAN | 1p78b12.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:2205407 3' similar to gb:X57522 ANTIGEN PEPTIDE TRANSPORTER 1 (HUMAN); |
| 4875 | 17892 | 30781 | 1.33 | 3.3E-01 | D64003.1 | NT | Synechocystis sp. PCC6803 complete genome, 22/27, 2765703-2868766 |
| 5397 | 18500 | 31377 | 2.48 | 3.3E-01 | X86819.1 | NT | R. norvegicus mRNA for 3'UTR of ubiquitin-like protein |
| 5397 | 18500 | 31378 | 2.48 | 3.3E-01 | X89819.1 | NT | R. norvegicus mRNA for 3'UTR of ubiquitin-like protein |
| 5664 | 18759 | 31928 | 0.55 | 3.3E-01 | P39055 | SWISSPROT | DYNAMIN |
| 5664 | 18759 | 31929 | 0.55 | 3.3E-01 | P39055 | SWISSPROT | DYNAMIN |
| 5884 | 18973 | 32166 | 0.61 | 3.3E-01 | BF213873.1 | EST_HUMAN | 601848090F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4078823 5' |
| 6056 | 19137 | 32347 | 1.75 | 3.3E-01 | BE119850.1 | EST_HUMAN | 601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875753 3' |
| 6056 | 19137 | 32348 | 1.75 | 3.3E-01 | BE119850.1 | EST_HUMAN | 601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875753 3' |
| 6154 | 19229 | 32459 | 0.82 | 3.3E-01 | P05691 | SWISSPROT | CIRCUMSPOROZOITE PROTEIN (CS) |
| 6960 | 20185 | 33508 | 0.63 | 3.3E-01 | AB034233.1 | NT | Flexibacter littoralis gyrB gene for DNA gyrase B subunit, partial cds |
| 6960 | 20185 | 33509 | 0.63 | 3.3E-01 | AB034233.1 | NT | Flexibacter littoralis gyrB gene for DNA gyrase B subunit, partial cds |
| 7073 | 20095 | 33404 | 4.16 | 3.3E-01 | AJ628131.1 | EST_HUMAN | 1p64h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element; contains element L1 repetitive element; |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 7073 | 20095 | 33405 | 4.16 | 3.3E-01 | AI628131.1 | EST_HUMAN | b84h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285609 3' similar to contains Alu repetitive element; contains element L1 repetitive element; |
| 8052 | 20998 | 34395 | 1.81 | 3.3E-01 | N85146.1 | EST_HUMAN | J2498F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2498 5' similar to TEGT |
| 8908 | 21874 | 35300 | 22.63 | 3.3E-01 | BF683954.1 | EST_HUMAN | 602140372F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301800 5' |
| 9030 | 22046 | 35469 | 0.66 | 3.3E-01 | BF210322.1 | EST_HUMAN | 601873281F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097180 5' |
| 9489 | 22433 | 35871 | 0.85 | 3.3E-01 | Q62926 | SWISSPROT | MITOGEN-ACTIVATED PROTEIN KINASE KINASE 1 (MAPK/ERK KINASE 1) (MEK KINASE 1) (MEKK 1) |
| 9733 | 22761 | 36215 | 0.98 | 3.3E-01 | BE828461.1 | EST_HUMAN | GM3-ET0041-180500-187-d10 ET0041 Homo sapiens cDNA |
| 9733 | 22761 | 36216 | 0.98 | 3.3E-01 | BE828461.1 | EST_HUMAN | GM3-ET0041-180500-187-d10 ET0041 Homo sapiens cDNA |
| 9859 | 22805 | 36258 | 2.8 | 3.3E-01 | N69866.1 | EST_HUMAN | za67h01.s1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:297649 3' |
| 9910 | 22731 | 36186 | 2.61 | 3.3E-01 | BF376745.1 | EST_HUMAN | RC4-TN0077-250800-011-g04 TN0077 Homo sapiens cDNA |
| 10350 | 23274 | | 2.12 | 3.3E-01 | L41044.1 | NT | Homo sapiens high-mobility group phosphoprotein (HMGI-C) gene, exons 1-3, complete cds |
| 11076 | 24038 | 37561 | 2.85 | 3.3E-01 | X63953.1 | NT | D.mauritiana Adh gene |
| 11076 | 24038 | 37562 | 2.85 | 3.3E-01 | X63953.1 | NT | D.mauritiana Adh gene |
| 11365 | 24313 | | 2.16 | 3.3E-01 | BF526499.1 | EST_HUMAN | 602070802F1 NCI_CGAP_Bn64 Homo sapiens cDNA clone IMAGE:4213585 5' |
| 11565 | 24605 | 38062 | 8.16 | 3.3E-01 | BE218351.1 | EST_HUMAN | hw51g02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176978 3' |
| 11673 | 24639 | 38218 | 3.19 | 3.3E-01 | P47953 | SWISSPROT | GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (CBP30) |
| 12027 | 24903 | | 3.43 | 3.3E-01 | AA806621.1 | EST_HUMAN | cb71g02.s1 NCI_CGAP_GCBT Homo sapiens cDNA clone IMAGE:1336850 3' |
| 12044 | 13135 | 26033 | 1.97 | 3.3E-01 | X07990.1 | NT | Rhizobium leguminosarum sym plasmid pRL5J nodX gene |
| 12248 | 25075 | 38170 | 1.84 | 3.3E-01 | | NT | Homo sapiens aldehyde oxidase 1 (AOX1), mRNA |
| 12658 | 25630 | | 4.92 | 3.3E-01 | AP000002.1 | NT | Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt. position (27) |
| 13113 | 25632 | 31621 | 1.59 | 3.3E-01 | BE312920.1 | EST_HUMAN | 601146730F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3162006 5' |
| 457 | 13530 | | 2.08 | 3.2E-01 | AF018261.1 | NT | Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds |
| 719 | 13781 | | 0.76 | 3.2E-01 | AL161561.2 | NT | Arabidopsis thaliana DNA chromosome 4, config fragment No. 61 |
| 1166 | 14207 | 27161 | 10.6 | 3.2E-01 | AF047013.1 | NT | Fusarium poae virus 1 RNA2 putative RNA dependent RNA polymerase gene, complete cds |
| 1287 | 14322 | 27285 | 1.77 | 3.2E-01 | Z50202.1 | NT | P.vulgaris arc5-1 gene |
| 1391 | 14425 | 27394 | 5.96 | 3.2E-01 | Q48624 | SWISSPROT | LACTOSE PERMEASE (LACTOSE-PROTON SYMPORTER) (LACTOSE TRANSPORT PROTEIN) |
| 1639 | 14071 | | 0.9 | 3.2E-01 | AF209730.1 | NT | Arabidopsis thaliana cultivar Columbia RPP13 (RPP13) gene, complete cds |
| 1789 | 14818 | 27803 | 1.5 | 3.2E-01 | Z36041.1 | NT | S.cerevisiae chromosome II reading frame ORF YBR172c |
| 1799 | 14828 | 27815 | 5.47 | 3.2E-01 | AW957194.1 | EST_HUMAN | EST369284 IMAGE resequences, MAGD Homo sapiens cDNA |
| 1799 | 14828 | 27816 | 5.47 | 3.2E-01 | AW957194.1 | EST_HUMAN | EST369284 IMAGE resequences, MAGD Homo sapiens cDNA |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 1860 | 14886 | 27882 | 1.03 | 3.2E-01 | AL111655.1 | NT | Botyils cinerea strain T4 cDNA library under conditions of nitrogen deprivation |
| 2168 | 15184 | 28205 | 2.33 | 3.2E-01 | BF203817.1 | EST_HUMAN | 601868804F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111512 5' |
| 2548 | 15549 | | 2.3 | 3.2E-01 | 7710079 | NT | Mus musculus Pbx/knotted 1 homeobox (Pbx1), mRNA |
| 2720 | 15714 | 28732 | 1.56 | 3.2E-01 | AF060568.1 | NT | Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds |
| 3622 | 16665 | | 0.79 | 3.2E-01 | D10872.1 | NT | Human h NAT allele 3-2 gene for arylamine N-acetyltransferase |
| 4367 | 17394 | 30273 | 0.93 | 3.2E-01 | 4759195 | NT | Homo sapiens symplekin (SYM) mRNA |
| 4422 | 17449 | 30340 | 1.62 | 3.2E-01 | M18818.1 | NT | Rabbit beta-like globin gene cluster encoding the epsilon, gamma, delta (pseudogene) and beta globin polypeptides, complete cds |
| 4526 | 17551 | 30439 | 1.3 | 3.2E-01 | Q10268 | SWISSPROT | HYPOTHETICAL 81.7 KD PROTEIN C13G7.04C IN CHROMOSOME 1 PRECURSOR |
| 4767 | 17787 | | 8.32 | 3.2E-01 | BF63817.1 | EST_HUMAN | 60208192F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4248505 5' |
| 4915 | 17932 | 30823 | 0.69 | 3.2E-01 | Q57081 | SWISSPROT | CYTADHERENCE HIGH MOLECULAR WEIGHT PROTEIN 3 (CYTADHERENCE ACCESSORY PROTEIN 3) (ACCESSORY ADHESIN PROTEIN 3) (P69) |
| 5250 | 18258 | 31127 | 0.96 | 3.2E-01 | AY008847.1 | NT | Homo sapiens interleukin 12 p40 subunit (IL12B) gene, IL12B-1 allele, complete cds |
| 5280 | 18288 | | 4.18 | 3.2E-01 | A1989472.1 | EST_HUMAN | w25808.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2498195 3' similar to contains Alu repetitive element; contains element PTR7 repetitive element ; |
| 5344 | 18449 | 31320 | 2.71 | 3.2E-01 | BE173964.1 | EST_HUMAN | GM0470569-060300-269-110 HT0569 Homo sapiens cDNA |
| 6068 | 19149 | 32361 | 1.36 | 3.2E-01 | L27221.1 | NT | Giardia intestinalis pyruvate:flavodoxin oxidoreductase and flanking genes |
| 6436 | 19602 | 32763 | 0.68 | 3.2E-01 | AF016494.1 | NT | Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P55), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete c> |
| 6749 | 19803 | 33084 | 0.91 | 3.2E-01 | AV718037.1 | EST_HUMAN | AV718037 FHTA Homo sapiens cDNA clone FHTAABH01 5' |
| 6897 | 19949 | | 1.03 | 3.2E-01 | AB002359.1 | NT | Human mRNA for KIAA0361 gene, KIAA0361 protein |
| 8189 | 21159 | 34588 | 0.44 | 3.2E-01 | AJ277861.1 | NT | Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1 |
| 8512 | 21480 | 34894 | 1.43 | 3.2E-01 | M60266.1 | NT | Rat ISO-alpha natriuretic factor gene, complete cds |
| 8609 | 21577 | 34993 | 0.45 | 3.2E-01 | AJ231001.1 | NT | Rattus norvegicus repeat; map NOS-D12Wox1 |
| 8710 | 21678 | 35103 | 16.12 | 3.2E-01 | X02508.1 | NT | H. sapiens gene fragment for acetylcholine receptor (AChR) alpha subunit exons 8, 9 and 3' flanking region |
| 8713 | 21681 | 35108 | 17.12 | 3.2E-01 | BF311635.1 | EST_HUMAN | 601897107F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128633 5' |
| 8805 | 21772 | | 1.54 | 3.2E-01 | AL161574.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 70 |
| 8845 | 21812 | 35231 | 1.13 | 3.2E-01 | BF246771.1 | EST_HUMAN | 601855580F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075627 5' |
| 8845 | 21812 | 35232 | 1.13 | 3.2E-01 | BF246771.1 | EST_HUMAN | 601855580F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075627 5' |
| 8919 | 21865 | 35311 | 2.13 | 3.2E-01 | AE002016.1 | NT | Deinococcus radiodurans R1 section 152 of 229 of the complete chromosome 1 |
| 9019 | 21985 | 35405 | 0.63 | 3.2E-01 | U51028.1 | NT | Oryctolagus cuniculus Ig H-chain pseudogene, V-region (VH6-a2) gene, partial cds |
| 9019 | 21985 | 35406 | 0.63 | 3.2E-01 | U51028.1 | NT | Oryctolagus cuniculus Ig H-chain pseudogene, V-region (VH6-a2) gene, partial cds |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 9422 | 22387 | 35826 | 0.49 | 3.2E-01 | AL163204.2 | NT | Homo sapiens chromosome 21 segment HS21C004 |
| 9432 | 22396 | | 2.28 | 3.2E-01 | M86511.1 | NT | Human monocyte antigen CD14 (CD14) mRNA, complete cds |
| 9505 | 22468 | 35911 | 0.45 | 3.2E-01 | AF041829.1 | NT | Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13 |
| 9505 | 22468 | 35912 | 0.45 | 3.2E-01 | AF041829.1 | NT | Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13 |
| 10353 | 23277 | 36752 | 3.37 | 3.2E-01 | U44914.1 | NT | Borrelia burgdorferi plasmid cp32-2, <i>erpC</i> and <i>erpD</i> genes, complete cds; and unknown genes |
| 10559 | 23481 | 36876 | 0.5 | 3.2E-01 | BE326230.1 | EST_HUMAN | hvb905.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181569 3' |
| 10674 | 23596 | | 3.71 | 3.2E-01 | AB011399.1 | NT | Homo sapiens gene for AF-6, complete cds |
| 11028 | 23992 | 37519 | 3.03 | 3.2E-01 | T08813.1 | EST_HUMAN | EST04702 Fetal brain, <i>Stratagene</i> (cat#938206) Homo sapiens cDNA clone HFBDZ21 |
| 12286 | 25890 | | 3.67 | 3.2E-01 | L07288.1 | NT | <i>Drosophila melanogaster</i> laminin A (Lam-A) mRNA, complete cds |
| 12674 | 25943 | | 1.39 | 3.2E-01 | BE86846.1 | EST_HUMAN | 601507820F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909532 5' |
| 12804 | 25431 | | 4.84 | 3.2E-01 | O83217 | SWISSPROT | ELONGATION FACTOR TU (EF-TU) |
| 12890 | 25719 | | 1.48 | 3.2E-01 | AF157625.1 | NT | Bos taurus Inositol 1,4,5-trisphosphate receptor type I mRNA, complete cds |
| 12938 | 25516 | | 1.57 | 3.2E-01 | L39874.1 | NT | Homo sapiens deoxycytidylate deaminase gene, complete cds |
| 13001 | 25925 | 31305 | 1.33 | 3.2E-01 | BE365776.1 | EST_HUMAN | 601275480F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3616746 5' |
| 13108 | 25628 | 31646 | 1.38 | 3.2E-01 | A1745111.1 | EST_HUMAN | t21c06.x1 NCI_CGAP_OV28 Homo sapiens cDNA clone IMAGE:2218954 3' similar to contains MER10.11 MER10 repetitive element; |
| 2679 | 15675 | 28696 | 3.02 | 3.1E-01 | R18051.1 | EST_HUMAN | ye90h06.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125051 5' similar to gb:M64241 QM PROTEIN (HUMAN); |
| 2708 | 15828 | 28717 | 4.64 | 3.1E-01 | 7661971 | NT | Homo sapiens KIAA0174 gene product (KIAA0174), mRNA |
| 2708 | 15828 | 28718 | 4.64 | 3.1E-01 | 7661971 | NT | Homo sapiens KIAA0174 gene product (KIAA0174), mRNA |
| 2869 | 15929 | | 1.63 | 3.1E-01 | AW629036.1 | EST_HUMAN | h146h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975391 3' |
| 3188 | 16243 | | 4.03 | 3.1E-01 | AB029099.1 | NT | Mus musculus gene for Ser/Thr kinase KKIAMRE, exon 6 |
| 3927 | 16967 | 29880 | 0.93 | 3.1E-01 | AJ251598.1 | NT | Daucus carota mRNA for transcription factor E2F (E2F gene) |
| 4989 | 18014 | 30901 | 1.25 | 3.1E-01 | AE003984.1 | NT | Xylella fastidiosa, section 130 of 229 of the complete genome |
| 5239 | 18247 | 31119 | 0.79 | 3.1E-01 | AF130370.1 | NT | Rattus norvegicus MEN1 tumor suppressor (Men1) mRNA, alternative splice product, complete cds |
| 5297 | 18320 | 31162 | 2.59 | 3.1E-01 | AL163203.2 | NT | Homo sapiens chromosome 21 segment HS21C003 |
| 5555 | 18652 | 31596 | 9.78 | 3.1E-01 | AF176111.1 | NT | Homo sapiens hepatocyte nuclear factor-3 alpha (HNF3A) gene, exon 1 |
| 5681 | 18776 | 31948 | 0.65 | 3.1E-01 | P44132 | SWISSPROT | HYPOPHOSPHATASE PROTEIN H1236 |
| 5682 | 18777 | 31949 | 0.87 | 3.1E-01 | Z74983.1 | NT | S.cerevisiae chromosome XV reading frame ORF YOL141W |
| 5693 | 18788 | | 1.01 | 3.1E-01 | Y13278.1 | NT | Mus musculus mRNA for polyomycin |
| 5666 | 18955 | 32142 | 2.3 | 3.1E-01 | AF184122.1 | NT | Homo sapiens filamin 2 (FLN2) gene, exons 10 through 22 |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 6416 | 25660 | 32732 | 0.61 | 3.1E-01 | R94322.1 | EST_HUMAN | y41704.r1 Soares fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:188367 5' |
| 6610 | 19668 | 32944 | 2.69 | 3.1E-01 | AW963549.1 | EST_HUMAN | RC3-HN0001-310300-011-b04 HN0001 Homo sapiens cDNA |
| 6683 | 19740 | 33015 | 0.85 | 3.1E-01 | A1264458.1 | EST_HUMAN | q39401.x1 NCI_CGAP_C68 Homo sapiens cDNA clone IMAGE:1874689 3' |
| 6840 | 19893 | 33188 | 0.88 | 3.1E-01 | X71887.1 | NT | H.sapiens gene for immunoglobulin kappa light chain variable region A8 and A9 |
| 6830 | 20154 | | 0.7 | 3.1E-01 | AW377354.1 | EST_HUMAN | MR2-CT0222-281098-005-H05 CT0222 Homo sapiens cDNA |
| 7162 | 25634 | 31238 | 2.55 | 3.1E-01 | BE737392.1 | EST_HUMAN | 601306121F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3640420 5' |
| 7942 | 20884 | 34275 | 0.56 | 3.1E-01 | 4885390 | NT | Homo sapiens hyaluronan synthase 2 (HAS2), mRNA |
| 8038 | 20975 | 34371 | 0.49 | 3.1E-01 | AF242431.1 | NT | Mus musculus neuronal apoptosis inhibitory protein 6 (Naip6) gene, complete cds; and Naip3 gene, exons 2-9 and 11-16 |
| 8166 | 21104 | 34502 | 0.54 | 3.1E-01 | AW850168.1 | EST_HUMAN | IL3-CT0219-271099-022-E03 CT0219 Homo sapiens cDNA |
| 8166 | 21104 | 34503 | 0.54 | 3.1E-01 | AW850168.1 | EST_HUMAN | IL3-CT0219-271099-022-E03 CT0219 Homo sapiens cDNA |
| 8995 | 21961 | 35386 | 0.83 | 3.1E-01 | R45318.1 | EST_HUMAN | y94601.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:35639 3' |
| 10262 | 23187 | 36671 | 0.52 | 3.1E-01 | 6679322 | NT | Mus musculus phosphatidylinositol-4-phosphate 5-kinase, type 1 gamma (Pip5k1c), mRNA |
| 10427 | 23349 | 36833 | 1 | 3.1E-01 | BF696639.1 | EST_HUMAN | 602124743F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281611 5' |
| 10427 | 23349 | 36834 | 1 | 3.1E-01 | BF696639.1 | EST_HUMAN | 602124743F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281611 5' |
| 10488 | 23410 | 36907 | 1.73 | 3.1E-01 | A1244001.1 | EST_HUMAN | q161011.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1863980 3' similar to gb:S55700 |
| 10666 | 23588 | | 0.56 | 3.1E-01 | T55325.1 | EST_HUMAN | HYDROXYMETHYLGLUTARYL-COA LYASE PRECURSOR (HUMAN); |
| 11186 | 24142 | 37676 | 2.35 | 3.1E-01 | BF216117.1 | EST_HUMAN | y647h08.s1 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:74367 3' similar to similar |
| 11864 | 24746 | 38328 | 2.3 | 3.1E-01 | 7662281 | NT | to gb:M91036_ma2 HEMOGLOBIN GAMMA-A AND GAMMA-G CHAINS (HUMAN) |
| 12133 | 25002 | 38608 | 1.68 | 3.1E-01 | AF048693.1 | NT | 601883592F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095814 5' |
| 12133 | 25002 | 38609 | 1.68 | 3.1E-01 | AF048693.1 | NT | Homo sapiens KIAA0764 gene product (KIAA0764), mRNA |
| 12415 | 25186 | | 1.57 | 3.1E-01 | AF294308.1 | NT | Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds |
| 12451 | 25210 | | 4.64 | 3.1E-01 | AF304162.1 | NT | Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds |
| 12592 | 25296 | | 4.19 | 3.1E-01 | AF195953.1 | NT | Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds |
| 12944 | 25523 | | 3.39 | 3.1E-01 | AF196779.1 | NT | Anolis opalinus isolate QS NADH dehydrogenase subunit 2 (ND2) gene, complete cds; mitochondrial gene for mitochondrial product |
| 73 | 15808 | 26112 | 1.78 | 3.0E-01 | 6755083 | NT | Stizostedion vitreum 40S ribosomal protein S11 mRNA, partial cds |
| 254 | 13351 | 26277 | 8.98 | 3.0E-01 | AJ271735.1 | NT | Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds |
| 1227 | 14265 | 27222 | 2.16 | 3.0E-01 | AW300400.1 | EST_HUMAN | Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a2 |
| 1508 | 14541 | 27512 | 5.96 | 3.0E-01 | AJ008755.1 | NT | Mus musculus protein kinase C, epsilon (Pkc), mRNA |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 2146 | 15182 | 28178 | 1.13 | 3.0E-01 | AF237778.1 | NT | Rattus norvegicus Ca2+/calmodulin-dependent protein kinase II, alpha subunit mRNA, 3' untranslated region |
| 3225 | 16280 | | 1.26 | 3.0E-01 | AB030481.1 | NT | Corynebacterium sp. ALY-1 alyPG gene for polyketonate lyase, complete cds |
| 3879 | 16918 | 29827 | 1.46 | 3.0E-01 | AW817785.1 | EST_HUMAN | PM1-ST0262-261199-001-g01 ST0262 Homo sapiens cDNA |
| 3998 | 17037 | 29944 | 1.02 | 3.0E-01 | AJ271736.1 | NT | Homo sapiens Xq pseudautosomal region; segment 2/2 |
| 4541 | 17564 | 30451 | 2.17 | 3.0E-01 | AJ008755.1 | NT | Balaenoptera physalus gene encoding atrial natriuretic peptide |
| 5425 | 18528 | 31407 | 5.19 | 3.0E-01 | BE741629.1 | EST_HUMAN | 601594960F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948734 5' |
| 5506 | 18606 | 31536 | 0.66 | 3.0E-01 | AF224689.1 | NT | Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds |
| 5510 | 18610 | 31541 | 0.76 | 3.0E-01 | AF229247.1 | NT | Canis lupus familiaris hemagglutinin gene, complete cds |
| 5582 | 18678 | 31641 | 3.81 | 3.0E-01 | BE693575.1 | EST_HUMAN | RC3-BT0333-180700-111-a03 BT0333 Homo sapiens cDNA |
| 5582 | 18678 | 31642 | 3.81 | 3.0E-01 | BE693575.1 | EST_HUMAN | RC3-BT0333-180700-111-a03 BT0333 Homo sapiens cDNA |
| 5619 | 18715 | 31874 | 4.05 | 3.0E-01 | U01247.1 | NT | Mus musculus 129/sv Clara cell 10 kd protein (mCC10) gene, complete cds |
| 7005 | 20131 | 33446 | 2.86 | 3.0E-01 | D16313.1 | NT | Mouse cyokeratin 15 gene, complete cds |
| 7041 | 18373 | 31261 | 0.71 | 3.0E-01 | U02369.1 | NT | Strongylocentrotus purpuratus 34/67 kDa laminin-binding protein mRNA, partial cds |
| 7111 | 20045 | 33347 | 0.96 | 3.0E-01 | AF229247.1 | NT | Canis lupus familiaris hemagglutinin gene, complete cds |
| 7196 | 20219 | 33551 | 0.59 | 3.0E-01 | X63941.1 | NT | S. Cerevisiae GAC1 |
| 7328 | 20299 | 33643 | 0.82 | 3.0E-01 | AL163206.2 | NT | Homo sapiens chromosome 21 segment HS21C006 |
| 7549 | 20512 | 33870 | 4.68 | 3.0E-01 | 10947007 | NT | Mus musculus midnolin (Mdn-pending), mRNA |
| 7744 | 20698 | 34084 | 1.33 | 3.0E-01 | AF071810.1 | NT | Streptococcus pneumoniae strain DBL5 PspA (pspA) gene, partial cds |
| 8259 | 21228 | 34638 | 1.28 | 3.0E-01 | AE001755.1 | NT | Thermotoga maritima section 67 of the complete genome |
| 8716 | 21684 | | 4.13 | 3.0E-01 | 9910161 | NT | Mus musculus C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9 (Clec4e9), mRNA |
| 8819 | 21786 | 35210 | 1.34 | 3.0E-01 | BE566083.1 | EST_HUMAN | 601339079F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3681594 5' |
| 9181 | 22147 | 35574 | 0.74 | 3.0E-01 | AF141876.1 | NT | Streptomyces sulfonolactis isopenicillin N synthase (pcbc) gene, partial cds |
| 9223 | 22189 | | 0.71 | 3.0E-01 | 7681685 | NT | Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA |
| 9573 | 22535 | 35986 | 0.95 | 3.0E-01 | AF220507.1 | NT | Anabaena PCC7120 cytosine-specific DNA methyltransferase (dmnB) gene, complete cds, putative |
| 9932 | 22859 | 36320 | 0.51 | 3.0E-01 | P76389 | SWISSPROT | entranilate phosphoribosyltransferase gene, partial cds; and unknown gene |
| 10327 | 23251 | 36730 | 0.73 | 3.0E-01 | BF574612.1 | EST_HUMAN | HYPOTHETICAL 59.5 KD PROTEIN IN WZA-ASMA INTERGENIC REGION |
| 10501 | 23423 | 36922 | 0.47 | 3.0E-01 | AF152598.3 | NT | 602133271F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288336 5' |
| 10501 | 23423 | 36922 | 0.47 | 3.0E-01 | AF152598.3 | NT | Actinobacillus actinomycetemcomitans Tada (tadA), TadB (tadB), TadC (tadC), TadD (tadD), TadE (tadE), TadF (tadF), and TadG (tadG) genes, complete cds |
| 10501 | 23423 | 36923 | 0.47 | 3.0E-01 | AF152598.3 | NT | Actinobacillus actinomycetemcomitans Tada (tadA), TadB (tadB), TadC (tadC), TadD (tadD), TadE (tadE), TadF (tadF), and TadG (tadG) genes, complete cds |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 10760 | 23681 | 37177 | 0.85 | 3.0E-01 | AW118111.1 | EST_HUMAN | xa03d10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2806035 3' |
| 10762 | 23683 | 37179 | 2.14 | 3.0E-01 | AB030231.1 | NT | Aspergillus oryzae bpaA gene for ER chaperone BIP, complete cds |
| 10782 | 23703 | 37207 | 0.82 | 3.0E-01 | BF683841.1 | EST_HUMAN | 602140133F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4301097 5' |
| 10782 | 23703 | 37202 | 0.82 | 3.0E-01 | BF683841.1 | EST_HUMAN | 602140133F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4301097 5' |
| 12081 | 24834 | 38529 | 2.5 | 3.0E-01 | JH51029.1 | EST_HUMAN | yp84b10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194107 5' |
| 12081 | 24834 | 38530 | 2.5 | 3.0E-01 | JH51029.1 | EST_HUMAN | yp84b10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194107 5' |
| 12696 | 25875 | | 1.57 | 3.0E-01 | AJ287631.1 | NT | Rattus norvegicus mRNA for glyceraldehyde-3-phosphate dehydrogenase type 2 (gapdh-2 gene) |
| 12979 | 25917 | | 2.52 | 3.0E-01 | 6877766 | NT | Mus musculus ribose 5-phosphate isomerase A (Rplp), mRNA |
| 1747 | 14778 | | 0.92 | 2.9E-01 | AJ248995.1 | NT | Mus musculus mas proto-oncogene and Igf2r gene for insulin-like growth factor type 2 and L41ps and Au78 pseudogenes |
| 2039 | 15058 | 28077 | 1.19 | 2.9E-01 | AE000736.1 | NT | Aquifex aeolicus section 68 of 109 of the complete genome |
| 2260 | 15274 | 28298 | 1.2 | 2.9E-01 | AF222718.1 | NT | Chrysothymus synnucleus mitochondrion, complete genome |
| 3265 | 16319 | 28240 | 1.92 | 2.9E-01 | AW754239.1 | EST_HUMAN | PM1-CT0326-171298-001-f12 CT0328 Homo sapiens cDNA |
| 3265 | 16319 | 28241 | 1.92 | 2.9E-01 | AW754239.1 | EST_HUMAN | PM1-CT0326-171298-001-f12 CT0328 Homo sapiens cDNA |
| 3912 | 16952 | 29863 | 1.03 | 2.9E-01 | AI610836.1 | EST_HUMAN | tp21a11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2188412 3' similar to gb.D15050 NIL-2-A ZINC FINGER PROTEIN (HUMAN); contains element L1 repetitive element |
| 3955 | 16995 | 29911 | 0.91 | 2.9E-01 | AI769472.1 | EST_HUMAN | w14d10.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402803 3' similar to WP:C34F8.7 CE15876 |
| 4112 | 17148 | | 0.7 | 2.9E-01 | AW002902.1 | EST_HUMAN | w02f10.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2480395 3' |
| 4511 | 17536 | 30420 | 1.24 | 2.9E-01 | AA284488.1 | EST_HUMAN | zs57d12.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701591 5' similar to contains Alu repetitive element |
| 4710 | 17731 | | 1.5 | 2.9E-01 | AL163207.2 | NT | Homo sapiens chromosome 21 segment HS21C007 |
| 5155 | 18166 | | 1.25 | 2.9E-01 | AI670899.1 | EST_HUMAN | wa06f03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2297309 3' similar to contains L1 L2 L1 repetitive element |
| 5275 | 18281 | 31145 | 3.3 | 2.9E-01 | AJ131017.1 | NT | Mus musculus SCL gene locus |
| 5277 | 18283 | 31148 | 1.12 | 2.9E-01 | BE741380.1 | EST_HUMAN | 601594241F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948178 5' |
| 5330 | 18436 | | 1.49 | 2.9E-01 | R37485.1 | EST_HUMAN | y77e12.s1 Soares infant brain INIB Homo sapiens cDNA clone IMAGE:28291 3' |
| 5469 | 20085 | 33372 | 0.75 | 2.9E-01 | AF321001.1 | NT | Suaeda maritima subsp. salina S-adenosylmethionine synthetase 2 mRNA, complete cds |
| 5858 | 18948 | 32133 | 5.1 | 2.9E-01 | X56098.1 | NT | B subtilis levanase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P18,18,28,30 and levanase |
| 5858 | 18948 | 32134 | 5.1 | 2.9E-01 | X56098.1 | NT | B subtilis levanase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P18,18,28,30 and levanase |
| 5871 | 18960 | 32149 | 6.12 | 2.9E-01 | 6879662 | NT | Mus musculus Eph receptor A8 (EphA8), mRNA |
| 6174 | 19249 | 32482 | 1.35 | 2.9E-01 | AA418145.1 | EST_HUMAN | z97b12.r1 Soares_NHIMPu_S1 Homo sapiens cDNA clone IMAGE:767711 5' |

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 6412 | 19480 | 32727 | 1.05 | 2.9E-01 | A1797128.1 | EST_HUMAN | we27c05.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:23423123 similar to contains L1.11 L1 repetitive element; |
| 6459 | 19524 | 32775 | 2.3 | 2.9E-01 | U03420.1 | NT | Bos taurus myosin I mRNA, complete cds |
| 6599 | 19659 | 32931 | 0.6 | 2.9E-01 | R09194.1 | EST_HUMAN | y39d08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:141615 5' |
| 6599 | 19659 | 32932 | 0.6 | 2.9E-01 | R09194.1 | EST_HUMAN | y39d08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:141615 5' |
| 6883 | 19935 | | 0.84 | 2.9E-01 | Z50156.1 | NT | D.discauleum: gene for 34 kD actin binding protein |
| 7043 | 20065 | 33372 | 0.58 | 2.9E-01 | AF321001.1 | NT | Suaeda maritima subsp. salsa S-adenosylmethionine synthetase 2 mRNA, complete cds |
| 7179 | 18410 | 31211 | 1.57 | 2.9E-01 | AF142329.1 | NT | Mus musculus Filth protein (Filth) gene, complete cds; and Ligin protein (Ligin) gene, partial cds |
| 7303 | 20274 | 33810 | 2.89 | 2.9E-01 | Q04399 | SWISSPROT | PUTATIVE MULTICOPPER OXIDASE YDR506C |
| 7367 | 20337 | 33887 | 1.88 | 2.9E-01 | AF100950.1 | NT | Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; Bing1 (BING1), tapasin (tapasin), RalGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3- galactosyl transferase (beta1,3-galactosyl tr> |
| 8252 | 21221 | 34630 | 1.67 | 2.9E-01 | BE540422.1 | EST_HUMAN | 601065830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5' |
| 8252 | 21221 | 34631 | 1.87 | 2.9E-01 | BE540422.1 | EST_HUMAN | 601065830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5' |
| 8489 | 21457 | 34874 | 0.49 | 2.9E-01 | AJ237937.1 | NT | Bos taurus partial stat5A gene, exons 5-19 |
| 8489 | 21457 | 34875 | 0.49 | 2.9E-01 | AJ237937.1 | NT | Bos taurus partial stat5A gene, exons 5-19 |
| 8502 | 21470 | | 1.16 | 2.9E-01 | BF217743.1 | EST_HUMAN | 601882570F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095113 5' |
| 8882 | 21650 | | 0.45 | 2.9E-01 | AF197456.1 | NT | Buchnera aphidicola plasmid pLeu isolate M1 2-isopropylmalate synthase (leuA) gene, partial cds; 3- isopropylmalate dehydrogenase (leuB) gene, complete cds; and isopropylmalate dehydratase subunit (leuC) gene, partial cds |
| 8942 | 21908 | 35333 | 0.77 | 2.9E-01 | AU150910.1 | EST_HUMAN | AU150910 NT2RP2 Homo sapiens cDNA clone NT2RP2003901 3' |
| 9277 | 22243 | 35672 | 1.01 | 2.9E-01 | AF225908.1 | NT | Arabidopsis thaliana sulfonylurea receptor-like protein mRNA, complete cds |
| 9388 | 22353 | 35784 | 0.6 | 2.9E-01 | M22452.1 | NT | Baboon lymphocyte homing/adhesion receptor mRNA, complete cds |
| 9601 | 22805 | 36053 | 0.78 | 2.9E-01 | AJ248287.1 | NT | Pyrococcus abyssi complete genome; segment 5/6 |
| 9601 | 22805 | 36054 | 0.76 | 2.9E-01 | AJ248287.1 | NT | Pyrococcus abyssi complete genome; segment 5/6 |
| 11240 | 24193 | 37711 | 1.7 | 2.9E-01 | AF128843.1 | NT | Trypanosoma cruzi stage-specific surface glycoprotein gp82 (gp82) mRNA, partial cds |
| 11497 | 24440 | 37899 | 1.86 | 2.9E-01 | V01394.1 | NT | Torpedo californica mRNA encoding acetylcholine receptor gamma subunit |
| 11497 | 24440 | 37990 | 1.86 | 2.9E-01 | V01394.1 | NT | Torpedo californica mRNA encoding acetylcholine receptor gamma subunit |
| 11913 | 24784 | 38385 | 2.98 | 2.9E-01 | AL139078.2 | NT | Campylobacter jejuni NCTC11168 complete genome; segment 5/6 |
| 12109 | 24979 | 38579 | 2.1 | 2.9E-01 | AW294742.1 | EST_HUMAN | U1-H-BW0-aim-f-10-0-U1.s1 NCI CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2729994 3' |
| 12651 | 25334 | 31760 | 1.47 | 2.9E-01 | AW005671.1 | EST_HUMAN | wz8805.x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2565921 3' similar to contains element MER29 repetitive element; |
| 12728 | 25381 | 31747 | 4 | 2.9E-01 | AF092453.1 | NT | Homo sapiens TNF- α -inducible RNA binding protein (TIRP) gene, complete cds |
| 13025 | 25573 | 31694 | 1.35 | 2.9E-01 | Y08937.1 | NT | Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 13025 | 25573 | 31695 | 1.35 | 2.9E-01 | Y08937.1 | NT | Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus |
| 570 | 13640 | | 2.2 | 2.8E-01 | U67136.1 | NT | Rattus norvegicus A-kinase anchoring protein AKAP150 mRNA, complete cds |
| 575 | 13644 | | 1.41 | 2.8E-01 | L28145.1 | NT | Prune dwarf virus movement protein, complete cds; coat protein, complete cds |
| 1085 | 14129 | 27083 | 3.9 | 2.8E-01 | AF168050.1 | NT | Guirra guirra oocyte maturation factor Mos (c-mos) gene, partial cds |
| 1282 | 14317 | 27279 | 1.06 | 2.8E-01 | BE313442.1 | EST_HUMAN | 801148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163888 5' |
| 1282 | 14317 | 27280 | 1.06 | 2.8E-01 | BE313442.1 | EST_HUMAN | 801148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163888 5' |
| 1295 | 14330 | 27291 | 2.65 | 2.8E-01 | D86550.1 | NT | Human mRNA for serine/threonine protein kinase, complete cds |
| 1740 | 14770 | 27758 | 2.22 | 2.8E-01 | AW860020.1 | EST_HUMAN | QV1-C10364-120200-065-b05 CT0384 Homo sapiens cDNA |
| 2028 | 15048 | 28062 | 2.08 | 2.8E-01 | AL047620.1 | EST_HUMAN | DKFZp586i2321 J1 588 (synonym: hute1) Homo sapiens cDNA clone DKFZp586i2321 |
| 2141 | 15158 | 28174 | 1.51 | 2.8E-01 | AW511195.1 | EST_HUMAN | h44403.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912333 3' |
| 2479 | 15483 | 28507 | 2.18 | 2.8E-01 | AE000494.1 | NT | Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome |
| 2479 | 15483 | 28508 | 2.18 | 2.8E-01 | AE000494.1 | NT | Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome |
| 2554 | 15556 | | 3.07 | 2.8E-01 | AL161565.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65 |
| 2674 | 15671 | 28639 | 1.35 | 2.8E-01 | AB020975.1 | NT | Arabidopsis thaliana mRNA for lipolytic transferase, complete cds |
| 2982 | 16040 | | 1.48 | 2.8E-01 | AF179480.1 | NT | Toxoplasma gondii 90kDa heat-shock protein (HSP90) mRNA, partial cds |
| 2983 | 16041 | 28963 | 2.57 | 2.8E-01 | Z14037.1 | NT | B. taurus microsatellite (ETH121) |
| 2983 | 16041 | 28964 | 2.57 | 2.8E-01 | Z14037.1 | NT | B. taurus microsatellite (ETH121) |
| 3390 | 16439 | 29365 | 1.16 | 2.8E-01 | AP000004.1 | NT | Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt, position (4/7) |
| 4021 | 17059 | 29960 | 1.72 | 2.8E-01 | AE001190.1 | NT | Borrelia burgdorferi (section 66 of 70) of the complete genome |
| 4150 | 17181 | | 0.87 | 2.8E-01 | AE004450.1 | NT | Pseudomonas aeruginosa PA01, section 11 of 529 of the complete genome |
| 4226 | 17265 | | 2.41 | 2.8E-01 | AID90868.1 | EST_HUMAN | ov44g10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640226 3' similar to contains Alu repetitive element; contains element MER22 repetitive element; |
| 4488 | 17513 | 30401 | 2.62 | 2.8E-01 | P13615 | SWISSPROT | RNA POLYMERASE BETA SUBUNIT (LARGE STRUCTURAL PROTEIN) (L PROTEIN) |
| 4822 | 17839 | 30737 | 0.92 | 2.8E-01 | D15050.1 | NT | Human mRNA for transcription factor AREB6, complete cds |
| 4822 | 17839 | 30738 | 0.92 | 2.8E-01 | D15050.1 | NT | Human mRNA for transcription factor AREB6, complete cds |
| 4866 | 17883 | 30771 | 2.71 | 2.8E-01 | AF030154.1 | NT | Human mRNA for transcription factor AREB6, complete cds |
| 4897 | 17914 | 30804 | 1.37 | 2.8E-01 | BF528188.1 | EST_HUMAN | Bovine adenovirus 3 complete genome |
| 4920 | 17937 | 30829 | 1.69 | 2.8E-01 | AI272669.1 | EST_HUMAN | 602042601F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4180129 5' |
| 5384 | 25637 | 31362 | 23.73 | 2.8E-01 | AA349997.1 | EST_HUMAN | q158c11.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1876628 3' similar to contains Alu repetitive element; contains element LTR5 repetitive element; |
| 5687 | 18782 | 31954 | 2.52 | 2.8E-01 | AB016625.1 | NT | EST57072 Infant brain Homo sapiens cDNA 5' end |
| 5915 | 19001 | | 1.04 | 2.8E-01 | AW992583.1 | EST_HUMAN | Homo sapiens OCTN2 gene, complete cds |
| | | | | | | EST_HUMAN | CM1-BN0024-150200-118-g12 BN0024 Homo sapiens cDNA |
| 6028 | 19111 | 32313 | 0.57 | 2.8E-01 | AA765296.1 | EST_HUMAN | oe01d08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1303691 3' similar to gb:M34539 FK506-BINDING PROTEIN (HUMAN); |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 6048 | 19129 | | 0.49 | 2.8E-01 | AA0404576.1 | EST_HUMAN | z41f01.r1 Soares ovary tumor NBH07 Homo sapiens cDNA clone IMAGE:724921 5' similar to contains Alu repetitive element |
| 6300 | 25994 | | 0.78 | 2.8E-01 | M36668.1 | NT | Bovine 680 bp repeated unit of 1.723 satellite DNA |
| 6343 | 19412 | 32653 | 2.02 | 2.8E-01 | AF003124.1 | NT | Mesembryanthemum crystallinum fructose-bisphosphate aldolase mRNA, complete cds |
| 6343 | 19412 | 32654 | 2.02 | 2.8E-01 | AF003124.1 | NT | Mesembryanthemum crystallinum fructose-bisphosphate aldolase mRNA, complete cds |
| 6895 | 19947 | 33244 | 8.31 | 2.8E-01 | BF611215.1 | EST_HUMAN | UI-H-B14-act-04-0-UJ.st NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085182 3' |
| 7201 | 20225 | 33557 | 0.52 | 2.8E-01 | U65300.1 | NT | Orthogeomys heterodus cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, complete cds |
| 7579 | 20541 | 33900 | 0.51 | 2.8E-01 | BE881455.1 | EST_HUMAN | 601490157F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3892142 5' |
| 7675 | 20633 | | 1.03 | 2.8E-01 | U05833.1 | NT | Marsilea quadrifolia ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) gene, chloroplast gene encoding chloroplast protein, partial cds |
| 7724 | 20680 | 34044 | 0.77 | 2.8E-01 | X69880.1 | NT | L. esculentum ypt2 mRNA for GTP-binding protein |
| 8429 | 21398 | 34808 | 1.12 | 2.8E-01 | A1346126.1 | EST_HUMAN | qp48h01.x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1926289 3' similar to gb:X06323_cds1 |
| 8429 | 21398 | 34809 | 1.12 | 2.8E-01 | A1346126.1 | EST_HUMAN | MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN); |
| 8551 | 21519 | 34938 | 2.25 | 2.8E-01 | U51688.1 | EST_HUMAN | qp48h01.x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1926289 3' similar to gb:X06323_cds1 |
| 8859 | 21826 | 35249 | 0.49 | 2.8E-01 | AA911629.1 | EST_HUMAN | MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN); |
| 8936 | 21902 | | 7.34 | 2.8E-01 | BF347847.1 | EST_HUMAN | Homo sapiens lanosterol 14-alpha demethylase cytochrome P450 (CYP51) gene, exon 5 |
| 9821 | 22670 | 36127 | 0.91 | 2.8E-01 | U17251.1 | NT | 602022987F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4156525 5' |
| 10089 | 22996 | | 0.95 | 2.8E-01 | L13654.1 | NT | Neurospora crassa negative regulator sulfur controller-2 (scon-2) gene, complete cds |
| 10248 | 23173 | 36662 | 0.93 | 2.8E-01 | AF132728.1 | NT | Lycopodium obscurum peroxidase (TPX1) mRNA, complete cds |
| 10248 | 23173 | 36663 | 0.93 | 2.8E-01 | AF132728.1 | NT | Escherichia coli translocated intimin receptor Tir (tir) gene, complete cds |
| 10310 | 23234 | 36716 | 0.6 | 2.8E-01 | AF294393.1 | NT | Escherichia coli translocated intimin receptor Tir (tir) gene, complete cds |
| 10420 | 23342 | 36828 | 4.98 | 2.8E-01 | 7706163 | NT | Rattus norvegicus glycerol-3-phosphate dehydrogenase gene, promoters A and B and exons 1a and 1b; nuclear gene for mitochondrial product |
| 10676 | 23598 | | 0.94 | 2.8E-01 | 9626154 | NT | Homo sapiens hypofibrinolytic protein (LOC51319), mRNA |
| 10718 | 23640 | 37133 | 0.44 | 2.8E-01 | BE969727.2 | EST_HUMAN | Fujinami sarcoma virus, complete genome |
| 11095 | 24055 | 37578 | 1.9 | 2.8E-01 | BF241092.1 | EST_HUMAN | 601654822R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3899785 3' |
| 11095 | 24055 | 37579 | 1.9 | 2.8E-01 | BF241092.1 | EST_HUMAN | 601890794F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109350 5' |
| 11125 | 24085 | 37612 | 2.96 | 2.8E-01 | BF695970.1 | EST_HUMAN | 601890794F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4109350 5' |
| 11608 | 24546 | | 4.02 | 2.8E-01 | BF674023.1 | EST_HUMAN | 601892148F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4076026 5' |
| 12312 | 25120 | 31843 | 1.39 | 2.8E-01 | AF268477.1 | NT | 602137418F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273953 5' |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 12684 | 25351 | | 23.54 | 2.8E-01 | D83329.1 | NT | Mus musculus DNA for prostaglandin D2 synthase, complete cds |
| 12788 | 25420 | 31738 | 3.09 | 2.8E-01 | BE178699.1 | EST_HUMAN | PM4-HT0606-030400-001-a07 HT0606 Homo sapiens cDNA |
| 12817 | 25439 | 31742 | 1.37 | 2.8E-01 | BE900116.1 | EST_HUMAN | 601673020F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3955996 5' |
| 12969 | 25879 | | 3.15 | 2.8E-01 | 11433629 | NT | Homo sapiens CDC42-binding protein kinase beta (DMPK-like) (CDC42BPB), mRNA |
| 13097 | 25973 | | 1.76 | 2.8E-01 | AW025400.1 | EST_HUMAN | wu96g05.x1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:2827928 3' |
| 477 | 13549 | 26477 | 2.95 | 2.7E-01 | Y17324.1 | NT | Rattus norvegicus CDK104 mRNA |
| 615 | 13680 | 26596 | 8.43 | 2.7E-01 | AA450061.1 | EST_HUMAN | z39b10.s1 Soares_tctal_fetus_Nb2HF8_Ov Homo sapiens cDNA clone IMAGE:788827 3' similar to contains Alu repetitive element |
| 1266 | 14301 | 27262 | 2.18 | 2.7E-01 | AB004906.1 | NT | Ipomoea purpurea transposable element Tip100 gene for transposase, complete cds |
| 1825 | 14658 | | 2.21 | 2.7E-01 | X79815.1 | NT | G.lambliia SR2 gene |
| 1742 | 14772 | 27757 | 2.88 | 2.7E-01 | W58067.1 | EST_HUMAN | z322h10.11 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:341443 5' |
| 1791 | 14820 | 27805 | 2.49 | 2.7E-01 | P03341 | SWISSPROT | GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10] |
| 2145 | 15885 | | 2.29 | 2.7E-01 | AF047575.1 | NT | Rattus norvegicus vesicular monoamine transporter type 2, promoter region and exon 1 |
| 2375 | 15383 | 28405 | 9.38 | 2.7E-01 | Y13868.1 | NT | Feline immunodeficiency virus env gene, isolate ITTO088PIU (M88), partial |
| 2481 | 15485 | 28488 | 3.97 | 2.7E-01 | AI310858.1 | EST_HUMAN | ta43c11.x2 NCL_CGAP_Lu25 Homo sapiens cDNA clone IMAGE:2046836 3' similar to contains element L1 repetitive element |
| 2909 | 15968 | 28891 | 1 | 2.7E-01 | AF251276.1 | NT | Mus musculus serine protease inhibitor 14 (Spi14) mRNA, complete cds |
| 2997 | 16055 | | 0.91 | 2.7E-01 | BF088284.1 | EST_HUMAN | CM1-HT0875-060900-385-e05 HT0875 Homo sapiens cDNA |
| 4038 | 17076 | 28976 | 1.74 | 2.7E-01 | AI828015.1 | EST_HUMAN | wc82a11.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462828 3' |
| 4053 | 17090 | 29985 | 0.76 | 2.7E-01 | AF216214.1 | NT | Drosophila buzzatii alpha-esterase 6 (aE6) gene, partial cds |
| 4053 | 17090 | 29986 | 0.76 | 2.7E-01 | AF216214.1 | NT | Drosophila buzzatii alpha-esterase 6 (aE6) gene, partial cds |
| 4061 | 17097 | 29991 | 2.33 | 2.7E-01 | L77569.1 | NT | Homo sapiens DJGeorge syndrome critical region, telomeric end |
| 4928 | 17945 | 30837 | 0.76 | 2.7E-01 | L27516.1 | NT | Triticum aestivum (Wc866) gene, complete cds |
| 5079 | 18089 | | 4.11 | 2.7E-01 | AW856131.1 | EST_HUMAN | RC1-CT0286-230200-016-a03 CT0286 Homo sapiens cDNA |
| 5339 | 18444 | 31197 | 2.13 | 2.7E-01 | P17277 | SWISSPROT | HOMEBOX PROTEIN HOXA4 (CHOX-1.4) |
| 5567 | 18664 | | 1.11 | 2.7E-01 | AB033171.1 | NT | Astrepura myriophthalma mitochondrial cytb gene for cytochrome b, partial cds |
| 6476 | 19541 | 32787 | 0.51 | 2.7E-01 | Q00918 | SWISSPROT | LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP-1) (TRANSFORMING GROWTH FACTOR BETA-1 MASKING PROTEIN, LARGE SUBUNIT) |
| 6476 | 19541 | 32788 | 0.51 | 2.7E-01 | Q00918 | SWISSPROT | LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP-1) (TRANSFORMING GROWTH FACTOR BETA-1 MASKING PROTEIN, LARGE SUBUNIT) |
| 6765 | 19819 | 33100 | 1.06 | 2.7E-01 | AE001094.1 | NT | Archaeoglobus fulgidus section 13 of 172 of the complete genome |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 6765 | 19819 | 33101 | 1.06 | 2.7E-01 | AE001094.1 | NT | Archaeoglobus fulgidus section 13 of 172 of the complete genome |
| 6948 | 20170 | 33494 | 2.1 | 2.7E-01 | Q61554 | SWISSPROT | FIBRILLIN 1 PRECURSOR |
| 7253 | 19988 | | 0.64 | 2.7E-01 | A1540070.1 | EST_HUMAN | td08h08.x1 NC1 CGAP CLL1 Homo sapiens cDNA clone IMAGE:2075103 3' |
| 7580 | 20842 | 33901 | 0.8 | 2.7E-01 | Q11079 | SWISSPROT | HYPOTHETICAL 20.9 KD PROTEIN B0863.3 IN CHROMOSOME X |
| 7811 | 20760 | 34135 | 0.86 | 2.7E-01 | Q01168 | SWISSPROT | NITROGEN REGULATORY PROTEIN NUT1 |
| 7811 | 20760 | 34136 | 0.86 | 2.7E-01 | Q01168 | SWISSPROT | NITROGEN REGULATORY PROTEIN NUT1 |
| 7952 | 20893 | 34285 | 1.9 | 2.7E-01 | AF248054.1 | NT | Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds |
| 7952 | 20893 | 34286 | 1.9 | 2.7E-01 | AF248054.1 | NT | Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds |
| 8012 | 20960 | 34343 | 0.86 | 2.7E-01 | AA351121.1 | EST_HUMAN | EST58740 Infant brain Homo sapiens cDNA 5' and similar to similar to myosin-binding protein H |
| 8012 | 20950 | 34344 | 0.86 | 2.7E-01 | AA351121.1 | EST_HUMAN | EST58740 Infant brain Homo sapiens cDNA 5' and similar to similar to myosin-binding protein H |
| 8084 | 21021 | 34421 | 0.63 | 2.7E-01 | L01081.1 | NT | Oryctolagus cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds |
| 8196 | 21166 | 34576 | 0.86 | 2.7E-01 | AA013147.1 | EST_HUMAN | ze35p11.s1 Soares retina N2b4-HR Homo sapiens cDNA clone IMAGE:360957 3' similar to contains Alu repetitive element. |
| 8360 | 21329 | | 0.52 | 2.7E-01 | AF048820.1 | NT | Carassius auratus pituitary adenylate cyclase activating polypeptide type 1 receptor precursor mRNA, complete cds |
| 8475 | 21444 | 34861 | 0.43 | 2.7E-01 | AW868503.1 | EST_HUMAN | MR1-SN0062-100500-002-409 SN0062 Homo sapiens cDNA |
| 8527 | 21495 | 34909 | 0.52 | 2.7E-01 | R39257.1 | EST_HUMAN | yc91h06.s1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:23511 3' |
| 8634 | 21602 | 35025 | 0.74 | 2.7E-01 | AL161552.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52 |
| 9112 | 22078 | 35505 | 0.52 | 2.7E-01 | Q14764 | SWISSPROT | MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN) |
| 9382 | 22347 | 35779 | 0.51 | 2.7E-01 | X03216.1 | NT | Staphylococcus aureus transposon Tn554 |
| 9688 | 22641 | 36098 | 11.09 | 2.7E-01 | O83809 | SWISSPROT | THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS) |
| 9688 | 22641 | 36099 | 11.09 | 2.7E-01 | O83809 | SWISSPROT | THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS) |
| 9891 | 22644 | | 2.17 | 2.7E-01 | P37928 | SWISSPROT | FIMBRIAE W PROTEIN |
| 10160 | 23085 | 36562 | 0.64 | 2.7E-01 | D89680.1 | NT | Rattus norvegicus DNA for peroxisome assembly factor-2, exon 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17 and complete cds |
| 10441 | 23363 | 36853 | 0.85 | 2.7E-01 | AF091848.1 | NT | Oryctolagus cuniculus calgranulin C mRNA, partial cds |
| 10477 | 23399 | 36896 | 2.83 | 2.7E-01 | AF087434.1 | NT | Mus musculus transcription factor NF-ATc isoform a (NF-ATc) mRNA, complete cds |
| 10611 | 23533 | 37029 | 1.06 | 2.7E-01 | AF156539.1 | NT | Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9 |
| 10611 | 23533 | 37030 | 1.06 | 2.7E-01 | AF156539.1 | NT | Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9 |
| 11163 | 24121 | 37648 | 4.87 | 2.7E-01 | AV705043.1 | EST_HUMAN | AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5' |
| 11163 | 24121 | 37649 | 4.87 | 2.7E-01 | AV705043.1 | EST_HUMAN | AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5' |

PCT/US 01/00668

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 11171 | 24128 | 37658 | 2.31 | 2.7E-01 | AJ133289.1 | NT | Homo sapiens cavedin-1/-2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2) |
| 12066 | 24939 | | 2.08 | 2.7E-01 | BE141035.1 | EST_HUMAN | MRO-HT0067-201099-002-c10 HT0067 Homo sapiens cDNA |
| 12090 | 24961 | | 1.52 | 2.7E-01 | O14181 | SWISSPROT | PUTATIVE 60S RIBOSOMAL PROTEIN C4F8.05C |
| 12509 | 25244 | 31802 | 1.39 | 2.7E-01 | AL163281.2 | NT | Homo sapiens chromosome 21 segment HS21C081 |
| 12757 | 25738 | | 1.46 | 2.7E-01 | AB008782.1 | NT | Arabidopsis thaliana mRNA for sulfate transporter, complete cds |
| 12851 | 25480 | | 1.63 | 2.7E-01 | Q63627 | SWISSPROT | CTD-BINDING SR-LIKE PROTEIN RA4 |
| 12948 | 25526 | | 3.16 | 2.7E-01 | AF217491.1 | NT | Homo sapiens fragile 16D oxidoreductase (FOR) gene, exon 6 |
| 470 | 15841 | 28470 | 1.97 | 2.8E-01 | P78411 | SWISSPROT | IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-2 |
| 481 | 13554 | | 1.5 | 2.8E-01 | D16459.1 | NT | Bos taurus mRNA for mb-1, complete cds |
| 1394 | 14428 | 27397 | 1.66 | 2.8E-01 | BE885087.1 | EST_HUMAN | 601510838F1 NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3912345 5' |
| 1431 | 14485 | 27441 | 1.36 | 2.8E-01 | AB013280.1 | NT | Glycine max pseudogene for 8d 30K |
| 1912 | 14936 | 27931 | 6.4 | 2.8E-01 | AL161472.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2 |
| 1912 | 14936 | 27932 | 6.4 | 2.8E-01 | AL161472.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2 |
| 2104 | 15121 | | 7.48 | 2.8E-01 | AW733152.1 | EST_HUMAN | bb04d10.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2958451 3' similar to gb:M36072 60S RIBOSOMAL PROTEIN L7A (HUMAN); gb:M14689_cds1 Mouse surfeit locus surfeit 3 protein gene (MOUSE); |
| 2490 | 15494 | | 0.99 | 2.8E-01 | Y12896.1 | NT | B. maritimus rbcL gene |
| 2553 | 15555 | | 8.24 | 2.8E-01 | BE272440.1 | EST_HUMAN | 361128016F1 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:2990043 5' |
| 3108 | 16165 | | 1.02 | 2.8E-01 | AW974531.1 | EST_HUMAN | EST366635 IMAGE resequences, MAGM Homo sapiens cDNA |
| 3594 | 16839 | 29559 | 1.02 | 2.8E-01 | M22342.1 | NT | Bacteriophage T2 DNA-(adenine-N6)methyltransferase (dam) gene, complete cds |
| 3657 | 16700 | 28618 | 2.11 | 2.8E-01 | AF229118.1 | NT | Homo sapiens acetylcholinesterase collagen-like tail subunit (COLO) gene, exons 1A, 2, 3, 4, and 5 |
| 3982 | 17022 | 28932 | 0.77 | 2.8E-01 | AJ012174.2 | NT | Chlamydia pneumoniae partial mpB gene for RNase P RNA subunit |
| 3982 | 17022 | 28933 | 0.77 | 2.8E-01 | AJ012174.2 | NT | Chlamydia pneumoniae partial mpB gene for RNase P RNA subunit |
| 4181 | 17212 | 30100 | 17.99 | 2.8E-01 | BE080598.1 | EST_HUMAN | QV1-BT0630-040400-132-e03 BT0630 Homo sapiens cDNA |
| 4394 | 17412 | 30296 | 1.39 | 2.8E-01 | AF175293.1 | NT | Enterococcus faecium strain N97-330 vanD glycopeptide resistance gene cluster, complete cds; and unknown gene |
| 4522 | 17547 | 30434 | 0.82 | 2.8E-01 | AB021180.1 | NT | Gallus gallus mRNA for skeletal myosin heavy chain, complete cds |
| 4522 | 17547 | 30435 | 0.82 | 2.8E-01 | AB021180.1 | NT | Gallus gallus mRNA for skeletal myosin heavy chain, complete cds |
| 4579 | 17601 | 30497 | 1.47 | 2.8E-01 | AA457617.1 | EST_HUMAN | aa89d07.r1 Stragene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838477 5' |
| 4671 | 17698 | 30585 | 2.31 | 2.8E-01 | U01103.1 | NT | Arabidopsis thaliana PSI type III chlorophyll a/b-binding protein (Lhca3*) mRNA, complete cds |
| 4745 | 17765 | 30659 | 1.46 | 2.8E-01 | AF142703.1 | NT | Ophrestia radicata maturase-like protein (matK) gene, complete cds; chloroplast gene for chloroplast product |

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Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 5007 | 18021 | 30909 | 4.38 | 2.6E-01 | H04858.1 | EST_HUMAN | y51e05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:152288 5' |
| 5081 | 18091 | | 0.78 | 2.6E-01 | AA884825.1 | EST_HUMAN | am33b711.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1488905 3' |
| 5414 | 18517 | | 1.06 | 2.6E-01 | AB035972.1 | NT | Paramacium caudatum gene for PAP, complete cds |
| 5524 | 18623 | 31558 | 0.69 | 2.6E-01 | M96060.1 | NT | Acetobacter xylinum cellulose synthase (bcsA) gene, partial cds, CMCax and CcpAx genes, complete cds |
| 5651 | 18747 | | 0.71 | 2.6E-01 | AI862398.1 | EST_HUMAN | td18a03.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2073788 3' similar to contains element MER35 repetitive element ; |
| 5889 | 18958 | 32148 | 0.68 | 2.6E-01 | AF207580.1 | NT | Homo sapiens protein translocase, JM26 protein, UDP-galactose translocator, pim-2 protooncogene homolog pim-2h, and shal-type potassium channel genes, complete cds; JM12 protein and transcription factor IGHM enhancer 3 genes, partial cds; and unknown g+ |
| 6189 | 25993 | | 2.61 | 2.6E-01 | AE001811.1 | NT | Thermotoga maritima section 123 of 136 of the complete genome |
| 6325 | 19395 | 32637 | 1.81 | 2.6E-01 | AI582557.1 | EST_HUMAN | ta02a12.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDF1_RAT Q84289 NEUROGENIC DIFFERENTIATION FACTOR 1 ; contains element LTR1 repetitive element ; |
| 6325 | 19395 | 32638 | 1.81 | 2.6E-01 | AI582557.1 | EST_HUMAN | ta02a12.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDF1_RAT Q84289 NEUROGENIC DIFFERENTIATION FACTOR 1 ; contains element LTR1 repetitive element ; |
| 6562 | 19822 | 32887 | 1.01 | 2.6E-01 | AL162757.2 | NT | Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 6/7 |
| 6825 | 19879 | 33169 | 0.6 | 2.6E-01 | BE792052.1 | EST_HUMAN | 601581754F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936156 5' |
| 6825 | 19879 | 33170 | 0.6 | 2.6E-01 | BE792052.1 | EST_HUMAN | 601581754F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936156 5' |
| 7238 | 20259 | 33593 | 0.75 | 2.6E-01 | AI914380.1 | EST_HUMAN | wd48c04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2331366 3' similar to gb:M37721 PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE PRECURSOR (HUMAN); |
| 7620 | 20580 | 33944 | 0.72 | 2.6E-01 | BE148961.1 | EST_HUMAN | CM0-HT0245-031199-086-f04 HT0245 Homo sapiens cDNA |
| 7663 | 25696 | | 0.73 | 2.6E-01 | AL139077.2 | NT | Campylobacter jejuni NCTC11168 complete genome; segment 4/6 |
| 7700 | 20658 | | 0.91 | 2.6E-01 | AA196149.1 | EST_HUMAN | zp92a01.r1 Stradiagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627672 5' |
| 8013 | 20951 | 34345 | 1.53 | 2.6E-01 | R10365.1 | EST_HUMAN | y37a03.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:129004 3' similar to gb:X12517 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C (HUMAN); |
| 8071 | 21008 | 34408 | 0.65 | 2.6E-01 | Q09855 | SWISSPROT | HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN C29E6.01 IN CHROMOSOME I |
| 8182 | 21152 | 34559 | 1.13 | 2.6E-01 | R02411.1 | EST_HUMAN | y82a07.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:124212 5' |
| 8236 | 21205 | 34610 | 1.17 | 2.6E-01 | BE144331.1 | EST_HUMAN | MRO-HT0186-181199-003-d12 HT0186 Homo sapiens cDNA |
| 8480 | 21449 | 34866 | 0.62 | 2.6E-01 | X82641.1 | NT | D.melanogaster mRNA for alpha 1,2 mannosidase (Berlin) |
| 8480 | 21449 | 34867 | 0.62 | 2.6E-01 | X82641.1 | NT | D.melanogaster mRNA for alpha 1,2 mannosidase (Berlin) |
| 8677 | 21645 | 35069 | 2.87 | 2.6E-01 | BF343588.1 | EST_HUMAN | 802014422F1 NCL_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4150396 5' |
| 8753 | 21721 | 35143 | 1.92 | 2.6E-01 | Q10199 | SWISSPROT | HYPOTHETICAL 75.2 KD PROTEIN C11C1.02 IN CHROMOSOME II |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 9042 | 22008 | 35428 | 4.09 | 2.6E-01 | BE830339.1 | EST_HUMAN | RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA |
| 9042 | 22008 | 35429 | 4.09 | 2.6E-01 | BE830339.1 | EST_HUMAN | RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA |
| 9822 | 22671 | 36128 | 0.99 | 2.6E-01 | X17604.1 | NT | S. occidentalis INV gene for Invertase (EC 3.2.1.26) |
| 10096 | 23022 | | 0.63 | 2.6E-01 | AF057121.1 | NT | Lontra canadensis cytochrome b (cyt) gene, mitochondrial gene encoding mitochondrial protein, complete cds |
| 10227 | 23152 | 36941 | 1.08 | 2.6E-01 | P87366 | SWISSPROT | GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KHF-G) |
| 10227 | 23152 | 36942 | 1.08 | 2.6E-01 | P87366 | SWISSPROT | GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KHF-G) |
| 10560 | 23472 | | 0.61 | 2.6E-01 | Q28295 | SWISSPROT | VON WILLEBRAND FACTOR PRECURSOR (VWF) |
| 10875 | 23786 | | 0.91 | 2.6E-01 | Y10196.1 | NT | Homo sapiens PHEX gene |
| 10978 | 23898 | | 0.48 | 2.6E-01 | Y15874.2 | NT | Danio rerio mRNA for RPTP-alpha protein |
| 11854 | 24736 | | 32.27 | 2.6E-01 | X51755.1 | NT | Human lambda-immunoglobulin constant region complex (germline) |
| 12688 | 26091 | | 2.77 | 2.6E-01 | 10190655 | NT | Mus musculus jerky (Jrk), mRNA |
| 12464 | 26883 | | 3.3 | 2.6E-01 | BE883491.1 | EST_HUMAN | 601511052F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912612 5' |
| 12528 | 26257 | 31806 | 4.42 | 2.6E-01 | AF318896.1 | NT | Homo sapiens Naik-A1Pase gamma subunit (FXD2) gene, complete cds, alternatively spliced |
| 12846 | 26458 | | 2.01 | 2.6E-01 | D88425.1 | NT | Caella cobaya mRNA for serine/threonine kinase, complete cds |
| 12974 | 26539 | | 1.74 | 2.6E-01 | AF141325.2 | NT | Homo sapiens Inositol polyphosphate 1-phosphatase (INPP1) gene, complete cds |
| 13010 | 26562 | | 3.07 | 2.6E-01 | P47285 | SWISSPROT | HYPOTHETICAL PROTEIN MG039 |
| 241 | 13340 | 26265 | 2.33 | 2.5E-01 | 4502296 | NT | Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA |
| 242 | 13340 | 26265 | 1.97 | 2.5E-01 | 4502296 | NT | Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA |
| 255 | 13352 | | 4.63 | 2.5E-01 | M26501.1 | NT | Starfish (P. ochraceus) cytoplasmic actin gene, complete cds |
| 833 | 13890 | 26844 | 1.87 | 2.5E-01 | U06984.1 | NT | Mus musculus ICR/Swiss glycerinaldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds |
| 1123 | 14107 | 27119 | 9.8 | 2.5E-01 | T88837.1 | EST_HUMAN | y011g07.r1 Stragene lung (#837210) Homo sapiens cDNA clone IMAGE:117468 5' |
| 1522 | 14564 | 27525 | 1.55 | 2.5E-01 | AL115624.1 | NT | Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation |
| 1741 | 14771 | | 5.06 | 2.5E-01 | 4885406 | NT | Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 4 (HCN4) mRNA |
| 1900 | 15680 | 27920 | 0.94 | 2.5E-01 | BE599604.1 | EST_HUMAN | PM4-CT0400-310700-005-d08 CT0400 Homo sapiens cDNA |
| 1900 | 15680 | 27921 | 0.94 | 2.5E-01 | BE599604.1 | EST_HUMAN | PM4-CT0400-310700-005-d08 CT0400 Homo sapiens cDNA |
| 2417 | 16424 | | 13.96 | 2.5E-01 | AE000675.1 | NT | Aquifex aeolicus section 7 of 109 of the complete genome |
| 2603 | 16506 | | 1.09 | 2.5E-01 | AA251987.1 | EST_HUMAN | 2s11a12.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684862 5' |
| 2644 | 15641 | 28065 | 0.94 | 2.5E-01 | X55310.1 | NT | B. taurus mRNA for D-aspartate oxidase |
| 3423 | 16471 | | 2.83 | 2.5E-01 | AW973471.1 | EST_HUMAN | EST385464 MAGe resequences, MAGM Homo sapiens cDNA |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 3545 | 16591 | 29516 | 0.87 | 2.5E-01 | AF233875.1 | NT | Danio rerio peptide YY precursor gene, complete cds |
| 3560 | 16606 | 29526 | 7.94 | 2.5E-01 | AL161517.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 29 |
| 3861 | 16900 | 29803 | 1.15 | 2.5E-01 | AJ741483.1 | EST_HUMAN | wg11c07.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364780 3' |
| 3861 | 16900 | 29804 | 1.15 | 2.5E-01 | AJ741483.1 | EST_HUMAN | wg11c07.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364780 3' |
| 4098 | 17130 | | 1.76 | 2.5E-01 | P32323 | SWISSPROT | A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR |
| 4346 | 17373 | | 0.99 | 2.5E-01 | Q03314 | SWISSPROT | RHIB PROTEIN |
| 4760 | 17800 | | 1.34 | 2.5E-01 | Q27225 | SWISSPROT | MOLT-INHIBITING HORMONE PRECURSOR (MIH) |
| 4768 | 17806 | 30698 | 4.71 | 2.5E-01 | AF007768.1 | NT | Chlorostoma fumiferana dipeptide associated protein 2 (DAP2) mRNA, complete cds |
| 4821 | 17838 | 30736 | 2.32 | 2.5E-01 | AE004416.1 | NT | Vibrio cholerae chromosome II, section 73 of 93 of the complete chromosome |
| 4840 | 17857 | | 3.69 | 2.5E-01 | AJ230113.1 | NT | Mus musculus annexin V gene, intron 4 segment containing 5' LTR and gap portion of MuERV-L (murine endogenous retrovirus) element |
| 4870 | 17887 | 30775 | 0.64 | 2.5E-01 | BE896785.1 | EST_HUMAN | h02111.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3922600 5' |
| 5086 | 18096 | 30972 | 0.84 | 2.5E-01 | AW873588.1 | EST_HUMAN | WP:Y71F9A_294.D CE22858 |
| 5243 | 18251 | | 0.96 | 2.5E-01 | AA768389.1 | EST_HUMAN | ca63a09.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1316920 3' similar to contains Alu repetitive element |
| 5399 | 18502 | 31380 | 13.58 | 2.5E-01 | S83390.1 | NT | T3 receptor-associated cofactor-1 [human, fetal liver, mRNA, 2630 nt] |
| 6070 | 19151 | 32363 | 0.64 | 2.5E-01 | AJ006346.1 | NT | Homo sapiens KVLQ11 gene |
| 6071 | 19152 | | 0.87 | 2.5E-01 | AL163207.2 | NT | Homo sapiens chromosome 21 segment HS21C007 |
| 6525 | 19588 | 32847 | 0.49 | 2.5E-01 | P22219 | SWISSPROT | PROTEIN KINASE VPS15 |
| 6760 | 19835 | 33118 | 0.86 | 2.5E-01 | AJ251973.1 | NT | Homo sapiens partial steirin-1 gene |
| 7245 | 19980 | 33277 | 0.8 | 2.5E-01 | 8394138 | NT | Rattus norvegicus rab3 (RABIN3), mRNA |
| 7575 | 20537 | 33896 | 0.79 | 2.5E-01 | U13992.1 | NT | Feline calicivirus CF168 RNA helicase/cysteine protease/RNA-dependent RNA polymerase polyprotein precursor and capsid protein precursor, genes, complete cds; and unknown gene |
| 7604 | 20565 | | 1.13 | 2.5E-01 | AF134119.1 | NT | Mus musculus SKD1 (Skd1) gene, complete cds |
| 7852 | 20798 | 34174 | 0.68 | 2.5E-01 | AL161506.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18 |
| 7898 | 20841 | 34223 | 3.88 | 2.5E-01 | AL163282.2 | NT | Homo sapiens chromosome 21 segment HS21C082 |
| 8177 | 21147 | 34556 | 2.72 | 2.5E-01 | BF109040.1 | EST_HUMAN | 7167a03.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3826198 3' |
| 8188 | 21158 | 34567 | 0.62 | 2.5E-01 | BE960712.1 | EST_HUMAN | 601653391R2 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826198 3' |
| 8568 | 21536 | 34956 | 2.02 | 2.5E-01 | BF038595.1 | EST_HUMAN | 601459238F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862809 5' |
| 8740 | 21708 | 35131 | 0.67 | 2.5E-01 | P04492 | SWISSPROT | E1B PROTEIN, SMALL T-ANTIGEN (E1B 19K) |
| 8983 | 21949 | 35373 | 3.37 | 2.5E-01 | H53236.1 | EST_HUMAN | y48407.f1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:202501 5' |
| 9227 | 22193 | 35623 | 0.81 | 2.5E-01 | M88626.1 | NT | Mouse testis-specific protein (TPX-1) gene, exon 10 |
| 9874 | 22827 | 36280 | 16.45 | 2.5E-01 | U89651.2 | NT | Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 9874 | 22827 | 36281 | 16.45 | 2.5E-01 | U90651.2 | NT | Homo sapiens matrix metalloproteinase MMP-1 gene, promoter region |
| 9831 | 22814 | 36268 | 2.03 | 2.5E-01 | AF085164.1 | NT | Hordeum vulgare receptor-like kinase LRK10 gene, partial cds |
| 9931 | 22814 | 36269 | 2.03 | 2.5E-01 | AF085164.1 | NT | Hordeum vulgare receptor-like kinase LRK10 gene, partial cds |
| 10458 | 23380 | 36873 | 1.7 | 2.5E-01 | AW591987.1 | EST_HUMAN | RC3-ST0186-130100-015-a07 ST0186 Homo sapiens cDNA |
| 10707 | 23629 | 37124 | 0.44 | 2.5E-01 | 11469652 | NT | Porphyra purpurea chloroplast, complete genome |
| 10909 | 23829 | 37342 | 1.58 | 2.5E-01 | AW152246.1 | EST_HUMAN | xg40c10.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2630034 3' similar to contains Alu repetitive element/contains element MSR1 repetitive element; |
| 10912 | 23832 | 37348 | 1.38 | 2.5E-01 | X58491.1 | NT | Mouse L1Md LINE DNA |
| 10992 | 23912 | 37427 | 0.45 | 2.5E-01 | A1934721.1 | EST_HUMAN | wp88e11.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2468878 3' similar to SW:CEBD_HUMAN P49716 COAAT/ENHANCER BINDING PROTEIN DELTA; |
| 10992 | 23912 | 37428 | 0.45 | 2.5E-01 | A1934721.1 | EST_HUMAN | wp88e11.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2468878 3' similar to SW:CEBD_HUMAN P49716 COAAT/ENHANCER BINDING PROTEIN DELTA; |
| 11413 | 24357 | 37892 | 4.47 | 2.5E-01 | D50914.1 | NT | Human mRNA for KIAA0124 gene, partial cds |
| 12120 | 24990 | 38591 | 2.34 | 2.5E-01 | AE000711.1 | NT | Aquifex aeolicus section 43 of 109 of the complete genome |
| 12204 | 25048 | 38625 | 4.55 | 2.5E-01 | AF200528.1 | NT | Zea mays cellulose synthase-4 (CesA-4) mRNA, complete cds |
| 12230 | 25959 | | 5.87 | 2.5E-01 | AL161541.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 41 |
| 12691 | 26805 | 31527 | 1.64 | 2.5E-01 | AF170072.1 | NT | Spodoptera frugiperda CALNUC mRNA, complete cds |
| 555 | 13825 | 26543 | 0.86 | 2.4E-01 | AA936316.1 | EST_HUMAN | on70d04.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1562023 3' |
| 849 | 13905 | 26864 | 2.87 | 2.4E-01 | BF576124.1 | EST_HUMAN | 602132442F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271578 5' |
| 1307 | 14343 | 27307 | 15.11 | 2.4E-01 | AJ289880.1 | NT | Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene |
| 1307 | 14343 | 27308 | 15.11 | 2.4E-01 | AJ289880.1 | NT | Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene |
| 1384 | 14418 | 27387 | 1.01 | 2.4E-01 | Y17293.1 | NT | Homo sapiens FLI-1 gene, partial |
| 1888 | 14893 | | 27.14 | 2.4E-01 | AF267753.1 | NT | Mesembryanthemum crystallinum putative potassium channel protein Mkt1p mRNA, complete cds |
| 1916 | 14940 | 27836 | 1.21 | 2.4E-01 | AF251708.1 | NT | Zaocys dhumnades fructose-1,6-bisphosphatase mRNA, complete cds |
| 2148 | 15164 | 28180 | 0.97 | 2.4E-01 | AF111168.2 | NT | Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes |
| 2178 | 15193 | | 1.04 | 2.4E-01 | P45384 | SWISSPROT | IMMUNOGLOBULIN A1 PROTEASE PRECURSOR (IGA1 PROTEASE) |
| 2271 | 15284 | 28310 | 2.23 | 2.4E-01 | AE000680.1 | NT | Aquifex aeolicus section 12 of 109 of the complete genome |
| 2391 | 15399 | 28424 | 1.65 | 2.4E-01 | BF002171.1 | EST_HUMAN | 7h23d04.x1 NCL_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:3316807 3' similar to SW:PRSB_XENLA |
| 2544 | 15546 | 28569 | 2.37 | 2.4E-01 | Z36534.1 | NT | O42586 26S PROTEASE REGULATORY SUBUNIT 6A; |
| 2772 | 15764 | 28785 | 2.11 | 2.4E-01 | X71783.1 | NT | D.discoidium (Ax3-K) ponA gene |
| 2787 | 15789 | 28807 | 3.03 | 2.4E-01 | AF030154.1 | NT | S.pombe swi6 gene |
| | | | | | | NT | Bovine adenovirus 3 complete genome |
| 3149 | 16206 | | 3.16 | 2.4E-01 | U72726.1 | NT | Oryza longistaminata receptor kinase-like protein, family member D, and retrofit (gap/pol) genes, complete cds |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 3163 | 16219 | 29134 | 1.71 | 2.4E-01 | X74209.1 | NT | H.sapiens AGT gene, PstI fragment of intron 4 |
| 3675 | 16718 | 29632 | 1 | 2.4E-01 | AF169793.1 | NT | Podocarpa anserina HET-C protein (Het-c) gene, complete cds |
| 3773 | 16815 | 29724 | 0.95 | 2.4E-01 | AE000312.1 | NT | Escherichia coli K-12 MG1655 section 202 of 400 of the complete genome |
| 4062 | 17098 | | 0.97 | 2.4E-01 | D29960.1 | NT | Rattus norvegicus mRNA for alphaB crystallin-related protein, complete cds |
| 4974 | 17989 | | 0.98 | 2.4E-01 | AL161589.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85 |
| 5099 | 18099 | 30975 | 0.95 | 2.4E-01 | D00944.1 | NT | Hepatitis C virus genomic RNA for polyprotein, complete cds |
| 5537 | 18634 | 31574 | 0.77 | 2.4E-01 | AI925707.1 | EST_HUMAN | wo33d05.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2457129 3' |
| 5537 | 18634 | 31575 | 0.77 | 2.4E-01 | AI925707.1 | EST_HUMAN | wo33d06.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2457129 3' |
| 5562 | 18659 | 31605 | 0.69 | 2.4E-01 | D50871.1 | NT | Glycine max mRNA for mitotic cyclin b1-type, complete cds |
| 5738 | 18832 | 32011 | 9.32 | 2.4E-01 | AF091216.1 | NT | Mus musculus Wm protein (Wm) gene, complete cds |
| 5738 | 18832 | 32012 | 9.32 | 2.4E-01 | AF091216.1 | NT | Mus musculus Wm protein (Wm) gene, complete cds |
| 5766 | 18858 | | 0.65 | 2.4E-01 | M83377.1 | NT | Gallus gallus brain-derived neurotrophic factor (BDNF) gene, 5' end |
| 5991 | 25649 | | 1.03 | 2.4E-01 | A133836.2 | NT | Branchiostoma floridae mRNA for calmodulin 2 (calM2) gene |
| | | | | | | | 7154d04.x1 NCI_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3338503 3' similar to SW:SFR4_HUMAN |
| | | | | | | | Q08170 SPLICING FACTOR, ARGININE/SERINE-RICH 4 ; contains element TAR1 TAR1 repetitive element |
| 5998 | 19082 | 32279 | 2.06 | 2.4E-01 | BF592336.1 | EST_HUMAN | |
| 6096 | 19177 | 32395 | 2.07 | 2.4E-01 | AF035548.1 | NT | Drosophila melanogaster p38a MAP kinase gene, complete cds |
| 6209 | 19283 | 32515 | 2.02 | 2.4E-01 | 7681801 | NT | Homo sapiens HSPC142 protein (HSPC142), mRNA |
| 6264 | 19337 | 32570 | 0.84 | 2.4E-01 | AV733787.1 | EST_HUMAN | AV733787 cda Homo sapiens cDNA clone cdaADE11 5' |
| 6523 | 19586 | 32844 | 0.69 | 2.4E-01 | AA399872.1 | EST_HUMAN | Z70402.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727683 3' |
| | | | | | | | wo62c11.x1 NCI_CGAP_Par1 Homo sapiens cDNA clone IMAGE:2323220 3' similar to gb:J03464 |
| 6685 | 19742 | 33018 | 1.72 | 2.4E-01 | AI698989.1 | EST_HUMAN | PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (HUMAN); |
| 7247 | 19982 | 33279 | 0.54 | 2.4E-01 | AF163863.1 | NT | Mustela vison tyrosine aminotransferase gene, complete cds |
| 7566 | 20529 | 33888 | 7.93 | 2.4E-01 | IL43001.1 | NT | Bos taurus guanidyl cyclase-activating protein 2 (guca2) mRNA, complete cds |
| 7748 | 20701 | 34068 | 0.55 | 2.4E-01 | N48732.1 | EST_HUMAN | yo55c11.1 Soares_multiple_sclerosis_2NbrHMSF Homo sapiens cDNA clone IMAGE:277460 5' |
| | | | | | | | |
| 7894 | 20833 | | 0.51 | 2.4E-01 | U05013.1 | NT | Rattus norvegicus Sprague-Dawley heme oxygenase-2 non-reducing isoform gene, complete cds |
| 7996 | 20935 | 34329 | 0.97 | 2.4E-01 | AF229844.1 | NT | Mus musculus DXImx48e protein (DXImx48e) mRNA, complete cds |
| 8416 | 21385 | 34792 | 0.51 | 2.4E-01 | X97252.1 | NT | M.musculus pah gene and promoter |
| 8416 | 21385 | 34793 | 0.51 | 2.4E-01 | X97252.1 | NT | M.musculus pah gene and promoter |
| 8692 | 21660 | 35083 | 1.5 | 2.4E-01 | AJ012585.1 | NT | Tetrahymena thermophila macronuclear gene encoding ribosomal protein L3, exons 1-2 |
| 8946 | 21912 | 35337 | 0.98 | 2.4E-01 | BF242794.1 | EST_HUMAN | 601877679F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106298 5' |
| 9001 | 21967 | | 0.57 | 2.4E-01 | BF678275.1 | EST_HUMAN | 602086188F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4260372 5' |
| 9487 | 22451 | 35891 | 0.51 | 2.4E-01 | AL139077.2 | NT | Campylobacter jejuni NCTC11168 complete genome, segment 4/6 |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|-----------------------------|-------------------------------|---|
| 9487 | 22451 | 35892 | 0.51 | 2.4E-01 | AL139077.2 | NT | Campylobacter jejuni NCTC11168 complete genome, segment 4/6 |
| 8921 | 22742 | 38193 | 7.63 | 2.4E-01 | AI693515.1 | EST_HUMAN | wd43e02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330808 3' similar to contains |
| 10062 | 22989 | 38457 | 0.57 | 2.4E-01 | AF220087.1 | NT | MER22.b1 TAR1 repetitive element ; |
| 10062 | 22989 | 38458 | 0.57 | 2.4E-01 | AF220087.1 | NT | Drosophila melanogaster SKPB gene, complete cds |
| 10805 | 23728 | 37227 | 1.69 | 2.4E-01 | Q03692 | SWISSPROT | Drosophila melanogaster SKPB gene, complete cds |
| 11119 | 24079 | 37603 | 2.89 | 2.4E-01 | AL161494.2 | NT | COLLAGEN ALPHA 1(X) CHAIN PRECURSOR |
| 11185 | 24141 | 37675 | 1.77 | 2.4E-01 | AF030198.1 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 8 |
| 11634 | 24475 | | 1.52 | 2.4E-01 | Z21847.1 | NT | Mus musculus type 1 sigma receptor gene, complete cds |
| 12096 | 24987 | 38564 | 4.86 | 2.4E-01 | P06900 | SWISSPROT | P. asiatica mosaic virus genomic RNA |
| 12160 | 25015 | 38617 | 2.5 | 2.4E-01 | AF217491.1 | NT | PROLINE RICH 33 KD EXTENSIN-RELATED PROTEIN PRECURSOR |
| 12294 | 25749 | | 1.93 | 2.4E-01 | AF004213.1 | NT | Homo sapiens Fragile 160 oxidoreductase (FOR) gene, exon 6 |
| 12361 | 25150 | | 2.1 | 2.4E-01 | AF004213.1 | NT | Arabidopsis thaliana ethylene-insensitive3-like1 (EIL1) mRNA, complete cds |
| 12575 | 25734 | | 2.27 | 2.4E-01 | V01507.1 | NT | Mus musculus mRNA for putative mc7 protein (mc7 gene) |
| 12782 | 26945 | | 1.31 | 2.4E-01 | BF228975.1 | EST_HUMAN | Gallus gallus gene coding for e-actin |
| 13006 | 25559 | | 8.49 | 2.4E-01 | AL163281.2 | NT | RC9-GT0413-100800-023-006 CT0413 Homo sapiens cDNA |
| 389 | 13464 | 26394 | 0.98 | 2.3E-01 | S75898.1 | NT | Homo sapiens chromosome 21 segment HS21C081 |
| 638 | 13704 | | 5.85 | 2.3E-01 | U39713.1 | NT | aromatase [Poephila guttata=zebra finches, ovary, mRNA, 3188 nt] |
| 668 | 13733 | 26658 | 21.34 | 2.3E-01 | U67598.1 | NT | Mycoplasma genitalium section 35 of 51 of the complete genome |
| 934 | 13987 | 26637 | 4.19 | 2.3E-01 | BE311893.1 | EST_HUMAN | Methanococcus jannaschii section 138 of 150 of the complete genome |
| 1511 | 14543 | 27514 | 1.33 | 2.3E-01 | 6877080 | NT | 601142073FT NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3505818 5' |
| 1588 | 14601 | | 1.02 | 2.3E-01 | U22837.2 | NT | Mus musculus vacuolar protein sorting 4b (Vps4b), mRNA |
| 1608 | 14640 | 27517 | 1.21 | 2.3E-01 | AJ245480.1 | NT | Yersinia pestis HmsH (hmsH), HmsF (hmsF), HmsR (hmsR), and HmsS (hmsS) genes, complete cds |
| 1636 | 14668 | 27644 | 2.62 | 2.3E-01 | Y10887.2 | NT | Brassica napus sig gene for S-locus glycoprotein, cultivar T2 |
| 2061 | 15079 | | 1.33 | 2.3E-01 | AJ235353.1 | NT | Mus musculus cdh5 gene, exon 1, partial |
| 2452 | 15457 | 28478 | 2.76 | 2.3E-01 | BE297718.1 | EST_HUMAN | Homo sapiens partial Intron 3 of the wild type AF-4/FEL gene |
| 2690 | 15657 | 28676 | 1.27 | 2.3E-01 | M11319.1 | NT | 601175562FT NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531015 5' |
| 2835 | 14422 | 27391 | 2.34 | 2.3E-01 | AB015033.1 | NT | Human erythropoietin gene, complete cds |
| 2974 | 16032 | 28855 | 1.25 | 2.3E-01 | AA601378.1 | EST_HUMAN | Martiniabilla agerovans gyrB gene for DNA gyrase subunit B, partial cds, strain:FO 14957 |
| 3100 | 16157 | | 7.15 | 2.3E-01 | R21732.1 | EST_HUMAN | no16006.s1 NCL_CGAP_Phet1 Homo sapiens cDNA clone IMAGE:1100843 3' similar to contains Alu |
| 3393 | 16432 | 28360 | 1.26 | 2.3E-01 | H69836.1 | EST_HUMAN | repetitive element; contains element TH-R repetitive element ; |
| | | | | | | | y921b07.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:130357 3' |
| | | | | | | | y97h10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213283 5' |

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Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 3854 | 16894 | 28798 | 1.05 | 2.3E-01 | S82821.1 | NT | GSTA5-glutathione S-transferase Yc2 subunit (5' region, Intron 1) [rats, Morris hepatoma cell line, Genomic, 2212 nt, segment 1 of 3] |
| 3956 | 16896 | | 5.02 | 2.3E-01 | 7662133 | NT | Homo sapiens KIAA0450 gene product (KIAA0450), mRNA |
| 4212 | 17241 | | 0.82 | 2.3E-01 | J03267.1 | NT | Rat et al. natriuretic factor (ANF) gene, 5' end |
| 4377 | 17405 | 30285 | 0.94 | 2.3E-01 | R82262.1 | EST_HUMAN | y17701.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:149017 5' |
| 4428 | 17455 | | 2.24 | 2.3E-01 | L78789.1 | NT | Mus musculus renin (Ren-1c) gene, promoter region |
| 4479 | 17504 | 30392 | 1.07 | 2.3E-01 | D90899.1 | NT | Synochocylis sp. PCC6803 complete genome, 1/27, 1-133859 |
| 4515 | 17540 | 30426 | 1.9 | 2.3E-01 | AF092535.1 | NT | Homo sapiens mitogen-activated protein kinase p38delta (PRKM13) mRNA, complete cds |
| 4584 | 17606 | 30502 | 7.42 | 2.3E-01 | 5031984 | NT | Homo sapiens nuclear transport factor 2 (nuclear protein 15) (NP15) mRNA |
| 5087 | 18097 | 30973 | 0.65 | 2.3E-01 | AB032400.1 | NT | Mus musculus tulip 1 mRNA, complete cds |
| 5200 | 18209 | 31083 | 0.91 | 2.3E-01 | U91328.1 | NT | Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds |
| 5377 | 18481 | 31356 | 2.19 | 2.3E-01 | AB040945.1 | NT | Homo sapiens mRNA for KIAA1612 protein, partial cds |
| 5503 | 18603 | 31532 | 2.51 | 2.3E-01 | BF058381.1 | EST_HUMAN | 7430606.x1 NCI CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3476699 3' similar to SW:GAG SMSAV |
| 5608 | 18704 | 31861 | 4.56 | 2.3E-01 | X96587.1 | NT | P03330 GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]; ; |
| 5733 | 18827 | | 1.01 | 2.3E-01 | L39112.1 | NT | C.familiaris rom1 gene |
| 5945 | 18835 | 32119 | 0.81 | 2.3E-01 | S60371.1 | NT | Vitiforma corneum small subunit ribosomal RNA gene |
| 6051 | 19132 | 32340 | 2.02 | 2.3E-01 | A1708840.1 | EST_HUMAN | 23S rRNA [Leuconostoc carnosum, Genomic, 2866 nt] |
| 6051 | 19132 | 32341 | 2.02 | 2.3E-01 | A1708840.1 | EST_HUMAN | as27e12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238 |
| 6812 | 19866 | 33154 | 0.76 | 2.3E-01 | AF198089.1 | NT | CYTCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN); |
| 7061 | 20083 | 33391 | 5.28 | 2.3E-01 | A1718148.1 | EST_HUMAN | as27e12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238 |
| 7318 | 20289 | 33632 | 0.69 | 2.3E-01 | 8923323 | NT | CYTCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN); |
| 7505 | 20470 | 33830 | 0.79 | 2.3E-01 | AF000227.1 | NT | as27e12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238 |
| 7646 | 20606 | 33972 | 2.65 | 2.3E-01 | AF178389.1 | NT | CYTCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN); |
| 7649 | 20609 | 33974 | 10.72 | 2.3E-01 | AV719681.1 | EST_HUMAN | Oryctolagus cuniculus cytochrome oxidase subunit VIIa (coxVIIa2) mRNA, complete cds; nuclear gene for mitochondrial product |
| 7649 | 20609 | 33975 | 10.72 | 2.3E-01 | AV719681.1 | EST_HUMAN | as42f12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319887 3' similar to contains Alu repetitive element; |
| 7866 | 20810 | | 3.39 | 2.3E-01 | 6754779 | NT | Homo sapiens hypothetical protein FLJ20345 (FLJ20345), mRNA |
| | | | | | | | Secale cereale omega secalin gene, complete cds |
| | | | | | | | Glycine max resistance protein LM17 precursor RNA, partial cds |
| | | | | | | | AV719681 GLC Homo sapiens cDNA clone GLDGB08 5' |
| | | | | | | | AV719681 GLC Homo sapiens cDNA clone GLDGB08 5' |
| | | | | | | | Mus musculus myosin XV (Myo15), mRNA |

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Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 7871 | 20815 | 34193 | 1.36 | 2.3E-01 | BE888071.1 | EST_HUMAN | 601511573F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912859 6' |
| 8028 | 20965 | | 2.99 | 2.3E-01 | N80983.1 | EST_HUMAN | za12608.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:292358 5' |
| 8073 | 21010 | 34408 | 0.63 | 2.3E-01 | 11416821 | NT | Homo sapiens protocadherin alpha cluster (LOC633960), mRNA |
| 8073 | 21010 | 34409 | 0.63 | 2.3E-01 | 11416821 | NT | Homo sapiens protocadherin alpha cluster (LOC633960), mRNA |
| 8184 | 21154 | 34562 | 0.8 | 2.3E-01 | AL161588.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 58 |
| 8328 | 21295 | 34710 | 2.02 | 2.3E-01 | M68931.1 | NT | Oxytricha nova macronuclear telomere-binding protein alpha subunit (tel-alpha alanine version) gene, complete cds |
| 8838 | 21805 | 35222 | 0.54 | 2.3E-01 | U57999.1 | NT | Mus musculus propepsin (psap SGP-1) gene, complete cds |
| 9125 | 22091 | 35519 | 0.46 | 2.3E-01 | AW590541.1 | EST_HUMAN | xc90806.x1 NCI_CGAP_Bn35 Homo sapiens cDNA clone IMAGE:2591554 3' |
| 9240 | 22208 | 35639 | 0.45 | 2.3E-01 | AW964460.1 | EST_HUMAN | EST376533 MAGE resequences, MAGH Homo sapiens cDNA |
| 9496 | 22460 | 35900 | 0.59 | 2.3E-01 | AA372164.1 | EST_HUMAN | EST84061 Rhadomyosarcoma Homo sapiens cDNA 5' end similar to DnaJ homolog (GB:X633368) |
| 9496 | 22460 | 35901 | 0.59 | 2.3E-01 | AA372164.1 | EST_HUMAN | EST84061 Rhadomyosarcoma Homo sapiens cDNA 5' end similar to DnaJ homolog (GB:X633368) |
| 9940 | 22857 | 36329 | 0.63 | 2.3E-01 | 6678318 | NT | Mus musculus phosphatidylinositol 3-kinase catalytic subunit delta (Pik3cd), mRNA |
| 10086 | 23013 | 36486 | 0.78 | 2.3E-01 | BE277690.1 | EST_HUMAN | 601120110F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2966739 5' |
| 10141 | 23087 | 36543 | 0.69 | 2.3E-01 | AW864460.1 | EST_HUMAN | EST376533 MAGE resequences, MAGH Homo sapiens cDNA |
| 10191 | 23116 | 36600 | 1.36 | 2.3E-01 | X52124.1 | NT | Haemophilus influenzae genes for HincII restriction-modification system (HincII methyltransferase (EC 2.1.1.72) and HincII endonuclease (EC 3.1.21.4)) |
| 10226 | 23151 | 36640 | 0.57 | 2.3E-01 | AW364633.1 | EST_HUMAN | PM2-DT0036-281299-001-704 DT0036 Homo sapiens cDNA |
| 10284 | 23218 | 36702 | 2.8 | 2.3E-01 | BE173060.1 | EST_HUMAN | MRO-HT0559-240400-014-g11 HT0559 Homo sapiens cDNA |
| 10351 | 23275 | 36749 | 2.33 | 2.3E-01 | AJ283261.1 | NT | Rhizobium leguminosarum partial genomic DNA for exopolysaccharide biosynthesis genes |
| 10809 | 23730 | 37232 | 0.8 | 2.3E-01 | AF201929.1 | NT | Murine hepatitis virus strain 2, complete genome |
| 10820 | 23741 | | 6.12 | 2.3E-01 | BF133577.1 | EST_HUMAN | 601646155R2 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4102092 3' |
| 11355 | 24305 | 37832 | 1.49 | 2.3E-01 | AF004833.1 | NT | Mus musculus tissue factor pathway inhibitor (TFPI) mRNA, complete cds |
| 11355 | 24305 | 37833 | 1.49 | 2.3E-01 | AF004833.1 | NT | Mus musculus tissue factor pathway inhibitor (TFPI) mRNA, complete cds |
| 11522 | 24463 | 38015 | 1.69 | 2.3E-01 | AJ250189.1 | NT | Mus musculus partial mRNA for muscle protein 534 (mg534 gene) |
| 11522 | 24463 | 38016 | 1.69 | 2.3E-01 | AJ250189.1 | NT | Mus musculus partial mRNA for muscle protein 534 (mg534 gene) |
| 11679 | 24945 | 38222 | 2.61 | 2.3E-01 | AE002167.2 | NT | Chlamydia pneumoniae AR39, section 4 of 94 of the complete genome |
| 12098 | 24969 | 38566 | 1.47 | 2.3E-01 | AE004668.1 | NT | Pseudomonas aeruginosa PA01, section 229 of 529 of the complete genome |
| 12278 | 25098 | | 5.42 | 2.3E-01 | U45426.1 | NT | Borrelia burgdorferi 2.9.8 locus, ORF-A-D genes, complete cds and REP+ gene, partial cds |
| 12370 | 25158 | | 6.49 | 2.3E-01 | T27231.1 | EST_HUMAN | HCOEST44 HT29M6 Homo sapiens cDNA clone HCOE44 5' |
| 12403 | 25176 | | 2.24 | 2.3E-01 | AW863940.1 | EST_HUMAN | PM4-SN0012-030400-001-b08 SN0012 Homo sapiens cDNA |
| 12460 | 25892 | 31417 | 2.82 | 2.3E-01 | AW303623.1 | EST_HUMAN | xi21d07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813773 3' similar to TR:Q9Z715 Q9Z7175 LYSYL OXIDASE-RELATED PROTEIN 2 : contains PTR5.b2 TAR1 repetitive element ; |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 12494 | 25937 | 31312 | 11.07 | 2.3E-01 | BE882464.1 | EST_HUMAN | 601607202F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:39086899 5' |
| 12544 | 25267 | | 2.36 | 2.3E-01 | BF663319.1 | EST_HUMAN | 602144450F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4297719 5' |
| 12591 | 26295 | | 3.71 | 2.3E-01 | AJ006519.1 | NT | Rattus norvegicus mRNA for acid gated ion channel |
| 12680 | 25348 | | 2.12 | 2.3E-01 | U49645.1 | NT | Pleurodeles waltl distal-less like protein PwDlx-3 (PwDlx-3) mRNA, complete cds |
| 12926 | 25511 | | 1.49 | 2.3E-01 | BF475611.1 | EST_HUMAN | mac30h12.x1 Lupski_sciatic_nerve Homo sapiens cDNA clone IMAGE:3395950 3' similar to contains element MER38 repetitive element; |
| 90 | 13206 | 26130 | 0.99 | 2.2E-01 | AJ052190.1 | EST_HUMAN | oz14a10.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1675290 3' similar to TR:Q13040 Q13040 A TP-BINDING CASSETTE PROTEIN ; |
| 1567 | 14600 | 27576 | 2.33 | 2.2E-01 | AF187850.1 | NT | Homo sapiens PPAR delta gene, promoter region |
| 2100 | 15117 | 28139 | 2.2 | 2.2E-01 | M34640.1 | NT | Fresh-water sponge Emf1 alpha collagen (COLF1) gene |
| 2412 | 15419 | 28443 | 8.18 | 2.2E-01 | BF677538.1 | EST_HUMAN | 602085009F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249989 5' |
| 2593 | 15594 | 28611 | 2.54 | 2.2E-01 | BE618258.1 | EST_HUMAN | 601462629F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866190 5' |
| 2593 | 15594 | 28612 | 2.54 | 2.2E-01 | BE618258.1 | EST_HUMAN | 601462629F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866190 5' |
| 2893 | 15952 | 28968 | 4.89 | 2.2E-01 | BE155625.1 | EST_HUMAN | PM2-HT0353-281289-003-a12 HT0353 Homo sapiens cDNA |
| 2893 | 15952 | 28969 | 4.89 | 2.2E-01 | BE155625.1 | EST_HUMAN | PM2-HT0353-281289-003-a12 HT0353 Homo sapiens cDNA |
| 2932 | 15990 | | 1.29 | 2.2E-01 | AF020503.1 | NT | Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5 |
| 3403 | 16452 | | 2.28 | 2.2E-01 | AL161562.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 62 |
| 3827 | 16967 | | 0.66 | 2.2E-01 | AF155728.1 | NT | Xiphophorus maculatus truncated Rex1 retrotransposon reverse transcriptase (RT) pseudogene |
| 4240 | 17269 | | 1.2 | 2.2E-01 | AF119102.1 | NT | Drosophila melanogaster UNC-119 (unc-119) gene, complete cds |
| 4247 | 17276 | 30158 | 5.86 | 2.2E-01 | AF155142.1 | NT | Mus musculus mixed lineage kinase 3 (Mlk3) and two pore domain K+ channel subunit (Kcnk6) genes, complete cds |
| 4292 | 17321 | 30200 | 2.33 | 2.2E-01 | AF117940.1 | NT | Mus musculus MAP kinase kinase 1 (Mek1) mRNA, complete cds |
| 4292 | 17321 | 30201 | 2.33 | 2.2E-01 | AF117340.1 | NT | Mus musculus MAP kinase kinase 1 (Mek1) mRNA, complete cds |
| 4383 | 17411 | 30294 | 1.21 | 2.2E-01 | U01307.1 | NT | Human scRNA (BC200 beta) pseudogene |
| 4383 | 17411 | 30295 | 1.21 | 2.2E-01 | U01307.1 | NT | Human scRNA (BC200 beta) pseudogene |
| 4456 | 17482 | 30370 | 23.17 | 2.2E-01 | AW361098.1 | EST_HUMAN | RC1-CT0249-141199-021-g04 CT0249 Homo sapiens cDNA |
| 4863 | 17890 | | 1.38 | 2.2E-01 | D50604.1 | NT | Human beta-cytoplasmic actin (ACTBP9) pseudogene |
| 4868 | 17865 | 30773 | 1.67 | 2.2E-01 | AA211216.1 | EST_HUMAN | z887c05.1 Stragene RNT neuron (#887233) Homo sapiens cDNA clone IMAGE:948968 5' |
| 5082 | 18092 | | 1.34 | 2.2E-01 | L13298.1 | NT | Mus musculus vinculin gene, exon 3 |
| 5160 | 18169 | 31048 | 1.22 | 2.2E-01 | BE141035.1 | EST_HUMAN | MRO-HT0067-201099-002-c10 HT0067 Homo sapiens cDNA |
| 5181 | 18190 | 31066 | 1.51 | 2.2E-01 | H60548.1 | EST_HUMAN | y42h09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:208001 5' similar to gb:Z14116.1.na1 CD59 GLYCOPROTEIN PRECURSOR (HUMAN); |
| 5263 | 18271 | | 1.06 | 2.2E-01 | AL163206.2 | NT | Homo sapiens chromosome 21 segment HS21C006 |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 5838 | 18928 | 32112 | 2.18 | 2.2E-01 | 5803002 | NT | Homo sapiens diaphanous (Drosophila, homolog) 2 (DIAPH2), transcript variant 156, mRNA |
| 5849 | 18939 | 32112 | 3.59 | 2.2E-01 | D84000.1 | NT | Synechocystis sp. PCC6803 complete genome, 19/27, 2382729-2538999 |
| 6114 | 19192 | 32415 | 0.61 | 2.2E-01 | U67087.1 | NT | Gallus gallus T-box containing protein (Ch-TbxT) mRNA, complete cds |
| 6114 | 19192 | 32416 | 0.61 | 2.2E-01 | U67087.1 | NT | Gallus gallus T-box containing protein (Ch-TbxT) mRNA, complete cds |
| 6864 | 19917 | 33211 | 0.7 | 2.2E-01 | AB038490.1 | NT | Homo sapiens gene for fukutin, complete cds |
| 6964 | 20189 | 33514 | 0.58 | 2.2E-01 | AA490106.1 | EST_HUMAN | ab02e09.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839656 3' |
| 6964 | 20189 | 33515 | 0.58 | 2.2E-01 | AA490106.1 | EST_HUMAN | ab02e09.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839656 3' |
| 7222 | 20244 | 33578 | 7.76 | 2.2E-01 | AV756238.1 | EST_HUMAN | AV756238 BM Homo sapiens cDNA clone BMFAHC06 5' |
| 7336 | 20307 | 33650 | 1.43 | 2.2E-01 | AF082738.1 | NT | Streptococcus pyogenes phosphatidylglycerophosphate synthase (pgsA) and ABC transporter ATP-binding protein (stpA) genes, complete cds; and unknown genes |
| 7336 | 20307 | 33651 | 1.43 | 2.2E-01 | AF082738.1 | NT | Streptococcus pyogenes phosphatidylglycerophosphate synthase (pgsA) and ABC transporter ATP-binding protein (stpA) genes, complete cds; and unknown genes |
| 7509 | 20474 | 33834 | 2.11 | 2.2E-01 | M24136.1 | NT | Human glycoprotein B gene, exon 4 |
| 7509 | 20474 | 33835 | 2.11 | 2.2E-01 | M24136.1 | NT | Human glycoprotein B gene, exon 4 |
| 7728 | 20684 | 34048 | 0.59 | 2.2E-01 | AE000036.2 | NT | Mycoplasma pneumoniae M129 section 45 of 63 of the complete genome |
| 7966 | 20905 | 34297 | 0.6 | 2.2E-01 | AF287967.1 | NT | Homo sapiens homeobox B7 (HOXB7) gene, partial cds; and homeobox B8 (HOXB8), homeobox B5 (HOXB5), homeobox B4 (HOXB4), and homeobox B3 (HOXB3) genes, complete cds |
| 8000 | 20939 | 34332 | 0.5 | 2.2E-01 | AB024553.1 | NT | Bacillus halodurans DNA, complete and partial cds, strain: C-125 |
| 8354 | 21323 | | 2.51 | 2.2E-01 | AF155143.1 | NT | Mus musculus nm23-M1 gene, promoter region |
| 8425 | 21394 | 34805 | 1 | 2.2E-01 | Z49933.1 | NT | E. coli sepA and sepB genes |
| 8896 | 21862 | 35284 | 0.49 | 2.2E-01 | AJ132918.1 | NT | Pan troglodytes MeCP2 gene 3'UTR |
| 9234 | 22200 | 35629 | 0.51 | 2.2E-01 | L23312.1 | NT | Mouse HD protein mRNA, complete cds |
| 9234 | 22200 | 35630 | 0.51 | 2.2E-01 | L23312.1 | NT | Mouse HD protein mRNA, complete cds |
| 9247 | 22213 | 35643 | 4.12 | 2.2E-01 | AE001713.1 | NT | Thermotoga maritima section 25 of 136 of the complete genome |
| 9267 | 22233 | 35663 | 0.47 | 2.2E-01 | U09964.1 | NT | Mus musculus ICR/Swiss glyceroldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds |
| 9376 | 22341 | | 3.89 | 2.2E-01 | AW856039.1 | EST_HUMAN | PM3-CT0263-241 299-009-b07 CT0263 Homo sapiens cDNA |
| 9470 | 22434 | 35872 | 1.4 | 2.2E-01 | 8393247 | NT | Mus musculus deformed epidermal autoregulatory factor 1 (Drosophila) (Dera1), mRNA |
| 9553 | 22615 | 35968 | 1.4 | 2.2E-01 | BF376354.1 | EST_HUMAN | MR1-TN0045-110900-008-c02 TN0045 Homo sapiens cDNA |
| 9644 | 22688 | 36037 | 1.3 | 2.2E-01 | W02988.1 | EST_HUMAN | za0408.11 Soares melanocyte 2NkHM Homo sapiens cDNA clone IMAGE:291591 5' |
| 9662 | 22819 | 36274 | 15.89 | 2.2E-01 | P48634 | SWISSPROT | LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2) |
| 9707 | 22860 | 36116 | 0.68 | 2.2E-01 | AJ008839.1 | NT | Xenopus laevis mRNA for kinesin-like protein 3 (xklp3) |
| 9718 | 22746 | 36197 | 0.78 | 2.2E-01 | 7657426 | NT | Mus musculus osteoblast specific factor 2 (OSF-2), mRNA |
| 9731 | 22759 | 36212 | 4.38 | 2.2E-01 | M89643.1 | NT | Brachydanio rerio ependymin beta and gamma chains (Epd) gene, complete cds |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|-----------------------------|-------------------------------|--|
| 9979 | 22906 | 36371 | 0.5 | 2.2E-01 | Q90980 | SWISSPROT | CYCLOC NUCLEOTIDE GATED CHANNEL, ROD PHOTORECEPTOR, ALPHA SUBUNIT (CNG CHANNEL 3) (CNG-3) (CNG3) |
| 10174 | 23099 | 36579 | 3.74 | 2.2E-01 | AF197941.1 | NT | Funaria hygrometrica chloroplast-localized small heat shock protein (CPsHSP21) mRNA, complete cds; nuclear gene for chloroplast product |
| 10313 | 23237 | 36719 | 1.76 | 2.2E-01 | BF206507.1 | EST_HUMAN | 601869724-F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100189 5' |
| 10537 | 23459 | 36956 | 1 | 2.2E-01 | 9625671 | NT | Human herpesvirus 5, complete genome |
| 10697 | 23619 | 37113 | 0.52 | 2.2E-01 | T59472.1 | EST_HUMAN | y663408.r1 Stratagene ovary (#637217) Homo sapiens cDNA clone IMAGE:75855 5' |
| 10697 | 23619 | 37114 | 0.52 | 2.2E-01 | T59472.1 | EST_HUMAN | y663408.r1 Stratagene ovary (#637217) Homo sapiens cDNA clone IMAGE:75855 5' |
| | | | | | | | Pseudomonas aeruginosa quinolone protein ethanol dehydrogenase (exaA) gene, partial cds; cytochrome c550 precursor (exaB), NAD+ dependent acetaldehyde dehydrogenase (exaC), and pyrroloquinoline quinone synthesis A (ppqA) genes, complete cds; and pyrroloquin> |
| 10735 | 23657 | 37150 | 0.51 | 2.2E-01 | AF068264.1 | NT | Mus musculus PHRT (Phrt) gene, partial cds |
| 10810 | 23731 | | 0.68 | 2.2E-01 | AF071001.1 | NT | Helicobacter pylori, strain J99 section 123 of 132 of the complete genome |
| 10856 | 23776 | 37274 | 0.67 | 2.2E-01 | AE001562.1 | NT | Helicobacter pylori, strain J99 section 123 of 132 of the complete genome |
| 10856 | 23776 | 37275 | 0.67 | 2.2E-01 | AE001562.1 | NT | Helicobacter pylori, strain J99 section 123 of 132 of the complete genome |
| 11751 | 24638 | 38215 | 3.77 | 2.2E-01 | X01918.1 | NT | Drosophila 86C glue gene cluster |
| 11789 | 23944 | 37466 | 3.41 | 2.2E-01 | 7706215 | NT | Homo sapiens H-2K binding factor-2 (LOC51580), mRNA |
| | | | | | | | Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), calretactin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI> |
| 12317 | 25950 | | 2.32 | 2.2E-01 | U82671.2 | NT | Vitis vinifera cultivar Pinot Noir plasma membrane aquaporin (PIP1a) mRNA, complete cds |
| 12406 | 25179 | | 3.88 | 2.2E-01 | AF188843.1 | NT | RC1-CT0249-141199-021-g04 CT0249 Homo sapiens cDNA |
| 12513 | 17482 | 30370 | 6.62 | 2.2E-01 | AW361098.1 | EST_HUMAN | h17602.x1 NCL_CGAP_GUT Homo sapiens cDNA clone IMAGE:2972523 3' |
| 12514 | 25246 | | 1.7 | 2.2E-01 | AW661922.1 | EST_HUMAN | Phodopus sungorus uncoupling protein 3 mRNA, partial cds |
| 13111 | 25946 | | 1.36 | 2.2E-01 | AF271265.1 | NT | nm31e11.s1 NCL_CGAP_Lp2 Homo sapiens cDNA clone IMAGE:1061804 |
| 972 | 14024 | 26978 | 1.58 | 2.1E-01 | AA569289.1 | EST_HUMAN | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18 |
| 975 | 14026 | 26980 | 1.06 | 2.1E-01 | AL161504.2 | NT | Ghlaurydia muridarum, section 45 of 85 of the complete genome |
| 1126 | 14169 | | 2.38 | 2.1E-01 | AE002314.2 | NT | Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA |
| 1203 | 14242 | 27199 | 0.88 | 2.1E-01 | 6754299 | NT | Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA |
| 1203 | 14242 | 27200 | 0.88 | 2.1E-01 | 6754299 | NT | Mus musculus mas proto-oncogene and Igf2r gene for insulin-like growth factor type 2 and L41ps and Au76 pseudogenes |
| 1512 | 14544 | 27515 | 1.05 | 2.1E-01 | AJ249895.1 | NT | pk73602.s1 NCL_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1519610 3' similar to gb:K02765 |
| 1929 | 14953 | 27949 | 1.94 | 2.1E-01 | AA906824.1 | EST_HUMAN | COMPLEMENT C3 PRECURSOR (HUMAN). |
| 2165 | 15181 | 28201 | 3.26 | 2.1E-01 | BF695073.1 | EST_HUMAN | 602083129F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247503 5' |
| 2489 | 15895 | 28516 | 2.19 | 2.1E-01 | H73968.1 | EST_HUMAN | y104070.s1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:232837 3' |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 2489 | 15895 | 28517 | 2.19 | 2.1E-01 | H73968.1 | EST_HUMAN | y004f07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:232837 3' |
| 2836 | 15984 | 28914 | 2 | 2.1E-01 | 6812445 | NT | Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 4 (KCNH4), mRNA |
| 3481 | 16507 | 29428 | 0.92 | 2.1E-01 | AA639482.1 | EST_HUMAN | nc90b10.s1 NCI_CGAP_Co9 Homo sapiens cDNA clone IMAGE:1159579 3' |
| 3819 | 16889 | | 6.5 | 2.1E-01 | 9838361 | NT | Beta vulgaris mitochondrion, complete genome |
| 4045 | 17083 | | 1.18 | 2.1E-01 | AE001793.1 | NT | Thermotoga maritima section 105 of 138 of the complete genome |
| 4084 | 17118 | 30013 | 1.48 | 2.1E-01 | P11675 | SWISSPROT | IMMEDIATE-EARLY PROTEIN IE180 |
| 4084 | 17118 | 30014 | 1.48 | 2.1E-01 | P11676 | SWISSPROT | IMMEDIATE-EARLY PROTEIN IE180 |
| 4403 | 17431 | | 1.62 | 2.1E-01 | AB033041.1 | NT | Homo sapiens pshp47 gene, complete cds |
| 4607 | 17628 | 30520 | 1.75 | 2.1E-01 | AB010273.1 | NT | Homo sapiens mRNA for KIAA1215 protein, partial cds |
| 5063 | 18073 | 30953 | 5.08 | 2.1E-01 | D13567.1 | NT | Lampetra japonica mRNA for alpha-2-macroglobulin, complete cds |
| 5110 | 18120 | 30994 | 1.13 | 2.1E-01 | Q01338 | SWISSPROT | ALPHA-2A ADRENERGIC RECEPTOR (ALPHA-2A ADRENOCEPTOR) (ALPHA-2AAR) |
| 5216 | 18225 | 31099 | 0.92 | 2.1E-01 | AE001526.1 | NT | Helicobacter pylori, strain J99 section 87 of 132 of the complete genome |
| 5374 | 18479 | 31362 | 5.48 | 2.1E-01 | BF672895.1 | EST_HUMAN | 602152001F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4283001 5' |
| 7071 | 20083 | 33403 | 1.16 | 2.1E-01 | AJ223392.1 | NT | Drosophila melanogaster 16S rRNA gene, partial |
| 7083 | 20017 | 33320 | 1.92 | 2.1E-01 | U04642.1 | NT | Human olfactory receptor (OR17-2) gene, partial cds |
| 7636 | 20596 | 33959 | 0.78 | 2.1E-01 | Q01956 | SWISSPROT | VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID) |
| 7636 | 20596 | 33960 | 0.78 | 2.1E-01 | Q01956 | SWISSPROT | VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID) |
| 7648 | 20608 | | 2.34 | 2.1E-01 | AE000972.1 | NT | Archaeoglobus fulgidus section 135 of 172 of the complete genome |
| 7973 | 20912 | 34303 | 1.77 | 2.1E-01 | AF000949.1 | NT | Canis familiaris keratin (KRT6) gene, complete cds |
| 8027 | 20964 | 34359 | 1.08 | 2.1E-01 | AF068687.1 | NT | Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds |
| 8027 | 20964 | 34360 | 1.08 | 2.1E-01 | AF068687.1 | NT | Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds |
| 8086 | 21022 | | 0.51 | 2.1E-01 | T87354.1 | EST_HUMAN | y83501.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:114793 5' |
| 8407 | 21376 | | 1.04 | 2.1E-01 | 7305030 | NT | Mus musculus erythrocyte protein band 4.1-like 3 (Epb4.1b3), mRNA |
| 8847 | 21814 | 35234 | | | | | Haemophilus influenzae hmcD, putative haemochromatosis protein (hmcA), and haemochromatosis protein (hmcB) genes, complete cds |
| 9149 | 22116 | 35540 | 0.84 | 2.1E-01 | U68399.1 | NT | DKFZp434H0814.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434H0814 5' |
| 9149 | 22116 | 35541 | 0.84 | 2.1E-01 | AL040537.1 | EST_HUMAN | DKFZp434H0814.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434H0814 5' |
| 9392 | 22357 | 35787 | 6.08 | 2.1E-01 | Z35786.1 | NT | S. cerevisiae chromosome II reading frame ORF YBL025W |
| 9862 | 22798 | 36251 | 0.59 | 2.1E-01 | N42538.1 | EST_HUMAN | y11e10.r1 Soares melanocyte 2Nblm Homo sapiens cDNA clone IMAGE:270954 5' |
| 9862 | 22798 | 36252 | 0.59 | 2.1E-01 | N42538.1 | EST_HUMAN | y11e10.r1 Soares melanocyte 2Nblm Homo sapiens cDNA clone IMAGE:270954 5' |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 9871 | 22824 | 36277 | 2.77 | 2.1E-01 | X97378.1 | NT | A.thaliana mRNA for ARRB1b protein |
| 9976 | 22903 | 36387 | 1.28 | 2.1E-01 | AB036529.1 | NT | Homo sapiens p53R2 gene for ribonucleotide reductase, exon 6 |
| 10692 | 23614 | 37109 | 1.13 | 2.1E-01 | Z97087.1 | NT | Beta vulgaris mRNA for elongation factor 1-beta |
| 10725 | 23647 | 37140 | 2.89 | 2.1E-01 | P52824 | SWISSPROT | DIACYLGLYCEROL KINASE, DELTA (DIGLYCERIDE KINASE)(DGK-DELTA) (DAG KINASE DELTA) |
| 10731 | 23653 | 37146 | 0.93 | 2.1E-01 | BF574254.1 | EST_HUMAN | (80 KD DIACYLGLYCEROL KINASE) |
| 11009 | 23974 | 37498 | 3.69 | 2.1E-01 | AF294296.1 | NT | Anolis lineatopus isolate NG NADH dehydrogenase subunit 2 (ND2) gene, complete cds; mitochondrial gene for mitochondrial product |
| 11890 | 24771 | | 2.15 | 2.1E-01 | 11036647 | NT | Homo sapiens pancreatic polypeptide 2 (PPY2), mRNA |
| 11905 | 24786 | 38376 | 1.61 | 2.1E-01 | BE180422.1 | EST_HUMAN | RC3-H1T0622-040500-013-b11 HT0622 Homo sapiens cDNA |
| 12137 | 25502 | | 1.38 | 2.1E-01 | X57624.1 | NT | Drosophila melanogaster ALA-E6 DNA, repeat region |
| 12680 | 25339 | | 1.94 | 2.1E-01 | AF217490.1 | NT | Homo sapiens fragile 16D oxidoreductase (FOR) gene, exons 8, 9, and partial cds |
| 12880 | 25860 | | 1.8 | 2.1E-01 | L32588.1 | NT | Human granulysin gene |
| 12914 | 25493 | | 2 | 2.1E-01 | BE622149.1 | EST_HUMAN | 601440712F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915675 5' |
| 13045 | 25586 | 31682 | 1.62 | 2.1E-01 | BE672330.1 | EST_HUMAN | 7a59a02.x1 NCL_CGAP_G06 Homo sapiens cDNA clone IMAGE:3223034 3' |
| 201 | 13302 | 26231 | 1.32 | 2.0E-01 | AB017437.1 | NT | Gallus gallus mRNA for avens, complete cds |
| 535 | 13608 | | 1.82 | 2.0E-01 | 7705601 | NT | Homo sapiens CGI-18 protein (LOC51008), mRNA |
| 700 | 13762 | 26594 | 1.25 | 2.0E-01 | M77085.1 | NT | O.cuniculus germline lgh heavy chain V-H pseudogene, allotype VH2 |
| 811 | 13869 | 26818 | 1.96 | 2.0E-01 | AF027865.1 | NT | Mus musculus Major Histocompatibility Locus class II region |
| 1013 | 14061 | 27012 | 0.72 | 2.0E-01 | D90005.1 | NT | Synechocystis sp. PCC6803 complete genome, 7/27, 781449-920915 |
| 1127 | 14170 | 27121 | 2.83 | 2.0E-01 | AL163213.2 | NT | Homo sapiens chromosome 21 segment HS21C013 |
| 1259 | 14294 | 27258 | 1.42 | 2.0E-01 | AJ132695.5 | NT | Homo sapiens rac1 gene |
| 1311 | 14347 | 27313 | 2.04 | 2.0E-01 | AW384937.1 | EST_HUMAN | PM1-HT0422-291298-002-c06 HT0422 Homo sapiens cDNA |
| 1454 | 14487 | | 1.39 | 2.0E-01 | AJ243957.1 | NT | Plum pox virus strain M, complete genome, isolate PS |
| 1483 | 14516 | 27490 | 15.27 | 2.0E-01 | 4503408 | NT | Homo sapiens dystrobrevin, alpha (DTNA), mRNA |
| 1555 | 14587 | 27559 | 2.13 | 2.0E-01 | AB007974.1 | NT | Homo sapiens mRNA, chromosome 1 specific transcript KIAA0605 |
| 1590 | 14592 | 27595 | 1.52 | 2.0E-01 | AF280700.1 | NT | Homo sapiens sodium/iodide symporter mRNA, partial cds |
| 1706 | 14758 | 27718 | 1.38 | 2.0E-01 | U22346.1 | NT | Human bradykinin B1 receptor (bradyb1) gene, complete cds |
| 1730 | 14780 | | 2.09 | 2.0E-01 | AF111170.3 | NT | Homo sapiens 14q32 Jagged2 gene, complete cds, and unknown gene |
| 1772 | 14801 | | 3.8 | 2.0E-01 | U67525.1 | NT | Methanococcus jannaschii section 67 of 150 of the complete genome |
| 1907 | 14931 | 27926 | 0.94 | 2.0E-01 | BE871330.1 | EST_HUMAN | 601449441F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:3863330 5' |
| 1907 | 14931 | 27927 | 0.94 | 2.0E-01 | BE871330.1 | EST_HUMAN | 601449441F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:3863330 5' |
| 2355 | 15364 | | 1.88 | 2.0E-01 | X82877.1 | NT | H.sapiens Nat-D-glucose cotransport regulator gene |

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Table 4
Single Exon Probes Expressed In Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 3499 | 16546 | 29472 | 0.74 | 2.0E-01 | P46607 | SWISSPROT | HOMEOBOX PROTEIN GLABRA2 (HOMEOBOX-LEUCINE ZIPPER PROTEIN ATHB-10) (HD-ZIP PROTEIN ATHB-10) |
| 3582 | 16627 | | 0.82 | 2.0E-01 | AW238005.1 | EST_HUMAN | xp15602.x1 NCL_CGAP_HN9 Homo sapiens cDNA clone IMAGE:2740395 3' similar to contains element |
| 3720 | 16763 | 29674 | 0.79 | 2.0E-01 | P34641 | SWISSPROT | MER21 repetitive element ; |
| 3855 | 16895 | 29799 | 1.14 | 2.0E-01 | AL163204.2 | NT | CED-11 PROTEIN |
| 3977 | 17017 | 29831 | 0.7 | 2.0E-01 | Z46906.1 | NT | Homo sapiens chromosome 21 segment HS21C004 |
| 4597 | 17618 | | 10.26 | 2.0E-01 | BE826165.1 | EST_HUMAN | Sus scrofa |
| 5078 | 18088 | 30968 | 7.06 | 2.0E-01 | 8922080 | NT | QV4-EN0032-190500-223-e03 EN0032 Homo sapiens cDNA |
| 5144 | 18153 | 31033 | 0.97 | 2.0E-01 | Y19216.1 | NT | Homo sapiens hypothetical protein ASH1 (ASH1), mRNA |
| 5298 | 18302 | 31163 | 0.93 | 2.0E-01 | BE439491.1 | EST_HUMAN | Homo sapiens putative pshHbD pseudogene for hair keratin, exons 1 to 9 |
| 5520 | 18619 | 31553 | 2.31 | 2.0E-01 | X56600.1 | NT | HTM1-122F1 HTM1 Homo sapiens cDNA |
| 5831 | 18921 | 32104 | 1.89 | 2.0E-01 | 11432540 | NT | Rat SOD-2 gene for manganese-containing superoxide dismutase |
| 5940 | 19026 | 32220 | 0.69 | 2.0E-01 | X91856.1 | NT | Homo sapiens dual oxidase-like domains 2 (DUOX2), mRNA |
| 6178 | 19253 | 32488 | 5.47 | 2.0E-01 | U15300.1 | NT | F.rubripes DNA encoding for valyl-RNA synthetase |
| 6298 | 19370 | | 0.79 | 2.0E-01 | M75967.1 | NT | Saccharomyces cerevisiae Halp (HAL5) mRNA, complete cds |
| 6417 | 19484 | 32733 | 0.56 | 2.0E-01 | P02467 | SWISSPROT | Human hepatocyte growth factor gene, exon 1 |
| 6569 | 19629 | 32895 | 3.05 | 2.0E-01 | X61033.1 | NT | COLLAGEN ALPHA 2(I) CHAIN PRECURSOR |
| 6679 | 19736 | 33012 | 4.25 | 2.0E-01 | AW360865.1 | EST_HUMAN | M.auratus mu class glutathione transferase gene |
| 7512 | 20477 | 33638 | 1.27 | 2.0E-01 | AF250371.1 | NT | PM1-CT0247-141099-001-g06 CT0247 Homo sapiens cDNA |
| 7679 | 20637 | 33989 | 0.72 | 2.0E-01 | P54422 | SWISSPROT | Mus musculus phosphoruclickinase-1 C isozyme (PfkC) gene, exons 3 through 7 |
| 8054 | 20991 | 34389 | 0.61 | 2.0E-01 | V00726.1 | NT | GAMMA-GLUTAMYL TRANSPEPTIDASE PRECURSOR |
| 8285 | 21254 | | 6.17 | 2.0E-01 | AF028026.1 | NT | Mouse germ line gene coding for beta-globin (Y2) |
| 8542 | 21510 | 34927 | 3.1 | 2.0E-01 | X91151.1 | NT | Andes virus strain Q123133 glycoprotein G1 and G2 precursor, gene, partial cds |
| 9074 | 22040 | | 0.43 | 2.0E-01 | BE562247.1 | EST_HUMAN | M.musculus scp2 gene exon 14 |
| 9706 | 22659 | 36115 | 1.09 | 2.0E-01 | U82511.1 | NT | 601344648F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677794 5' |
| 9745 | 22686 | 36141 | 0.76 | 2.0E-01 | U71122.1 | NT | Dictyostelium discoideum elug cDNA19 protein (rsc19) mRNA, partial cds |
| 9914 | 22735 | | 6.23 | 2.0E-01 | AE001278.1 | NT | Arabidopsis pyruvate decarboxylase-2 (Pdc2) gene, complete cds |
| 10103 | 23029 | 36506 | 0.62 | 2.0E-01 | P11420 | SWISSPROT | Chlamydia trachomatis section 5 of 87 of the complete genome |
| 10251 | 23176 | | 1.94 | 2.0E-01 | AF146692.1 | NT | DAUGHTERLESS PROTEIN |
| 10401 | 23323 | 36807 | 1.94 | 2.0E-01 | AF086907.1 | NT | DAUGHTERLESS PROTEIN |
| 10401 | 23323 | 36808 | 1.94 | 2.0E-01 | AF086907.1 | NT | Homo sapiens filamin 2 (FLN2) mRNA, complete cds |
| 10528 | 23450 | 36948 | 0.64 | 2.0E-01 | AF157814.1 | NT | Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds |
| | | | | | | NT | Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds |
| | | | | | | NT | Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12 |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 10528 | 23450 | 36949 | 0.64 | 2.0E-01 | AF157814.1 | NT | Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12 |
| 10575 | 23497 | | 0.78 | 2.0E-01 | X78388.1 | NT | D.melanogaster DNA mobile element (hoppe) |
| 10770 | 23691 | 37188 | 0.97 | 2.0E-01 | X97121.1 | NT | R.norvegicus mRNA for NTR2 receptor |
| 11189 | 24145 | 37678 | 2.24 | 2.0E-01 | D89088.1 | NT | Salvelinus pluvius mRNA for transferrin, complete cds |
| 11189 | 24145 | 37679 | 2.24 | 2.0E-01 | D89088.1 | NT | Salvelinus pluvius mRNA for transferrin, complete cds |
| 12641 | 25325 | | 1.42 | 2.0E-01 | AF206637.2 | NT | Pimephales promelas liver glucose-6-phosphate-1-dehydrogenase mRNA, partial cds |
| 12828 | 25779 | | 1.66 | 2.0E-01 | AF302773.1 | NT | Homo sapiens ninein-Lm isoform (ninein) mRNA, complete cds |
| 12837 | 25711 | 31609 | 1.34 | 2.0E-01 | AW975287.1 | EST_HUMAN | EST387405 MAGE resequences, MAGN Homo sapiens cDNA |
| 12875 | 25508 | 31707 | 4.12 | 2.0E-01 | AI023592.1 | EST_HUMAN | ov60a10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1643610 3' |
| 12898 | 25483 | | 2.98 | 2.0E-01 | AF078184.2 | NT | Homo sapiens Ku70-binding protein (KUB3) mRNA, partial cds |
| 110 | 13221 | | 8.9 | 1.9E-01 | 7549743 | NT | Rattus norvegicus Aryl hydrocarbon receptor nuclear translocator 1 (Ahr1), mRNA |
| 352 | 13441 | 26366 | 6.09 | 1.9E-01 | AF004353.1 | NT | Mus musculus pale ear (ep) gene, wild type allele, 3' region, partial cds |
| 857 | 13723 | 26647 | 2.66 | 1.9E-01 | U32581.2 | NT | Homo sapiens lamda/ota protein kinase C-interacting protein mRNA, complete cds |
| 657 | 13723 | 26648 | 2.66 | 1.9E-01 | U32581.2 | NT | Homo sapiens lamda/ota protein kinase C-interacting protein mRNA, complete cds |
| 664 | 13730 | 26655 | 8.69 | 1.9E-01 | BE070801.1 | EST_HUMAN | RC3-BT0502-251199-011-d01 BT0502 Homo sapiens cDNA |
| 665 | 13730 | 26655 | 6.99 | 1.9E-01 | BE070801.1 | EST_HUMAN | RC3-BT0502-251199-011-d01 BT0502 Homo sapiens cDNA |
| 898 | 14039 | | 1.18 | 1.9E-01 | 7305180 | NT | Mus musculus interleukin 2 receptor, gamma chain (il2rg), mRNA |
| 1106 | 14150 | 27101 | 9.93 | 1.9E-01 | AA358813.1 | EST_HUMAN | EST67784 Fetal Lung II Homo sapiens cDNA 5' end |
| 1372 | 14406 | 27378 | 2.9 | 1.9E-01 | AF081282.1 | NT | Sorghum bicolor 22 kDa kafirin cluster |
| 1430 | 14464 | | 3.22 | 1.9E-01 | AF184623.1 | NT | Plasmodium vivax reticulocyte binding protein-2 (rpb-2) gene, complete cds |
| 2390 | 15398 | 28423 | 3.89 | 1.9E-01 | U68066.1 | NT | Homo sapiens hypothetical protein FLJ10581 (FLJ10581), mRNA |
| 2934 | 16992 | 28912 | 3.47 | 1.9E-01 | J00922.1 | NT | Sigmodon hispidus p53 gene, partial cds |
| 2949 | 16006 | | 4.89 | 1.9E-01 | J00922.1 | NT | Gallus gallus ovalbumin (Y) gene, complete cds |
| 3406 | 16455 | 29378 | 4 | 1.9E-01 | D13197.1 | NT | Mouse gene for immunoglobulin diversity region D1 |
| 3492 | 16539 | 29464 | 5.36 | 1.9E-01 | R18467.1 | EST_HUMAN | Y42F10.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129547 5' |
| 3817 | 16857 | 29763 | 0.87 | 1.9E-01 | AF284017.1 | NT | Rattus norvegicus arylacetamide deacetylase gene, complete cds |
| 3848 | 16888 | 29791 | 2.26 | 1.9E-01 | P39768 | SWISSPROT | PAIR RULE PROTEIN ODD-PAIRED |
| 4018 | 17057 | 29959 | 3.91 | 1.9E-01 | AB006784.1 | NT | Schizosaccharomyces pombe DNA for cytoplasmic dynein heavy chain, complete cds |
| 4110 | 17144 | 30038 | 1.42 | 1.9E-01 | AW754108.1 | EST_HUMAN | CM3-CT0315-271199-045-b11 CT0315 Homo sapiens cDNA |
| 4259 | 17288 | 30169 | 1.24 | 1.9E-01 | BE834943.1 | EST_HUMAN | MR1-FN0010-290700-007-404 FN0010 Homo sapiens cDNA |
| 4496 | 17521 | 30408 | 0.83 | 1.9E-01 | AL161493.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 5 |
| 5047 | 18080 | | 1.15 | 1.9E-01 | AF223842.1 | NT | Rattus norvegicus chemokine receptor CXCR3 mRNA, complete cds |
| 5231 | 18239 | | 1.01 | 1.9E-01 | AI631199.1 | EST_HUMAN | ts93g12.x1 NCI_GGAP_G06 Homo sapiens cDNA clone IMAGE:2288886 3' similar to gb:M21674 ALPHA PLATELET-DERIVED GROWTH FACTOR RECEPTOR PRECURSOR (HUMAN); |

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 5885 | 18780 | | 5.2 | 1.9E-01 | AW130149.1 | EST_HUMAN | x129a07.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:2618444 3' similar to gb:M73779 RETINOIC ACID RECEPTOR ALPHA-1 (HUMAN); |
| 5728 | 18822 | 32002 | 8.11 | 1.9E-01 | AF127937.1 | NT | Homo sapiens DNA polymerase epsilon catalytic subunit protein (POLE1) gene, exon 1a |
| 5839 | 19025 | 32219 | 0.71 | 1.9E-01 | AF091216.1 | NT | Mus musculus Wrm protein (Wrm) gene, complete cds |
| 5887 | 19072 | | 2.15 | 1.9E-01 | AU133116.1 | EST_HUMAN | AU133116 NT2RP4 Homo sapiens cDNA clone NT2RP4001328 5' |
| 6461 | 19526 | 32776 | 0.95 | 1.9E-01 | A1762391.1 | EST_HUMAN | w154h02.x1 NCL CGAP_Cot16 Homo sapiens cDNA clone IMAGE:2394099 3' |
| 6527 | 19590 | 32850 | 0.88 | 1.9E-01 | AW148452.1 | EST_HUMAN | x114c08.x1 NCL CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2618030 3' similar to gb:X03559 ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR (HUMAN); |
| 7164 | 18395 | 31240 | 1.46 | 1.9E-01 | R43212.1 | EST_HUMAN | y09a12.s1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:31663 3' similar to contains MER13 repetitive element ; |
| 7193 | 20217 | 33547 | 0.95 | 1.9E-01 | AF034920.1 | NT | Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11 |
| 7193 | 20217 | 33548 | 0.95 | 1.9E-01 | AF034920.1 | NT | Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11 |
| 7474 | 20440 | 33798 | 0.65 | 1.9E-01 | U73846.1 | NT | Drosophila melanogaster testis-specific RNA-binding protein (bruno) mRNA, complete cds |
| 7709 | 20868 | 34033 | 0.75 | 1.9E-01 | U93688.1 | NT | Staphylococcus aureus toxic shock syndrome toxin-1 (tst), enterotoxin (ent), and integrase (int) genes, complete cds |
| 7734 | 20889 | 34053 | 1.35 | 1.9E-01 | U80922.1 | NT | Arabidopsis thaliana serine/threonine protein phosphatase type one (TOPP8) gene, complete cds |
| 7784 | 20737 | 34109 | 2.54 | 1.9E-01 | AF072724.1 | NT | Zea mays starch branching enzyme I (sbe1) gene, complete cds |
| 8318 | 21287 | 34701 | 1.41 | 1.9E-01 | AL161557.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 57 |
| 9034 | 22000 | 35421 | 12.98 | 1.9E-01 | AB033024.1 | NT | Homo sapiens mRNA for KIAA1198 protein, partial cds |
| 9297 | 22263 | 35692 | 1.32 | 1.9E-01 | M14568.1 | NT | Marasipal cat beta-globin gene mRNA, partial cds |
| 9297 | 22263 | 35693 | 1.32 | 1.9E-01 | M14568.1 | NT | Marasipal cat beta-globin gene mRNA, partial cds |
| 10234 | 23159 | 36847 | 0.67 | 1.9E-01 | AA912486.1 | EST_HUMAN | q96g10.s1 NCL CGAP_PNS1 Homo sapiens cDNA clone IMAGE:1537506 3' similar to contains Alu repetitive element; |
| 10602 | 23524 | 37019 | 0.72 | 1.9E-01 | BE830353.1 | EST_HUMAN | RC5-ET0082-060700-022-A02 ET0082 Homo sapiens cDNA |
| 10602 | 23524 | 37020 | 0.72 | 1.9E-01 | BE830353.1 | EST_HUMAN | RC5-ET0082-060700-022-A02 ET0082 Homo sapiens cDNA |
| 11106 | 24066 | 37598 | 1.87 | 1.9E-01 | AF223391.1 | NT | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced |
| 11831 | 24714 | 38298 | 1.47 | 1.9E-01 | M22253.1 | NT | Rattus norvegicus sodium channel 1 mRNA, complete cds |
| 12033 | 24909 | 38504 | 3.54 | 1.9E-01 | AJ243213.1 | NT | Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5 |
| 12049 | 24922 | 38519 | 1.53 | 1.9E-01 | L07344.1 | NT | Influenza A/Guangdong/243/72 nucleoprotein (seg 5) gene, 5' end |
| 12975 | 25540 | | 1.62 | 1.9E-01 | AF036959.1 | NT | Rattus norvegicus nuclear serine/threonine protein kinase mRNA, complete cds |
| 34 | 13154 | 26055 | 2.78 | 1.8E-01 | U73200.1 | NT | Mus musculus p116Rip mRNA, complete cds |
| 260 | 15837 | 26281 | 1.39 | 1.8E-01 | AB022090.1 | NT | Mus musculus Cctg gene for chaperonin containing TCP-1 gamma subunit, partial cds |

Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 370 | 13456 | 26386 | 1.91 | 1.8E-01 | 4502532 | NT | Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2) mRNA, and translated products |
| 983 | 14034 | 26986 | 0.89 | 1.8E-01 | AI912212.1 | EST_HUMAN | wf7102.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2337051 3' |
| 1093 | 14136 | 27087 | 1.05 | 1.8E-01 | AF000580.1 | NT | Dicotyledon discalium plasmid Ddp5, complete genome |
| 1293 | 14328 | 27290 | 9.43 | 1.8E-01 | AL117189.1 | NT | Yersinia pestis plasmid pCD1 |
| 1503 | 14536 | 27507 | 1.17 | 1.8E-01 | 6753947 | NT | Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA |
| 1503 | 14536 | 27508 | 1.17 | 1.8E-01 | 6753947 | NT | Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA |
| 1864 | 14889 | | 1.37 | 1.8E-01 | 4505036 | NT | Homo sapiens latent transforming growth factor beta binding protein 4 (LTBP4) mRNA |
| 1882 | 14907 | | 1.47 | 1.8E-01 | AI733708.1 | EST_HUMAN | qg22d10.x5 NCI_CGAP_Ki63 Homo sapiens cDNA clone IMAGE:1761811 3' similar to TR:075936 O75936 GAMMA BUTYROBETAINE HYDROXYLASE ; |
| 1930 | 14954 | 27950 | 1.66 | 1.8E-01 | AB051897.1 | NT | Mus musculus Scya6, Scya9, Scya16-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds |
| 2702 | 16698 | | 3.94 | 1.8E-01 | AW935728.1 | EST_HUMAN | QV3-DT0018-081299-036-g04 DT0018 Homo sapiens cDNA |
| 2908 | 15967 | | 1.95 | 1.8E-01 | AF184589.1 | NT | Jonopsidium acule LEAFY protein (LEAFY2) gene, partial cds |
| 2914 | 15972 | 28896 | 0.85 | 1.8E-01 | AW182300.1 | EST_HUMAN | x41a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659756 3' |
| 3141 | 16198 | 29108 | 1.35 | 1.8E-01 | AW995178.1 | EST_HUMAN | QV0-BN0041-070300-147-c04 BN0041 Homo sapiens cDNA |
| 3379 | 16428 | 29354 | 0.82 | 1.8E-01 | BF183582.1 | EST_HUMAN | 601809723R1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040821 3' |
| 3637 | 16680 | 29594 | 1.89 | 1.8E-01 | H03369.1 | EST_HUMAN | y45e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element; |
| 3637 | 16680 | 29595 | 1.89 | 1.8E-01 | H03369.1 | EST_HUMAN | y45e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element; |
| 4360 | 17387 | | 0.75 | 1.8E-01 | D37954.1 | NT | Bovine NB26 mRNA for MHC class II (BoLA-DQB), complete cds |
| 4586 | 17608 | 30503 | 6.42 | 1.8E-01 | AL161556.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 56 |
| 4806 | 17823 | 30718 | 2.5 | 1.8E-01 | AB051897.1 | NT | Mus musculus Scya6, Scya9, Scya16-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds |
| 5051 | 18063 | 30941 | 2.11 | 1.8E-01 | X79794.1 | NT | N.tabacum mRNA pNLA-35 |
| 5084 | 18094 | 30970 | 1.96 | 1.8E-01 | AW814270.1 | EST_HUMAN | MP3-ST0203-151299-112-g08 ST0203 Homo sapiens cDNA |
| 5099 | 18109 | 30982 | 0.93 | 1.8E-01 | AF192382.1 | EST_HUMAN | en28g07.y5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700028 5' |
| 5131 | 18140 | 31018 | 2.96 | 1.8E-01 | AF181258.1 | NT | Mesocricetus auratus Na-tetraololate cotransporting polypeptide mRNA, partial cds |
| 5214 | 18223 | | 0.73 | 1.8E-01 | U66150.1 | NT | Loligo forbesi TTA repeat microsatellite region Lfor4 |
| 5371 | 18476 | 31349 | 0.84 | 1.8E-01 | BE082628.1 | EST_HUMAN | RC6-BT0641-300300-011-H03 BT0641 Homo sapiens cDNA |
| 5906 | 18992 | 32163 | 1.91 | 1.8E-01 | AL161594.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90 |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 12301 | 25112 | 31840 | 1.88 | 1.8E-01 | BF348623.1 | EST_HUMAN | 602019928F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4155318 5' |
| 12752 | 25398 | | 2.05 | 1.8E-01 | Q96882 | SWISSPROT | DNA TERMINAL PROTEIN (BELLETT PROTEIN) (PTP PROTEIN) |
| 12868 | 25489 | | 1.85 | 1.8E-01 | R24494.1 | EST_HUMAN | yt48t10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133027 5' |
| 12907 | 25489 | | 1.56 | 1.8E-01 | Y11114.1 | NT | E. dispar mRNA for hexokinase (hxd1) |
| 579 | 13648 | 26561 | 1.77 | 1.7E-01 | BE385184.1 | EST_HUMAN | 601274604F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3616768 5' |
| 808 | 13684 | 26814 | 2.22 | 1.7E-01 | X53330.1 | NT | P. dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4 |
| 962 | 14015 | | 1.83 | 1.7E-01 | P36816 | SWISSPROT | NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L) |
| 1998 | 15019 | | 3.18 | 1.7E-01 | AF255051.1 | NT | Homo sapiens BNIP3H (BNIP3H) gene, complete cds; nuclear gene for mitochondrial product |
| 2871 | 15931 | 28848 | 2.3 | 1.7E-01 | AF000716.1 | NT | Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds |
| 2871 | 15931 | 28849 | 2.3 | 1.7E-01 | AF000716.1 | NT | Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds |
| 2838 | 15996 | 28917 | 1.89 | 1.7E-01 | AA336909.1 | EST_HUMAN | EST41651 Endometrial tumor Homo sapiens cDNA 5' end |
| 3010 | 16068 | 28988 | 1.22 | 1.7E-01 | AJ238736.1 | NT | Naja naja atra cdx-1 gene, exons 1-3 |
| 3010 | 16068 | 28989 | 1.22 | 1.7E-01 | AJ238736.1 | NT | Naja naja atra cdx-1 gene, exons 1-3 |
| 3122 | 19179 | 29089 | 1.68 | 1.7E-01 | AF081514.1 | NT | Taxus canadensis geranylgeranyl diphosphate synthase mRNA, complete cds |
| 3378 | 16427 | 29353 | 0.92 | 1.7E-01 | N55763.1 | EST_HUMAN | J2348F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2346 5' |
| 3482 | 16508 | 29429 | 1.48 | 1.7E-01 | AJ269505.1 | NT | Anabaena sp. ORF4 (partial), ORF3, ORF2, ORF1, adpA gene, adpB gene, adpC gene, adpD gene, adpE gene and adpF gene |
| 3989 | 16999 | 29914 | 5.69 | 1.7E-01 | AJ235377.1 | NT | Homo sapiens derivative 11 breakpoint fragment: partial intron 10 of the ALL-1/MLL/HRX gene fused to intron 5 of the AF-4/FEL gene |
| 4591 | 17812 | | 1.9 | 1.7E-01 | X52836.1 | NT | Schistosoma gregaria alpha repetitive DNA |
| 4878 | 17893 | 30782 | 1.21 | 1.7E-01 | AJ247635.1 | EST_HUMAN | qt67c09.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848808 3' similar to contains ORF.b1 ORF repetitive element |
| 5165 | 18174 | | 0.92 | 1.7E-01 | AF072725.1 | NT | Zea mays starch branching enzyme 1b (ae) gene, complete cds |
| 5270 | 18219 | 31095 | 0.74 | 1.7E-01 | BF030010.1 | EST_HUMAN | 601557256F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827197 5' |
| 5482 | 18582 | 31493 | 1.88 | 1.7E-01 | AA470886.1 | EST_HUMAN | ne13a02.s1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:881066 3' similar to gb:M17886 60S |
| 5482 | 18582 | 31494 | 1.88 | 1.7E-01 | AA470886.1 | EST_HUMAN | ne13a02.s1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:881066 3' similar to gb:M17886 60S |
| 5874 | 18769 | 31941 | 0.74 | 1.7E-01 | U43599.1 | NT | ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN); |
| 6463 | 19528 | 32777 | 12.89 | 1.7E-01 | H72118.1 | EST_HUMAN | Brugia pahangi microfilarial sheath protein SHP3 (shp3) gene, complete cds |
| | | | | | | | ys02g06.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213656 3' |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 6526 | 19589 | 32848 | 0.9 | 1.7E-01 | AI370976.1 | EST_HUMAN | ta29c11.x1 Soares fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:2045492 3' |
| 6526 | 19589 | 32849 | 0.9 | 1.7E-01 | AI370976.1 | EST_HUMAN | ta29c11.x1 Soares fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:2045492 3' |
| 7031 | 18363 | 31250 | 0.78 | 1.7E-01 | BE300286.1 | EST_HUMAN | 600944067T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2980248 3' |
| 7063 | 20085 | | 1.76 | 1.7E-01 | AF026552.3 | NT | Mesocricetus auratus oviductin precursor (OVI) gene, complete cds |
| 7196 | 20220 | | 0.79 | 1.7E-01 | Z92910.1 | NT | Homo sapiens HFE gene |
| 7430 | 20397 | 33749 | 1.56 | 1.7E-01 | AP000422.1 | NT | Escherichia coli O157:H7 genomic DNA, Sakai-VT2 prophage inserted region |
| 7515 | 20480 | 33841 | 8.55 | 1.7E-01 | BE734179.1 | EST_HUMAN | 601569022F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843964 5' |
| 7721 | 20678 | 34043 | 1.42 | 1.7E-01 | P16724 | SWISSPROT | PROBABLE PROCESSING AND TRANSPORT PROTEIN UL56 (HFLF0 PROTEIN) |
| 7739 | 25688 | 34057 | 0.71 | 1.7E-01 | Q01955 | SWISSPROT | COLLAGEN ALPHA 3(IV) CHAIN PRECURSOR |
| 8194 | 21184 | 34573 | 1.24 | 1.7E-01 | AF000573.1 | NT | Homo sapiens homogenitase 1, 2-dioxygenase gene, complete cds |
| 8296 | 21265 | 34676 | 0.62 | 1.7E-01 | AF150659.1 | NT | Pseudomonas putida long-chain-fatty-acid-CoA ligase (fadD) gene, complete cds |
| 8620 | 21688 | 35004 | 7.37 | 1.7E-01 | 7706426 | NT | Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA |
| 8620 | 21688 | 35005 | 7.37 | 1.7E-01 | 7706426 | NT | Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA |
| 9045 | 22011 | 35433 | 0.6 | 1.7E-01 | AW992873.1 | EST_HUMAN | RC2-BN0032-120200-011-a10 BN0032 Homo sapiens cDNA |
| 9079 | 22045 | 35468 | 3.22 | 1.7E-01 | D00384.1 | NT | Rat (SHR strain) SX1 gene |
| 9196 | 22162 | 35590 | 0.81 | 1.7E-01 | AF217413.1 | NT | Homo sapiens neuroigin 3 isoform gene, complete cds, alternatively spliced |
| 9196 | 22162 | 35591 | 0.81 | 1.7E-01 | AF217413.1 | NT | Homo sapiens neuroigin 3 isoform gene, complete cds, alternatively spliced |
| 9348 | 22314 | 35739 | 0.44 | 1.7E-01 | R77002.1 | EST_HUMAN | y66g02.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:144242 5' |
| 9523 | 22486 | 35933 | 0.43 | 1.7E-01 | BE253142.1 | EST_HUMAN | 601116672F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357184 5' |
| 9523 | 22486 | 35934 | 0.43 | 1.7E-01 | BE253142.1 | EST_HUMAN | 601116672F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357184 5' |
| 9948 | 22875 | 36337 | 8.16 | 1.7E-01 | AP001508.1 | NT | Bacillus halodurans genomic DNA, section 2/14 |
| 10056 | 22983 | 36451 | 0.47 | 1.7E-01 | AW977455.1 | EST_HUMAN | EST389564 IMAGE resequences, MAGO Homo sapiens cDNA |
| 10056 | 22983 | 36452 | 0.47 | 1.7E-01 | AW977455.1 | EST_HUMAN | EST389564 IMAGE resequences, MAGO Homo sapiens cDNA |
| 10073 | 23000 | 36470 | 1.93 | 1.7E-01 | U16288.1 | NT | Human class IV alcohol dehydrogenase (ADH7) gene, exon 3 |
| 10148 | 23074 | 36548 | 0.59 | 1.7E-01 | Z34508.1 | NT | Human immunodeficiency virus type 1 (B7.05) env gene (partial) |
| 10148 | 23074 | 36549 | 0.59 | 1.7E-01 | Z34508.1 | NT | Human immunodeficiency virus type 1 (B7.05) env gene (partial) |
| 10167 | 23092 | 36570 | 0.7 | 1.7E-01 | AJ251749.1 | NT | Drosophila melanogaster mRNA for serine protease inhibitor (serpin-6), (sp6 gene) |
| 10593 | 23515 | | 2.43 | 1.7E-01 | AL163284.2 | NT | Homo sapiens chromosome 21 segment HS21C084 |
| 10759 | 23680 | 37176 | 1.24 | 1.7E-01 | 11427203 | NT | Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 2 (SLC7A2), mRNA |
| 10761 | 23682 | 37178 | 1.61 | 1.7E-01 | AA627972.1 | EST_HUMAN | nc6007.st NCI_CGAP_C08 Homo sapiens cDNA clone IMAGE:1148282 3' similar to gbL25081 TRANSFORMING PROTEIN RHOC (HUMAN); |
| 10968 | 23886 | | 0.42 | 1.7E-01 | AL161542.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 42 |
| 11040 | 24004 | 37530 | 8.17 | 1.7E-01 | BE390835.1 | EST_HUMAN | 601286547F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3813258 5' |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 11157 | 24115 | 37841 | 2.51 | 1.7E-01 | AA814617.1 | EST_HUMAN | cl43a03.s1 NCI_CGAP_CNS1 Homo sapiens cDNA clone IMAGE:1428924 3' |
| 11447 | 24390 | 37833 | 8.03 | 1.7E-01 | 7106300 | NT | Mus musculus adenomatosis polyposis coli binding protein Eb1 (Eb1), mRNA |
| 11447 | 24390 | 37834 | 8.03 | 1.7E-01 | 7106300 | NT | Mus musculus adenomatosis polyposis coli binding protein Eb1 (Eb1), mRNA |
| 11703 | 24668 | 38245 | 1.6 | 1.7E-01 | AA883376.1 | EST_HUMAN | cl45f09.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460297 3' |
| 12021 | 24898 | | 1.66 | 1.7E-01 | P15272 | SWISSPROT | AMP NUCLEOSIDASE |
| 12141 | 25005 | 38615 | 1.74 | 1.7E-01 | 11418157 | NT | Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA |
| 12273 | 25893 | | 1.54 | 1.7E-01 | AL163278.2 | NT | Homo sapiens chromosome 21 segment HS21C078 |
| 12437 | 25736 | 31618 | 1.55 | 1.7E-01 | AA847421.1 | EST_HUMAN | oe18h02.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1386281 |
| 12555 | 25739 | | 1.69 | 1.7E-01 | A1824404.1 | EST_HUMAN | b68g05.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2274872 3' similar to gb:M73779 RETINOIC |
| 12833 | 25450 | 31723 | 14.15 | 1.7E-01 | U01317.1 | NT | ACID RECEPTOR ALPHA-1 (HUMAN); |
| 128 | 13233 | 26162 | 2.02 | 1.6E-01 | AF217632.1 | NT | Human beta globin region on chromosome 11 |
| 680 | 15814 | 26670 | 1.56 | 1.6E-01 | R31497.1 | EST_HUMAN | Homo sapiens mevalonate kinase gene, exon 6 and 7 |
| 1504 | 14537 | 27509 | 1.4 | 1.6E-01 | AA548863.1 | EST_HUMAN | yh75f12.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:135599 5' |
| 1525 | 14557 | 27528 | 4.54 | 1.6E-01 | AF298117.1 | NT | nk28d12.s1 NCI_CGAP_Co11 Homo sapiens cDNA clone IMAGE:1014839 3' |
| 1941 | 14965 | 27962 | 1.79 | 1.6E-01 | P22063 | SWISSPROT | Homo sapiens homeobox protein OTX2 gene, complete cds |
| 2001 | 15022 | | 1 | 1.6E-01 | U10334.1 | NT | AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1) |
| 2393 | 15892 | 28427 | 0.99 | 1.6E-01 | X94232.1 | NT | Craosotrea gigas RNA polymerase II largest subunit mRNA, partial cds |
| 2501 | 15504 | 28531 | 1.19 | 1.6E-01 | AB037729.1 | NT | H. sapiens mRNA for novel T-cell activation protein |
| 2902 | 15961 | 28881 | 10.42 | 1.6E-01 | AF185589.1 | NT | Homo sapiens mRNA for KIAA1308 protein, partial cds |
| 2902 | 15961 | 28882 | 10.42 | 1.6E-01 | AF185589.1 | NT | Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region |
| 3649 | 16692 | 29607 | 1.2 | 1.6E-01 | AJ003165.1 | NT | Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region |
| 3649 | 16692 | 29608 | 1.2 | 1.6E-01 | AJ003165.1 | NT | Populus trichocarpa cv. Trichobel ABI3 gene |
| 3786 | 16827 | 29734 | 0.78 | 1.6E-01 | AE000962.1 | NT | Populus trichocarpa cv. Trichobel ABI3 gene |
| 4025 | 17063 | | 2.81 | 1.6E-01 | AE004413.1 | NT | Archaeoglobus fulgidus section 145 of 172 of the complete genome |
| 4356 | 17383 | 30265 | 10.43 | 1.6E-01 | AF179680.1 | NT | Vibrio cholerae chromosome II, section 70 of 93 of the complete chromosome |
| 4494 | 17509 | | 3.1 | 1.6E-01 | AW968601.1 | EST_HUMAN | Homo sapiens apelin gene, complete cds |
| 4491 | 17516 | | 4.57 | 1.6E-01 | 6753319 | NT | EST380677 MAGe resequences, MAGJ Homo sapiens cDNA |
| 4916 | 17933 | 30824 | 1.43 | 1.6E-01 | Z28330.1 | NT | Mus musculus chaperonin subunit 3 (gamma) (Cot3), mRNA |
| 4916 | 17933 | 30825 | 1.43 | 1.6E-01 | Z28330.1 | NT | S. cerevisiae chromosome XI reading frame ORF YKR105c |
| 4982 | 17997 | 30895 | 4.36 | 1.6E-01 | AA088343.1 | EST_HUMAN | S. cerevisiae chromosome XI reading frame ORF YKR105c |
| 5004 | 18018 | 30905 | 1.94 | 1.6E-01 | AJ006356.1 | NT | z184f09.s1 Stragene cdon (#837204) Homo sapiens cDNA clone IMAGE:511361 3' similar to TR:E221955 |
| 5004 | 18018 | 30906 | 1.94 | 1.6E-01 | AJ006356.1 | NT | E221955 38,855 BP SEGMENT OF CHROMOSOME XIV. ; |
| | | | | | | | Lycopersicon esculentum RsaI fragment 2, satellite region |
| | | | | | | | Lycopersicon esculentum RsaI fragment 2, satellite region |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 5069 | 18079 | 30960 | 1.16 | 1.6E-01 | BE018707.1 | EST_HUMAN | bb83h08.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3049023 5' similar to gb:M61715 |
| 5461 | 18563 | 31475 | 0.87 | 1.6E-01 | L40808.1 | NT | TRYPTOPHANYL-TRNA SYNTHETASE (HUMAN); gb:XG9957 M.musculus (MOUSE); |
| 5600 | 18596 | 31668 | 2.82 | 1.6E-01 | AW197496.1 | EST_HUMAN | Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds |
| 5600 | 18596 | 31667 | 2.82 | 1.6E-01 | AW197496.1 | EST_HUMAN | xm4301.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2686960 3' similar to TR:O75984 O75984 |
| 5612 | 18708 | 31865 | 2.31 | 1.6E-01 | AF034716.1 | NT | HYPOPHOSPHATASE 1 (HUMAN); |
| 6144 | 19219 | 32449 | 0.9 | 1.6E-01 | BE925803.1 | EST_HUMAN | Rattus norvegicus CCAAT/enhancer binding protein epsilon (cebp) gene, complete cds |
| 6385 | 19453 | 32697 | 0.57 | 1.6E-01 | BF183584.1 | EST_HUMAN | RC3-BN0034-310800-113-01 BN0034 Homo sapiens cDNA |
| 6385 | 19453 | 32698 | 0.57 | 1.6E-01 | BF183584.1 | EST_HUMAN | 601809725R1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040335 3' |
| 6568 | 19628 | 32893 | 1.99 | 1.6E-01 | AL161588.2 | NT | 601809725R1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040335 3' |
| 6568 | 19628 | 32894 | 1.99 | 1.6E-01 | AL161588.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84 |
| 6950 | 20174 | 33498 | 0.55 | 1.6E-01 | AA398047.1 | EST_HUMAN | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84 |
| 6969 | 20192 | 33519 | 0.66 | 1.6E-01 | AB046786.1 | NT | z88904.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728511 5' |
| 7156 | 18388 | 31232 | 4.63 | 1.6E-01 | AW291215.1 | EST_HUMAN | Homo sapiens mRNA for KIAA1566 protein, partial cds |
| 8056 | 20993 | 34390 | 1.59 | 1.6E-01 | AW246359.1 | EST_HUMAN | UH-B12-agi-b-06-0.U1.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724418 3' |
| 8090 | 21026 | 34425 | 0.57 | 1.6E-01 | 6752237 | NT | S.cerevisiae chromosome X reading frame ORF YJR132w |
| 8102 | 21038 | | 1.15 | 1.6E-01 | AU136525.1 | EST_HUMAN | 2822248.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822248 5' |
| 8201 | 21171 | 34582 | 1.28 | 1.6E-01 | L49349.1 | NT | Mus musculus Cer-2<+>-dependent activator protein for secretion (Cadps), mRNA |
| 8359 | 21328 | | 0.51 | 1.6E-01 | BE244087.1 | EST_HUMAN | AU136525 PLACE1 Homo sapiens cDNA clone PLACE1004468 5' |
| 8456 | 21425 | 34841 | 0.66 | 1.6E-01 | U38243.1 | NT | Gorilla gorilla androgen receptor gene, partial exon |
| 8979 | 21945 | 35369 | 0.85 | 1.6E-01 | Z99119.1 | EST_HUMAN | TCBAP1E0607 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0607 |
| 9178 | 22144 | 35571 | 0.71 | 1.6E-01 | R13673.1 | EST_HUMAN | Bacteroides vulgatus beta-lactamase (cbxA) gene, complete cds and mobilization protein (mobA) gene, complete cds |
| 9285 | 22251 | | 0.63 | 1.6E-01 | L36881.1 | NT | Bacillus subtilis complete genome (section 16 of 21): from 2997771 to 3213410 |
| 9322 | 22287 | 35717 | 1.9 | 1.6E-01 | Z49501.1 | NT | y60h08.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:26873 5' |
| 9468 | 22430 | | 0.63 | 1.6E-01 | AF111167.2 | NT | Homo sapiens guanylate cyclase activating protein (GCAP) gene exons 1-4, complete cds |
| 10009 | 22936 | | 2.05 | 1.6E-01 | BF375171.1 | EST_HUMAN | S.cerevisiae chromosome X reading frame ORF YJR001w |
| 10012 | 22939 | 36404 | 2 | 1.6E-01 | Z49501.1 | NT | Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene |
| 10048 | 22979 | | 0.96 | 1.6E-01 | BE155664.1 | EST_HUMAN | RC3-ST0200-041189-011-h01 ST0200 Homo sapiens cDNA |
| | | | | | | | S.cerevisiae chromosome X reading frame ORF YJR001w |
| | | | | | | | PM2-HT0353-270100-004-f11 HT0353 Homo sapiens cDNA |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 11017 | 23982 | 37509 | 2.59 | 1.6E-01 | AW850853.1 | EST_HUMAN | IL3-CT0220-111199-028-G01 CT0220 Homo sapiens cDNA |
| 11122 | 24082 | 37607 | 1.82 | 1.6E-01 | Z28073.1 | NT | S.cerevisiae chromosome XI reading frame ORF YKL073w |
| 11122 | 24082 | 37608 | 1.82 | 1.6E-01 | Z28073.1 | NT | S.cerevisiae chromosome XI reading frame ORF YKL073w |
| 11344 | 24294 | 37820 | 1.5 | 1.6E-01 | BE258649.1 | EST_HUMAN | 601145793F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3161183 5' |
| 11451 | 24394 | | 3.84 | 1.6E-01 | AF106064.1 | NT | Plasmodium falciparum calcium-dependent protein kinase-3 (cdpk3) gene, complete cds |
| 11740 | 24625 | 38204 | 6.59 | 1.6E-01 | 6671552 | NT | Mus musculus adaptor-related protein complex AP-1, beta 1 subunit (Ap1b1), mRNA |
| 12155 | 25906 | | 1.75 | 1.6E-01 | 6679466 | NT | Mus musculus protein kinase, cGMP-dependent, type II (Prkg2), mRNA |
| 12275 | 25095 | 38179 | 6.75 | 1.6E-01 | AV719585.1 | EST_HUMAN | AV719585 GLC Homo sapiens cDNA clone GLCEMF07 5' |
| 12608 | 25307 | | 1.62 | 1.6E-01 | AW839711.1 | EST_HUMAN | RC1-LT0074-120200-014-H01_1 LT0074 Homo sapiens cDNA |
| 12697 | 25721 | | 22.15 | 1.6E-01 | AB045310.1 | NT | Cucumis sativus KS mRNA for ent-kaurene synthase, complete cds |
| 12856 | 25463 | | 2.73 | 1.6E-01 | AK024496.1 | NT | Homo sapiens mRNA for FLJ00104 protein, partial cds |
| 12945 | 25524 | | 2.66 | 1.6E-01 | AF287344.1 | NT | Fuchsia hybrid cultivar Qu 94208 ribosomal protein S10 gene, partial cds; nuclear gene for mitochondrial product |
| 12971 | 25537 | 31716 | 2.24 | 1.6E-01 | 8506522 | NT | Rattus norvegicus chondroitin sulfate proteoglycan 5 (neuroglycan C) (Cspg5), mRNA |
| 12978 | 25543 | | 1.93 | 1.6E-01 | BE267894.1 | EST_HUMAN | 601125459F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345038 5' |
| 248 | 13345 | 26270 | 1.73 | 1.5E-01 | BE710087.1 | EST_HUMAN | IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA |
| 248 | 13345 | 26271 | 1.73 | 1.5E-01 | BE710087.1 | EST_HUMAN | IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA |
| 589 | 15813 | | 2.4 | 1.5E-01 | AV711696.1 | EST_HUMAN | AV711696 DCA Homo sapiens cDNA clone DCAADH06 5' |
| 783 | 13843 | 26788 | 1.51 | 1.5E-01 | AL163284.2 | NT | Homo sapiens chromosome 21 segment HS21C084 |
| 1094 | 14138 | 27089 | 1.01 | 1.5E-01 | AJ009735.1 | NT | Cyprinus carpio mRNA for EGG522 myosin heavy chain, 3'UTR |
| 1099 | 14143 | 27093 | 2.55 | 1.5E-01 | AJ251885.1 | NT | Homo sapiens partial SLC22A2 gene for organic cation transporter (OCT2), exon 1 |
| 1115 | 14189 | | 1.57 | 1.5E-01 | L36125.1 | NT | Rattus norvegicus insulin-responsive glucose transporter (GLUT4) gene, 5' end |
| 1280 | 14315 | 27276 | 3.58 | 1.5E-01 | D26635.1 | NT | Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15) |
| 1280 | 14315 | 27277 | 3.58 | 1.5E-01 | D26635.1 | NT | Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15) |
| 1478 | 14511 | 27487 | 2.54 | 1.5E-01 | AF117340.1 | NT | Mus musculus MAP kinase kinase 1 (Meck1) mRNA, complete cds |
| 1923 | 14947 | 27943 | 1.65 | 1.5E-01 | AW444451.1 | EST_HUMAN | UI-H-B13-akt-b-09-0-UI.s1 NCI CGAP Sub5 Homo sapiens cDNA clone IMAGE:2733641 3' |
| 2723 | 15717 | 28735 | 1.47 | 1.5E-01 | BF695381.1 | EST_HUMAN | 602083269F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247537 5' |
| 2924 | 15982 | | 1.1 | 1.5E-01 | AW572516.1 | EST_HUMAN | xx56a02.x2 NCI CGAP Pan1 Homo sapiens cDNA clone IMAGE:2831978 3' similar to gb:X56072_ma1 |
| 3048 | 16105 | 28019 | 0.76 | 1.5E-01 | M81441.1 | NT | THYROID HORMONE RECEPTOR ALPHA-1 (HUMAN); |
| | | | | | | NT | Bos taurus factor V variant 2 (factor V) mRNA, complete cds |
| 3363 | 16413 | 29338 | 5.55 | 1.5E-01 | AA955049.1 | EST_HUMAN | oo68405.s1 NCI CGAP GC4 Homo sapiens cDNA clone IMAGE:1671337 3' similar to gb:M11433 |
| 3381 | 16430 | 29357 | 0.74 | 1.5E-01 | Z23104.1 | NT | RETINOL-BINDING PROTEIN 1, CELLULAR (HUMAN); |
| 3381 | 16430 | 29358 | 0.74 | 1.5E-01 | Z23104.1 | NT | L. stagnalis mRNA for G protein-coupled receptor |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 3440 | 16487 | 29405 | 0.97 | 1.5E-01 | AW612237.1 | EST_HUMAN | ht2902.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2956539 3' similar to contains element MER16 repetitive element; |
| 3768 | 16810 | 29719 | 2.22 | 1.5E-01 | U09864.1 | NT | Mus musculus ICR/Swiss glyceroldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 1 (PDK1), nuclear gene encoding mitochondrial protein, mRNA |
| 3782 | 16823 | 29731 | 0.8 | 1.5E-01 | 7108358 | NT | XYNA; Thermoaerobacterium; xynA; 4182 base-pairs |
| 3795 | 16835 | 29740 | 0.66 | 1.5E-01 | M97882.1 | NT | h10106.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2981411 3' |
| 3881 | 16920 | 29829 | 2.25 | 1.5E-01 | AW665983.1 | EST_HUMAN | Populus trichocarpa cv. Trichobel ABI3 gene |
| 3896 | 16936 | 29846 | 0.71 | 1.5E-01 | AJ003165.1 | NT | Populus trichocarpa cv. Trichobel ABI3 gene |
| 3896 | 16936 | 29847 | 0.71 | 1.5E-01 | AJ003165.1 | NT | Populus trichocarpa cv. Trichobel ABI3 gene |
| 4090 | 17115 | 30011 | 2.53 | 1.5E-01 | AW366659.1 | EST_HUMAN | RC2-HT0149-191088-012-c09 HT0149 Homo sapiens cDNA |
| 4213 | 17242 | 30127 | 9.83 | 1.5E-01 | AL163284.2 | NT | Homo sapiens chromosome 21 segment HS21C084 |
| 4513 | 17538 | 30422 | 0.91 | 1.5E-01 | BE791253.1 | EST_HUMAN | 601583988F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938345 5' |
| 4513 | 17538 | 30423 | 0.91 | 1.5E-01 | BE791253.1 | EST_HUMAN | 601583988F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938345 5' |
| 4756 | 17776 | 30672 | 1.88 | 1.5E-01 | BF687665.1 | EST_HUMAN | 602067192F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4066223 5' |
| 4783 | 15717 | 28735 | 2.86 | 1.5E-01 | BF689381.1 | EST_HUMAN | 602083289F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247537 5' |
| 4830 | 17847 | 30747 | 1 | 1.5E-01 | BE173796.1 | EST_HUMAN | GM0-HT0565-280200-245-b10 HT0565 Homo sapiens cDNA |
| 4830 | 17847 | 30748 | 1 | 1.5E-01 | BE173796.1 | EST_HUMAN | GM0-HT0565-280200-245-b10 HT0565 Homo sapiens cDNA |
| 5034 | 18048 | 30828 | 1.2 | 1.5E-01 | AL161560.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60 |
| 5134 | 18143 | 31023 | 1.07 | 1.5E-01 | 5579451 | NT | Homo sapiens calbindin 1, (28kD) (CALB1), mRNA |
| 5328 | 18434 | 31186 | 2.46 | 1.5E-01 | P07996 | SWISSPROT | THROMBOSPONDIN 1 PRECURSOR |
| 5357 | 18462 | 31331 | 1.03 | 1.5E-01 | AF256652.1 | NT | Calman crocodilus MHC class II beta chain (hclibeta) gene, complete cds |
| 5401 | 18504 | | 5.5 | 1.5E-01 | P15196 | SWISSPROT | SEX HORMONE-BINDING GLOBULIN PRECURSOR (SHBG) (SEX STEROID-BINDING PROTEIN) |
| 5618 | 18712 | 31870 | 4.35 | 1.5E-01 | AW850754.1 | EST_HUMAN | (SBP) (TESTIS-SPECIFIC ANDROGEN-BINDING PROTEIN) (ABP) |
| 5659 | 18755 | 31922 | 7.17 | 1.5E-01 | U65016.1 | NT | IL3-CT0219-160200-064-F10 CT0219 Homo sapiens cDNA |
| 5659 | 18755 | 31923 | 7.17 | 1.5E-01 | U65016.1 | NT | Mus musculus transforming growth factor alpha (TGFa) mRNA, complete cds |
| 6012 | 19095 | 32285 | 0.79 | 1.5E-01 | 4506810 | NT | Mus musculus transforming growth factor alpha (TGFa) mRNA, complete cds |
| 6120 | 19198 | 32422 | 1.74 | 1.5E-01 | 6753659 | NT | Homo sapiens sodium channel, voltage-gated, type VI, alpha polypeptide (SCN6A) mRNA |
| 6120 | 19198 | 32423 | 1.74 | 1.5E-01 | 6753659 | NT | Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA |
| 6161 | 19236 | 32487 | 1.96 | 1.5E-01 | AJ276505.1 | NT | Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA |
| 6319 | 19390 | 32630 | 3.25 | 1.5E-01 | BE727658.1 | EST_HUMAN | Mus musculus genomic fragment, 279 Kb, chromosome 7 |
| 6375 | 19443 | | 1.86 | 1.5E-01 | 4506396 | NT | 601564322F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833981 5' |
| | | | | | | | Homo sapiens RAD54 (S.cerevisiae)-like (RAD54L) mRNA |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 6478 | 19543 | 32791 | 1.7 | 1.5E-01 | AF134907.1 | NT | Influenza B virus (BN/anchang/480/94) NB protein gene, complete cds; and neuraminidase gene, partial cds |
| 6661 | 25664 | 32985 | 1.8 | 1.5E-01 | AE001039.1 | NT | Archaeoglobus fulgidus section 68 of 172 of the complete genome |
| 6681 | 19736 | 33013 | 4.63 | 1.5E-01 | 11417236 | NT | Homo sapiens chromosome 5 open reading frame 3 (C5ORF3), mRNA |
| 6692 | 19749 | 33026 | 1.8 | 1.5E-01 | P48508 | SWISSPROT | GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT (GAMMA-GLUTAMYL-CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN) |
| 6740 | 19796 | 33075 | 2.35 | 1.5E-01 | Q28462 | SWISSPROT | AMELOGENIN |
| 6842 | 19895 | 33189 | 0.85 | 1.5E-01 | AA714760.1 | EST_HUMAN | rw30d10.st NCL CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241971 3' |
| 6871 | 19924 | 33220 | 1.8 | 1.5E-01 | P30143 | SWISSPROT | HYPOTHETICAL 51.7 KD PROTEIN IN THRC-TALB INTERGENIC REGION (ORF8) |
| 7171 | 18402 | 31247 | 5.15 | 1.5E-01 | AW970295.1 | EST_HUMAN | EST382378 IMAGE resequences, MAGK Homo sapiens cDNA |
| 7214 | 25678 | | 0.71 | 1.5E-01 | AA811545.1 | EST_HUMAN | ob73f02.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1337019 3' similar to contains element LTR2 repetitive element; |
| 7424 | 20391 | | 1.91 | 1.5E-01 | AF210842.1 | NT | Homo sapiens HARP (HARP) gene, exon 17 and complete cds |
| 7621 | 20681 | 33945 | 1.68 | 1.5E-01 | AI973157.1 | EST_HUMAN | wf52608.xt NCL CGAP_Ur1 Homo sapiens cDNA clone IMAGE:2491310 3' |
| 7846 | 20763 | 34169 | 0.98 | 1.5E-01 | AF299073.1 | NT | Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds |
| 7849 | 20793 | 34170 | 0.96 | 1.5E-01 | AF299073.1 | NT | Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds |
| 7857 | 20802 | 34177 | 1.84 | 1.5E-01 | AW500611.1 | EST_HUMAN | UI-HF-BN0-akk-d-05-0-UI.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5' |
| 7857 | 20802 | 34178 | 1.84 | 1.5E-01 | AW500611.1 | EST_HUMAN | UI-HF-BN0-akk-d-05-0-UI.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5' |
| 8014 | 20952 | 34348 | 0.71 | 1.5E-01 | U46560.1 | NT | Saccharomyces cerevisiae weak multicopy suppressor of lost-1 (SOL3) gene, complete cds |
| 8393 | 21382 | 34769 | 1.21 | 1.5E-01 | P21303 | SWISSPROT | MEROZONTE RECEPTOR PK66 PRECURSOR (66 KD PROTECTIVE MINOR SURFACE ANTIGEN) |
| 8562 | 21530 | 34950 | 0.97 | 1.5E-01 | AA970317.1 | EST_HUMAN | cc85g12.s1 NCL CGAP_Kids Homo sapiens cDNA clone IMAGE:1573030 3' similar to gb:M26062 |
| 8655 | 21623 | | 1.01 | 1.5E-01 | BE884799.1 | EST_HUMAN | INTERLEUKIN-2 RECEPTOR BETA CHAIN PRECURSOR (HUMAN); |
| 8743 | 21711 | | 13.33 | 1.5E-01 | C16800.1 | EST_HUMAN | 601510523FT NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912004 5' |
| 8776 | 21743 | 35163 | 1.69 | 1.5E-01 | L27835.1 | NT | C16800 Clontech human aorta polyA+ mRNA (#8572) Homo sapiens cDNA clone GEN-528H09 5' |
| 8940 | 21806 | 35330 | 1.79 | 1.5E-01 | D84476.1 | NT | Pangasanodon gigas growth hormone (GH) mRNA, complete cds |
| 8962 | 21928 | | 0.74 | 1.5E-01 | P43446 | SWISSPROT | Homo sapiens mRNA for ASK1, complete cds |
| 9190 | 22166 | 35585 | 1.31 | 1.5E-01 | 4501972 | NT | WNT-10A PROTEIN PRECURSOR |
| 9460 | 22424 | 35982 | 3.06 | 1.5E-01 | N74226.1 | EST_HUMAN | Homo sapiens adaptor-related protein complex 1, beta 1 subunit (ADTB1), mRNA |
| 9548 | 22511 | 35960 | 1.03 | 1.5E-01 | BF585465.1 | EST_HUMAN | za59c06.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:286868 3' similar to |
| 9655 | 22517 | | 2.73 | 1.5E-01 | AV754819.1 | EST_HUMAN | PIR:S44443 S44443 RAD23 protein homolog2 - human ; |
| 9760 | 22701 | | 0.87 | 1.5E-01 | AU130007.1 | EST_HUMAN | GVO000404 Human Psoriasis Differential Display Homo sapiens cDNA |
| 9808 | 21131 | 34534 | 6.92 | 1.5E-01 | U00455.1 | NT | AV754819 TP Homo sapiens cDNA clone TPAAHB12 5' |
| | | | | | | | AU130007 NT2RP3 Homo sapiens cDNA clone NT2RP3000080 5' |
| | | | | | | | Acipenser transmontano vitellogenin mRNA, partial cds |

Table 4

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| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 10176 | 23101 | 36581 | 0.58 | 1.5E-01 | M77144.1 | NT | Human type II 3-beta hydroxysteroid dehydrogenase/ 5-delta - 4-delta isomerase gene, complete cds |
| 10281 | 23206 | 36590 | 6.22 | 1.5E-01 | AF007570.1 | NT | Aplysia californica carboxypeptidase D mRNA, complete cds |
| 10281 | 23206 | 36591 | 6.22 | 1.5E-01 | AF007570.1 | NT | Aplysia californica carboxypeptidase D mRNA, complete cds |
| 10563 | 23485 | 36979 | 2.67 | 1.5E-01 | X88852.1 | NT | P. leniusculus mRNA for integrin beta subunit |
| 10651 | 23573 | | 0.52 | 1.5E-01 | AB027759.1 | NT | Mesocricetus auratus mRNA for collagen type XVII, complete cds |
| 10671 | 23593 | 37089 | 2.49 | 1.5E-01 | AI814046.1 | EST_HUMAN | wk53h12.x1 NC1_CGAP_P122 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA |
| 10671 | 23593 | 37090 | 2.49 | 1.5E-01 | AI814046.1 | EST_HUMAN | GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN); |
| 10753 | 23675 | 37172 | 2.19 | 1.5E-01 | U40932.1 | NT | wk53h12.x1 NC1_CGAP_P122 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA |
| 10906 | 23826 | 37338 | 2.14 | 1.5E-01 | AJ011964.1 | NT | GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN); |
| 10906 | 23826 | 37339 | 2.14 | 1.5E-01 | AJ011964.1 | NT | Danio rerio transcription factor Pax9b (Pax9) mRNA, complete cds |
| 11173 | 24130 | 37680 | 4.35 | 1.5E-01 | AL163280.2 | NT | Claviceps purpurea ps1 gene |
| 11173 | 24130 | 37689 | 4.35 | 1.5E-01 | AL163280.2 | NT | Claviceps purpurea ps1 gene |
| 11412 | 24356 | 37891 | 1.71 | 1.5E-01 | AW841915.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C080 |
| 11449 | 24392 | 37937 | 3.86 | 1.5E-01 | AA425488.1 | EST_HUMAN | IL5-CN0024-030300-025-D04 CN0024 Homo sapiens cDNA |
| 11501 | 20581 | 33945 | 1.69 | 1.5E-01 | AI973157.1 | EST_HUMAN | contains element MER22 repetitive element; |
| 12229 | 25769 | | 11.17 | 1.5E-01 | BF700582.1 | EST_HUMAN | wk52c08.x1 NC1_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2491310 3' |
| 12607 | 25306 | | 1.82 | 1.5E-01 | AF030358.2 | NT | 602128753F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285549 5' |
| 12610 | 25309 | | 1.81 | 1.5E-01 | AJ238332.1 | NT | Rattus norvegicus chemokine CX3C mRNA, complete cds |
| 12688 | 25791 | | 12.47 | 1.5E-01 | R83077.1 | EST_HUMAN | Mus musculus mRNA for death inducer-obliterat-1 (Dio-1) |
| 12748 | 25814 | | 2.45 | 1.5E-01 | AV741272.1 | EST_HUMAN | yp87s04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194430 5' |
| 12855 | 25722 | 31613 | 7.87 | 1.5E-01 | AL139074.2 | NT | AV741272 CB Homo sapiens cDNA clone CBDA GD04 5' |
| 13073 | 25606 | 31689 | 1.53 | 1.5E-01 | AJ276242.1 | NT | Campylobacter jejuni NCTC11168 complete genome; segment 1/6 |
| 299 | 13393 | | 2.07 | 1.4E-01 | AF009683.1 | NT | Sus scrofa mRNA for sodium iodide symporter |
| 911 | 13966 | | 3.95 | 1.4E-01 | DF8638.1 | NT | Homo sapiens T cell receptor beta locus, TCRBV8SSGP to TCRBV21S2A2 region |
| 1264 | 14299 | | 2.77 | 1.4E-01 | T81964.1 | EST_HUMAN | Xenopus laevis mRNA for DNA (cytosine-5)-methyltransferase, complete cds |
| 1763 | 14792 | | 1.61 | 1.4E-01 | 6879980 | NT | yd54c01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:112032 3' |
| 1766 | 14793 | 27780 | 1.82 | 1.4E-01 | AE001710.1 | NT | Mus musculus growth differentiation factor 5 (Gdf5), mRNA |
| 2002 | 15023 | | 12.82 | 1.4E-01 | AA720615.1 | EST_HUMAN | Thermotoga maritima section 22 of 136 of the complete genome |
| 2482 | 19486 | 28509 | 1.15 | 1.4E-01 | P30706 | SWISSPROT | iny72d07.s1 NC1_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1283821 3' |
| 2804 | 15796 | 28816 | 7.57 | 1.4E-01 | AI933496.1 | EST_HUMAN | GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPAT) |

Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 3914 | 16954 | 29865 | 0.93 | 1.4E-01 | R59232.1 | EST_HUMAN | y97a03.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:41487 5' |
| 3914 | 16954 | 29866 | 0.93 | 1.4E-01 | R59232.1 | EST_HUMAN | y97a03.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:41487 5' |
| 4202 | 17233 | 30120 | 11.04 | 1.4E-01 | A1699094.1 | EST_HUMAN | bx56c02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3' |
| 4202 | 17233 | 30121 | 11.04 | 1.4E-01 | A1699094.1 | EST_HUMAN | bx56c02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3' |
| 4265 | 17294 | 30173 | 3.96 | 1.4E-01 | AE001710.1 | NT | Thermidoga maritima section 22 of 136 of the complete genome |
| | | | | | | | z450b01.s1 Soares fetal liver spleen 1NFLS_S1 Homo sapiens cDNA clone IMAGE:453873 3' similar to gb:U01057.mn1 INTERLEUKIN-2 RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN); contains Alu repetitive element |
| 4440 | 17466 | | 0.71 | 1.4E-01 | AA776287.1 | EST_HUMAN | Homo sapiens phosphodiesterase 4A, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E2) (PDE4A), mRNA |
| 4703 | 17724 | 30618 | 0.89 | 1.4E-01 | 5453861 | NT | AV689659 GKC Homo sapiens cDNA clone GKCDUG09 5' |
| 4907 | 17924 | 30817 | 0.92 | 1.4E-01 | AV689659.1 | EST_HUMAN | ye15c11.s1 Stratiogene lung (H937210) Homo sapiens cDNA clone IMAGE:117812 3' |
| 5379 | 18483 | 31358 | 4.72 | 1.4E-01 | T90677.1 | EST_HUMAN | Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds |
| 5402 | 18505 | 31381 | 4.08 | 1.4E-01 | AB004556.1 | NT | Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds |
| 5402 | 18505 | 31382 | 4.06 | 1.4E-01 | AB004556.1 | NT | hr7c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3135638 3' |
| 6430 | 19496 | 32749 | 2.9 | 1.4E-01 | BE328891.1 | EST_HUMAN | AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5' |
| 6629 | 19687 | 32965 | 5.1 | 1.4E-01 | AU117147.1 | EST_HUMAN | AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5' |
| 6629 | 19687 | 32966 | 5.1 | 1.4E-01 | AU117147.1 | EST_HUMAN | xb7d12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2581751 3' |
| 6723 | 19779 | 33058 | 3.48 | 1.4E-01 | AW082796.1 | EST_HUMAN | QV1-UM0036-080300-103-409 UM0036 Homo sapiens cDNA |
| 6737 | 19793 | 33058 | 1.26 | 1.4E-01 | BE266536.1 | EST_HUMAN | DKFZp761A0910_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A0910 5' |
| 6759 | 19813 | 33093 | 2.02 | 1.4E-01 | BF378633.1 | EST_HUMAN | UI-H-B10-aat-c-09-0-UI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710289 3' |
| 7333 | 20304 | | 0.74 | 1.4E-01 | AL118568.1 | EST_HUMAN | HSC1DB011 normalized infant brain cDNA Homo sapiens cDNA clone c-1db01 |
| 7615 | 20576 | | 1.67 | 1.4E-01 | AW015373.1 | EST_HUMAN | w04f12.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2389295 3' similar to SW:ICE4_HUMAN |
| 7841 | 20601 | 33965 | 0.51 | 1.4E-01 | F08745.1 | EST_HUMAN | P49662 CASPASE-4 PRECURSOR ; |
| 7694 | 20652 | | 0.91 | 1.4E-01 | A1762827.1 | EST_HUMAN | Oryctolagus cuniculus fructose 1,6-bisphosphate aldolase 1.6, bisphosphate aldolase (AldB) gene, complete cds |
| 7883 | 20827 | 34203 | 0.82 | 1.4E-01 | U85645.1 | NT | q160b12.x1 Soares_NHIMPu_S1 Homo sapiens cDNA clone IMAGE:1879583 3' |
| 8029 | 20966 | 34361 | 1.24 | 1.4E-01 | A1305192.1 | EST_HUMAN | AV659047 GLC Homo sapiens cDNA clone GLCFSH06 3' |
| 8818 | 21785 | | 1.24 | 1.4E-01 | AV659047.1 | EST_HUMAN | th92b12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126111 3' similar to |
| 9136 | 22102 | | 0.97 | 1.4E-01 | A1436063.1 | EST_HUMAN | TR:002710 002710 GAG POLYPROTEIN. ; |
| 9264 | 22230 | 35661 | 4.68 | 1.4E-01 | AA307073.1 | EST_HUMAN | EST1178192 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end |
| 9346 | 22310 | 35735 | 0.56 | 1.4E-01 | AW023636.1 | EST_HUMAN | df58b03.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2487485 5' |
| 9478 | 22442 | 35883 | 0.94 | 1.4E-01 | R62746.1 | EST_HUMAN | y10h05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138873 5' |
| 9478 | 22442 | 35884 | 0.94 | 1.4E-01 | R62746.1 | EST_HUMAN | y10h05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138873 5' |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 9541 | 22504 | 35953 | 9.19 | 1.4E-01 | BF310959.1 | EST_HUMAN | 601895465F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124824 5' |
| 9630 | 22574 | 36024 | 1.19 | 1.4E-01 | W93411.1 | EST_HUMAN | z09404.1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:357102 5' similar to contains element KER repetitive element; |
| 9702 | 22655 | 36109 | 0.43 | 1.4E-01 | X73283.1 | NT | M.vannelli genes rpoH, rpoB and rpoA |
| 9702 | 22655 | 36110 | 0.43 | 1.4E-01 | X73283.1 | NT | M.vannelli genes rpoH, rpoB and rpoA |
| 9713 | 22666 | 36123 | 1.44 | 1.4E-01 | Y10196.1 | NT | Homo sapiens PH1X gene |
| 9713 | 22666 | 36124 | 1.44 | 1.4E-01 | Y10196.1 | NT | Homo sapiens PH1X gene |
| 9805 | 21128 | 34532 | 2.06 | 1.4E-01 | AF121361.1 | NT | Drosophila melanogaster signal transducing adaptor protein (STAM), serine threonine kinase Ial (IAL), and zinc finger protein (DNZ1) genes, complete cds |
| 10164 | 23089 | 36567 | 0.56 | 1.4E-01 | X66092.1 | NT | C.perfringens ORF for putative membrane transport protein |
| 10346 | 23270 | 36747 | 1.12 | 1.4E-01 | AF023813.1 | NT | Macromitrium levatum small ribosomal protein 4 (ps4) gene, chloroplast gene encoding chloroplast protein, partial cds |
| 10448 | 23370 | 36861 | 0.57 | 1.4E-01 | AW021908.1 | EST_HUMAN | df29h08.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485094 5' |
| 10448 | 23370 | 36862 | 0.57 | 1.4E-01 | AW021908.1 | EST_HUMAN | df29h08.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485094 5' |
| 10619 | 23541 | 37039 | 0.67 | 1.4E-01 | BF375285.1 | EST_HUMAN | MR3-ST0218-211299-013-a08 ST0218 Homo sapiens cDNA |
| 10619 | 23541 | 37040 | 0.67 | 1.4E-01 | BF375285.1 | EST_HUMAN | MR3-ST0218-211299-013-a08 ST0218 Homo sapiens cDNA |
| 10829 | 23750 | | 0.56 | 1.4E-01 | T84283.1 | EST_HUMAN | y047d03.1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:111366 5' |
| 10962 | 23882 | 37395 | 0.71 | 1.4E-01 | Z99117.1 | NT | Bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870 |
| 11191 | 24147 | 37680 | 2.59 | 1.4E-01 | R53400.1 | EST_HUMAN | y70c05.1 Soares breast 2NHBst Homo sapiens cDNA clone IMAGE:154088 5' |
| 11432 | 24376 | 37916 | 2.53 | 1.4E-01 | P08648 | SWISSPROT | INTEGRIN ALPHA-5 PRECURSOR (FIBRONECTIN RECEPTOR ALPHA SUBUNIT) (INTEGRIN ALPHA-F) |
| 11752 | 24637 | | 1.59 | 1.4E-01 | AL161496.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 8 |
| 11797 | 23952 | 37474 | 2.38 | 1.4E-01 | U28760.1 | NT | Borrelia burgdorferi glyceraldehyde-3-phosphate dehydrogenase (GAPDH), phosphoglycerate kinase (PGK), triosephosphate isomerase (TPI) genes, complete cds |
| 11855 | 24737 | | 1.55 | 1.4E-01 | X52102.1 | NT | M.musculus p16K gene for 16 kDa protein |
| 12549 | 25272 | 31776 | 2.33 | 1.4E-01 | X74773.1 | NT | P.salina plastid gene secY |
| 12562 | 25280 | | 2.24 | 1.4E-01 | 11988117 | NT | Rattus norvegicus desmin (Des), mRNA |
| 12605 | 25994 | | 2.35 | 1.4E-01 | BE513802.1 | EST_HUMAN | 601315638F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634329 5' |
| 12702 | 25362 | | 2.29 | 1.4E-01 | D64004.1 | NT | Synechocystis sp. PCC6803 complete genome, 23/27, 2868767-3002965 |
| 12776 | 25981 | | 4.86 | 1.4E-01 | P10447 | SWISSPROT | TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN ABL |
| 12996 | 25792 | | 3.72 | 1.4E-01 | D82983.1 | NT | Mus musculus mRNA for prolidase, complete cds |
| 13067 | 25601 | | 2.63 | 1.4E-01 | AW377998.1 | EST_HUMAN | MR0-HT0208-221296-204-c08 HT0208 Homo sapiens cDNA |
| 322 | 13414 | 26338 | 2.48 | 1.3E-01 | 4758467 | NT | Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA |
| 322 | 13414 | 26339 | 2.48 | 1.3E-01 | 4758467 | NT | Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA |

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Table 4
Single Exon Probes Expressed in Bone Marrow.

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 530 | 13601 | 26519 | 2.91 | 1.3E-01 | AB013139.1 | NT | Homo sapiens gene for NBS1, complete cds |
| 637 | 13703 | 26624 | 0.78 | 1.3E-01 | AJ277606.1 | NT | Human calicivirus HUNLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93/UK |
| 637 | 13703 | 26625 | 0.78 | 1.3E-01 | AJ277606.1 | NT | Human calicivirus HUNLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93/UK |
| 845 | 13901 | 26859 | 1.04 | 1.3E-01 | XS3330.1 | NT | P. dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4 |
| 895 | 13950 | 26908 | 1.76 | 1.3E-01 | AF139518.1 | NT | Rattus norvegicus A-kinase anchor protein mRNA, complete cds |
| 1028 | 14074 | 27024 | 1.8 | 1.3E-01 | AL117078.1 | NT | Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation |
| 1129 | 14172 | | 2.88 | 1.3E-01 | AL115285.1 | NT | Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation |
| 1220 | 14258 | 27215 | 1.51 | 1.3E-01 | AV712467.1 | EST_HUMAN | AV712467 DCA Homo sapiens cDNA clone DCAAF05 5' |
| 1438 | 14471 | | 0.93 | 1.3E-01 | AF146277.1 | NT | Homo sapiens adapter protein CMS mRNA, complete cds |
| 1876 | 14987 | 27999 | 2.07 | 1.3E-01 | AL117078.1 | NT | Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation |
| 2180 | 15195 | | 1.69 | 1.3E-01 | AJ243578.1 | NT | Rhodospseudomonas acidophila pucB5, pucA5, pucB6, pucA6, pucB7, pucA8, pucB8, pucA7 and pucC genes and ORF151 |
| 2298 | 16310 | | 0.96 | 1.3E-01 | AW812104.1 | EST_HUMAN | RC4-ST0173-191099-032-d12 ST0173 Homo sapiens cDNA |
| 2389 | 15397 | | 3.94 | 1.3E-01 | AE001016.1 | NT | Archaeoglobus fulgidus section 91 of 172 of the complete genome |
| 2592 | 15593 | 28610 | 2.23 | 1.3E-01 | M86918.1 | NT | Carassius auratus keratin type I mRNA, complete cds |
| 3465 | 16511 | 29432 | 0.98 | 1.3E-01 | M21572.1 | NT | Bovine branched chain alpha-keto acid dihydrolipoyl transacylase mRNA, complete cds |
| 3735 | 16777 | 29689 | 0.91 | 1.3E-01 | AP000001.1 | NT | Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7) |
| 3735 | 16777 | 29690 | 0.91 | 1.3E-01 | AP000001.1 | NT | Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7) |
| 3741 | 16783 | 29695 | 0.89 | 1.3E-01 | AB032159.1 | NT | Homo sapiens DD4 gene for dihydrolipoyl transacylase mRNA, complete cds |
| 3794 | 16777 | 29689 | 0.67 | 1.3E-01 | AP000001.1 | NT | Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7) |
| 3794 | 16777 | 29690 | 0.67 | 1.3E-01 | AP000001.1 | NT | Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7) |
| 3816 | 16868 | 29762 | 0.74 | 1.3E-01 | 6878840 | NT | Rattus norvegicus Fibrinogen, gamma polypeptide (Fgg), mRNA |
| 4014 | 17053 | | 1.48 | 1.3E-01 | AL161581.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77 |
| 4081 | 13703 | 26624 | 7.11 | 1.3E-01 | AJ277606.1 | NT | Human calicivirus HUNLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93/UK |
| 4081 | 13703 | 26625 | 7.11 | 1.3E-01 | AJ277606.1 | NT | Human calicivirus HUNLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93/UK |
| 4163 | 17194 | | 1.12 | 1.3E-01 | AF020713.1 | NT | Bacteriophage SPBc2 complete genome |
| 4185 | 17216 | | 4.1 | 1.3E-01 | AW364341.1 | EST_HUMAN | QV3-DT0018-081299-036-e03 DT0018 Homo sapiens cDNA |
| 4194 | 17228 | 30114 | 2.47 | 1.3E-01 | AF028805.1 | NT | Schistosoma mansoni fructose biphosphate aldolase mRNA, complete cds |
| 4215 | 17244 | 30129 | 20.19 | 1.3E-01 | AW273741.1 | EST_HUMAN | xc23f10 xt Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813995 3' |
| 4343 | 17370 | | 1.49 | 1.3E-01 | AL163280.2 | NT | Homo sapiens chromosome 21 segment HS21C080 |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 4505 | 17530 | 30414 | 0.8 | 1.3E-01 | M21572.1 | NT | Bovine branched chain alpha-keto acid dihydrolylpyl transacylase mRNA, complete cds |
| 4504 | 17587 | 30479 | 2.72 | 1.3E-01 | BE272339.1 | EST_HUMAN | 601126096F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2990063 5' |
| 5014 | 18028 | | 0.91 | 1.3E-01 | AU136619.1 | EST_HUMAN | AU136619 PLACE1 Homo sapiens cDNA clone PLACE1004693 5' |
| 5050 | 18070 | | 0.63 | 1.3E-01 | BF091980.1 | EST_HUMAN | RC4-TN0077-180900-012-c05 TN0077 Homo sapiens cDNA |
| 5398 | 18501 | 31379 | 0.76 | 1.3E-01 | AW469988.1 | EST_HUMAN | ha07b06.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2872979 3' similar to contains L1.b1 L1 |
| 5436 | 18538 | 31446 | 1.98 | 1.3E-01 | AW804417.1 | EST_HUMAN | L1 repetitive element |
| 5579 | 18675 | | 0.91 | 1.3E-01 | AF107783.1 | NT | QV0-UM0093-100400-189-a06 UM0093 Homo sapiens cDNA |
| 5665 | 18760 | | 0.68 | 1.3E-01 | AF056980.1 | NT | Emertella nidulans DNA-dependent RNA polymerase II RPB140 (RPB2) gene, partial cds |
| 5813 | 18803 | 32086 | 0.85 | 1.3E-01 | BF210920.1 | EST_HUMAN | Hepatitis C virus 88_C1.10 genome polyprotein gene, partial cds |
| 6099 | 19178 | 32396 | 0.58 | 1.3E-01 | BF527281.1 | EST_HUMAN | 601874591F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4101119 5' |
| 6098 | 19178 | 32397 | 0.58 | 1.3E-01 | BF527281.1 | EST_HUMAN | 602039337F2 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4177233 5' |
| 6630 | 19688 | 32987 | 17.29 | 1.3E-01 | AB031326.1 | EST_HUMAN | 602039337F2 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4177233 5' |
| 6720 | 19776 | 33055 | 2.08 | 1.3E-01 | X88891.1 | NT | Schizosaccharomyces pombe gene for Alp41, complete cds |
| 6940 | 20184 | 33487 | 0.64 | 1.3E-01 | H73425.1 | EST_HUMAN | Cjacchus intron 4 of visual pigment gene (red allele) |
| 6955 | 20180 | | 0.82 | 1.3E-01 | W26367.1 | EST_HUMAN | yu02401.11 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:232609 5' |
| 7009 | 20135 | 33450 | 1.04 | 1.3E-01 | BE782826.1 | EST_HUMAN | 2613 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA |
| 7009 | 20135 | 33451 | 1.04 | 1.3E-01 | BE782826.1 | EST_HUMAN | 601465957F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3869079 5' |
| 7211 | 20234 | | 0.72 | 1.3E-01 | BF528560.1 | EST_HUMAN | 601465957F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3869079 5' |
| 7477 | 20443 | | 2.15 | 1.3E-01 | H48664.1 | EST_HUMAN | 602044345F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4181866 5' |
| 8292 | 21261 | | 0.97 | 1.3E-01 | BE272339.1 | EST_HUMAN | y33402.11 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:207075 5' |
| 8306 | 21275 | 34686 | 1.59 | 1.3E-01 | 11423284 | NT | 601126096F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2990063 5' |
| 8336 | 21305 | 34720 | 1.18 | 1.3E-01 | BF690522.1 | EST_HUMAN | Homo sapiens PRO0611 protein (PRO0611), mRNA |
| 8580 | 21548 | | 0.56 | 1.3E-01 | BE562528.1 | EST_HUMAN | 602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4299074 3' |
| 8617 | 21585 | 35001 | 0.6 | 1.3E-01 | 11421558 | NT | 601335828F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3689934 5' |
| 8688 | 21656 | | 4.68 | 1.3E-01 | Z74102.1 | NT | Homo sapiens TED protein (TED), mRNA |
| 8729 | 21697 | | 4.2 | 1.3E-01 | 8923919 | NT | S.cerevisiae chromosome IV reading frame ORF YDL054c |
| 8873 | 21840 | 35263 | 1.05 | 1.3E-01 | BF690522.1 | EST_HUMAN | Homo sapiens core histone macroH2A.2 (MACROH2A2), mRNA |
| 9300 | 22265 | 35694 | 0.55 | 1.3E-01 | R11172.1 | EST_HUMAN | 602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4299074 3' |
| 9300 | 22265 | 35695 | 0.55 | 1.3E-01 | R11172.1 | EST_HUMAN | y339g11.11 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:129284 5' similar to |
| 9574 | 22536 | 35987 | 0.65 | 1.3E-01 | 11068003 | NT | SP:RL2B_RAT P29316 60S RIBOSOMAL PROTEIN ; |
| 9574 | 22536 | 35988 | 0.65 | 1.3E-01 | 11068003 | NT | y339g11.11 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:129284 5' similar to |
| | | | | | | | SP:RL2B_RAT P29316 60S RIBOSOMAL PROTEIN ; |
| | | | | | | | Plutella xylostella granulovirus, complete genome |
| | | | | | | | Plutella xylostella granulovirus, complete genome |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 9827 | 22678 | 36132 | 3.9 | 1.3E-01 | AF023126.1 | NT | Oryctolagus cuniculus H ₂ K ₂ -ATPase alpha 2c subunit mRNA, complete cds |
| 10129 | 23055 | | 0.74 | 1.3E-01 | N86348.1 | EST_HUMAN | J7837F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J7837 5' similar to B-CELL |
| 10411 | 23333 | | 0.89 | 1.3E-01 | 8393940 | NT | RECEPTOR ASSOCIATED PROTEIN (BAP) 29 |
| 10489 | 23411 | 36908 | 0.86 | 1.3E-01 | AW851599.1 | EST_HUMAN | Rattus norvegicus peptidyl arginine deiminase, type IV (Pd4), mRNA |
| 10757 | 25702 | 37173 | 1.06 | 1.3E-01 | AL163246.2 | NT | MR2-C10222-201089-001-e01 C10222 Homo sapiens cDNA |
| 10891 | 23811 | 37318 | 0.86 | 1.3E-01 | AU121237.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C046 |
| 10938 | 23858 | 37372 | 0.45 | 1.3E-01 | AW247836.1 | EST_HUMAN | AU121237 HEMBB1 Homo sapiens cDNA clone HEMBB1002387 5' |
| 10996 | 23962 | | 2.57 | 1.3E-01 | BF330999.1 | EST_HUMAN | 2820637.3prime NIH_MGC 7 Homo sapiens cDNA clone IMAGE:2820637 3' |
| 11581 | 24519 | | 3.56 | 1.3E-01 | 6871745 | NT | MR4-BT0358-130700-010-K08 BT0358 Homo sapiens cDNA |
| 11670 | 24606 | 38182 | 1.77 | 1.3E-01 | AW082636.1 | EST_HUMAN | Mus musculus cofilin 2, muscle (Cf2), mRNA |
| 11670 | 24608 | 38183 | 1.77 | 1.3E-01 | AW082636.1 | EST_HUMAN | xc20709.x1 NCI_CGAP_Co19 Homo sapiens cDNA clone IMAGE:2584841 3' |
| 11922 | 24803 | 38395 | 2.33 | 1.3E-01 | BE279446.1 | EST_HUMAN | xc20709.x1 NCI_CGAP_Co19 Homo sapiens cDNA clone IMAGE:2584841 3' |
| 12397 | 25171 | 31817 | 1.83 | 1.3E-01 | BE618349.1 | EST_HUMAN | 601156052F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3504804 5' |
| 12535 | 25260 | | 3.3 | 1.3E-01 | AJ242790.1 | NT | 601462741F1 NIH_MGC 57 Homo sapiens cDNA clone IMAGE:3866003 5' |
| 12692 | 25357 | 31766 | 1.37 | 1.3E-01 | BF572303.1 | EST_HUMAN | Gallus gallus scyl gene for lymphotactin, exons 1-3 |
| 12885 | 25475 | | 1.48 | 1.3E-01 | AB028829.1 | NT | 602077752F1 NIH_MGC 52 Homo sapiens cDNA clone IMAGE:4252082 5' |
| 12915 | 25494 | | 2.52 | 1.3E-01 | AW001114.1 | EST_HUMAN | Ephydratia fluviatilis mRNA for sALK-6, complete cds |
| 383 | 13496 | 26428 | 14.68 | 1.2E-01 | A1421744.1 | EST_HUMAN | wu24d09.x1 Soares Dieckgraefe_cdon_NHCD Homo sapiens cDNA clone IMAGE:2520877 3' similar to |
| 424 | 13119 | | 1.38 | 1.2E-01 | U68912.1 | NT | TR:O60287 O60287 KIAA0539 PROTEIN ; |
| 549 | 13819 | | 2.78 | 1.2E-01 | AF039442.1 | NT | tf39b02.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2098539 3' similar to gb:U05760_rna1 |
| 1377 | 14411 | 27381 | 2.19 | 1.2E-01 | AU149146.1 | EST_HUMAN | ANNEXIN V (HUMAN); |
| 1377 | 14411 | 27382 | 2.19 | 1.2E-01 | AU149146.1 | EST_HUMAN | Dicystelium discoideum ORF DG1016 gene, partial cds |
| 1383 | 14417 | | 4.89 | 1.2E-01 | AV735249.1 | EST_HUMAN | Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds |
| 1388 | 14421 | | 0.92 | 1.2E-01 | AL445066.1 | NT | AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3' |
| 1507 | 14540 | | 1.23 | 1.2E-01 | AA897474.1 | EST_HUMAN | AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3' |
| 1635 | 14667 | 27643 | 1.62 | 1.2E-01 | Q14934 | SWISSPROT | AV735249 cda Homo sapiens cDNA clone cdAAJB11 5' |
| 1658 | 14690 | 27668 | 2.99 | 1.2E-01 | A1285402.1 | EST_HUMAN | Thermoplasma acidophilum complete genome, segment 4/5 |
| 1783 | 14812 | | 18.69 | 1.2E-01 | X89211.1 | NT | al48609.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460584 3' similar to TR:Q16671 |
| 1934 | 14958 | | 1.76 | 1.2E-01 | AW446968.1 | EST_HUMAN | Q16671 ANTI-MULLERIAN HORMONE TYPE II RECEPTOR PRECURSOR ; |
| | | | | | | | NUCLEAR FACTOR OF ACTIVATED T-CELLS, CYTOPLASMIC 4 (T CELL TRANSCRIPTION FACTOR |
| | | | | | | | NFAT3) (NF-ATC3) (NF-AT3) |
| | | | | | | | q16909.x1 NCI_CGAP_Esc2 Homo sapiens cDNA clone IMAGE:1060583 3' |
| | | | | | | | H.sapiens DNA for endogenous retroviral like element |
| | | | | | | | UI-H-B13-akt-10-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734554 3' |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 2183 | 15208 | 28227 | 1.65 | 1.2E-01 | BF248490.1 | EST_HUMAN | 601821567F1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4046224 5' |
| 2294 | 15308 | 28329 | 1.21 | 1.2E-01 | AL163213.2 | NT | Homo sapiens chromosome 21 segment HS21C013 |
| 2595 | 15596 | 28614 | 2.05 | 1.2E-01 | AW996556.1 | EST_HUMAN | QV3-BN0046-220300-129-f10 BN0046 Homo sapiens cDNA |
| 2602 | 15602 | 28624 | 1.61 | 1.2E-01 | BE219989.1 | EST_HUMAN | hV6504.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3178303 3' |
| 2738 | 15732 | 28748 | 37.59 | 1.2E-01 | A1823388.1 | EST_HUMAN | ts18g07.x1 NCI_CGAP_Par1 Homo sapiens cDNA clone IMAGE:2228988 3' similar to TR:Q14048 Q14048 COLLAGEN VI ALPHA-2 ALTERNATIVE C-TERMINAL DOMAIN. [1] contains element PTR5 repetitive element; |
| 2855 | 15915 | 28838 | 1.4 | 1.2E-01 | U18018.1 | NT | Human E1A enhancer binding protein (E1A-F) mRNA, partial cds |
| 2913 | 15971 | 28895 | 2.03 | 1.2E-01 | A1720470.1 | EST_HUMAN | as80c09.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2335024 3' similar to gb.L05095 60S RIBOSOMAL PROTEIN L30 (HUMAN); |
| 2946 | 16004 | 28929 | 2.52 | 1.2E-01 | M16394.1 | NT | Human creatine Kinase-B mRNA, complete cds |
| 3017 | 16075 | 28998 | 0.73 | 1.2E-01 | X56882.1 | NT | Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA) |
| 3244 | 16299 | 29224 | 1.34 | 1.2E-01 | AW370668.1 | EST_HUMAN | QV1-BT0259-261099-021-d05 BT0259 Homo sapiens cDNA |
| 3271 | 16325 | | 0.82 | 1.2E-01 | U67800.1 | NT | Methanococcus jannaschii section 142 of 150 of the complete genome |
| 3533 | 16579 | 29502 | 0.86 | 1.2E-01 | X56882.1 | NT | Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA) |
| 3533 | 16579 | 29503 | 0.86 | 1.2E-01 | X56882.1 | NT | Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA) |
| 3620 | 16538 | | 1.05 | 1.2E-01 | Z99118.1 | NT | Bacillus subtilis complete genome (section 15 of 21); from 2795131 to 3013540 |
| 3780 | 16821 | | 0.7 | 1.2E-01 | BF128551.1 | EST_HUMAN | 601810796R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053698 3' |
| 4211 | 17240 | 30125 | 2.16 | 1.2E-01 | Z54255.1 | NT | P. clarkii mRNA; repeat region (ID 2MRT7) |
| 4211 | 17240 | 30126 | 2.16 | 1.2E-01 | Z54255.1 | NT | P. clarkii mRNA; repeat region (ID 2MRT7) |
| 4751 | 17771 | 30667 | 0.98 | 1.2E-01 | Z48183.1 | NT | L. esculentum mRNA for glycylase-1 |
| 5116 | 18128 | | 1 | 1.2E-01 | P16466 | SWISSPROT | HEMOLYSIN PRECURSOR |
| 5150 | 18159 | 31038 | 0.91 | 1.2E-01 | AL163227.2 | NT | Homo sapiens chromosome 21 segment HS21C027 |
| 5150 | 18159 | 31039 | 0.91 | 1.2E-01 | AL163227.2 | NT | Homo sapiens chromosome 21 segment HS21C027 |
| 5164 | 18173 | 31052 | 1 | 1.2E-01 | AL161518.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 30 |
| 5234 | 18242 | 31114 | 0.81 | 1.2E-01 | BE974502.1 | EST_HUMAN | 601880493R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950711 3' |
| 5322 | 18428 | 31178 | 0.75 | 1.2E-01 | AA744369.1 | EST_HUMAN | hV63c04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1282950 3' |
| 5373 | 18478 | 31351 | 0.91 | 1.2E-01 | AF228391.1 | NT | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced |
| 5383 | 18487 | 31361 | 2.27 | 1.2E-01 | W33035.1 | EST_HUMAN | zcd0d02.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:321699 5' |
| 5442 | 18544 | 31456 | 2.15 | 1.2E-01 | Z98296.1 | NT | Homo sapiens gene encoding plakophilin (exons 1-13) |
| 5583 | 18679 | 31643 | 0.95 | 1.2E-01 | Z48234.1 | NT | M. domestica Borkh. Granny Smith adh mRNA for alcohol dehydrogenase |
| 6324 | 19394 | 32636 | 2.66 | 1.2E-01 | BE620945.1 | EST_HUMAN | 601493518F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895613 5' |
| 6376 | 19444 | 32686 | 1.1 | 1.2E-01 | P10842 | SWISSPROT | MATING-TYPE P-SPECIFIC POLYPEPTIDE PI |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 6431 | 19497 | 32750 | 2.19 | 1.2E-01 | AW845275.1 | EST_HUMAN | IL0-CT0031-221099-113-e04 CT0031 Homo sapiens cDNA |
| 6499 | 19563 | 32815 | 1.38 | 1.2E-01 | M26925.1 | NT | Muscle galactosyltransferase mRNA, complete cds |
| 6804 | 19658 | 33145 | 0.89 | 1.2E-01 | BF347985.1 | EST_HUMAN | 602023112F1 NCI_CGAP_Brm67 Homo sapiens cDNA clone IMAGE:4158386 5' |
| 6868 | 20180 | 33517 | 0.55 | 1.2E-01 | AF295739.1 | NT | JC virus agnoprotein, VP2, VP3, VP1, large T antigen, and small t antigen genes, complete cds |
| 7210 | 20233 | 33567 | 0.67 | 1.2E-01 | H47799.1 | EST_HUMAN | yp80f04.1 Scores fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:193759 5' |
| 7210 | 20233 | 33568 | 0.67 | 1.2E-01 | H47799.1 | EST_HUMAN | yp80f04.1 Scores fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:193759 5' |
| 7854 | 20799 | 34175 | 0.62 | 1.2E-01 | AJ271741.1 | NT | Homo sapiens partial ILF3 gene for interleukin enhancer binding factor 3 (alternative transcripts drbp76, drbp76 gamma, drbp76 alpha and ILF3) |
| 8063 | 21000 | 34396 | 0.9 | 1.2E-01 | BF680613.1 | EST_HUMAN | 602155195F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4286382 5' |
| 8088 | 21034 | 34433 | 0.57 | 1.2E-01 | D87458.1 | NT | Human mRNA for KIAA0282 gene, partial cds |
| 8098 | 21034 | 34434 | 0.57 | 1.2E-01 | D87458.1 | NT | Human mRNA for KIAA0282 gene, partial cds |
| 8224 | 21193 | | 1.24 | 1.2E-01 | BE007072.1 | EST_HUMAN | PM3-BN0137-290300-002-f09 BN0137 Homo sapiens cDNA |
| 8295 | 21264 | 34675 | 3.1 | 1.2E-01 | A1913753.1 | EST_HUMAN | wc98g03.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2328804 3' similar to SW:GST2_HUMAN |
| 8341 | 21310 | 34724 | 0.76 | 1.2E-01 | Q02369 | SWISSPROT | Q99735 MICROSOMAL GLUTATHIONE S-TRANSFERASE II; |
| 8652 | 21620 | 35040 | 0.61 | 1.2E-01 | A1832681.1 | EST_HUMAN | NADH-JUBIQUINONE OXIDOREDUCTASE B22 SUBUNIT (COMPLEX I-B22) (CI-B22) |
| 8739 | 21707 | | 10.85 | 1.2E-01 | AW083652.1 | EST_HUMAN | at171b10.x1 Barslead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2377435 3' |
| | | | | | | | xc49d07.x1 NCI_CGAP_Esc2 Homo sapiens cDNA clone IMAGE:2587597 3' similar to gb:M13452 LAMIN A (HUMAN); |
| 8759 | 21726 | | | | | | Staphylococcus aureus plasmid pSK23 putative recombinase Sin (sin) gene, partial cds; and transcriptional regulator QacR (qacR) and multidrug efflux protein QacB (qacB) genes, complete cds |
| 8798 | 21765 | 35187 | 3.98 | 1.2E-01 | AF053772.1 | NT | N.crassa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds |
| 8798 | 21765 | 35188 | 0.99 | 1.2E-01 | J03956.1 | NT | N.crassa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds |
| 8948 | 21914 | | 0.81 | 1.2E-01 | AJ271736.1 | NT | Homo sapiens Xq pseudautosomal region, segment 2/2 |
| 9037 | 22003 | | 2.01 | 1.2E-01 | U32714.1 | NT | Haemophilus influenzae Rd section 29 of 163 of the complete genome |
| 9073 | 22039 | | 0.64 | 1.2E-01 | X15191.1 | NT | M.musculus DNA fragment of Apolipoprotein B gene |
| 9830 | 22813 | 36287 | 1.69 | 1.2E-01 | X77961.1 | NT | S.cerevisiae HXT5 gene |
| 10365 | 23288 | 36765 | 1.84 | 1.2E-01 | AV710857.1 | EST_HUMAN | AV710857 Cu Homo sapiens cDNA clone CUAKE08 5' |
| 11232 | 24185 | | 2.36 | 1.2E-01 | D26184.1 | NT | Yeast MPT5 gene for suppressor protein, complete cds |
| 11404 | 24348 | | 2.55 | 1.2E-01 | BF662324.2 | EST_HUMAN | 601655578R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846283 3' |
| 11482 | 24425 | | 1.57 | 1.2E-01 | BF314481.1 | EST_HUMAN | 601900763F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5' |
| 11584 | 24522 | 38077 | 2.45 | 1.2E-01 | AF190493.1 | NT | Homo sapiens dynein intermediate chain DNAI1 (DNAI1) gene, exon 17 |
| 11738 | 24623 | 38201 | 1.6 | 1.2E-01 | 9994174 | NT | Homo sapiens UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 4 (B4GALT4), mRNA |

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|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 11838 | 24719 | | 1.54 | 1.2E-01 | M65109.1 | NT | Rabbit glycogen-associated protein phosphatase regulatory subunit (RG1) mRNA, complete cds |
| 12162 | 25016 | | 3.66 | 1.2E-01 | AV658033.1 | EST_HUMAN | AV658033 GLC Homo sapiens cDNA clone GLCFIB12.3' |
| 12517 | 25248 | | 2.78 | 1.2E-01 | AJ271736.1 | NT | Homo sapiens Xq pseudautosomal region: segment 2/2 |
| 12593 | 25922 | 31304 | 6.17 | 1.2E-01 | Q04912 | SWISSPROT | MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON) (CDW136) (CD136 ANTIGEN) |
| 12805 | 25432 | | 2.66 | 1.2E-01 | X53981.1 | NT | R.norvegicus NF68 gene for 68kDa neurofilament |
| 12867 | 25935 | 31310 | 1.58 | 1.2E-01 | BE061418.1 | EST_HUMAN | QV4-BT0234-111199-031-g10 BT0234 Homo sapiens cDNA |
| 12889 | 25477 | 31731 | 9.62 | 1.2E-01 | AI296903.1 | EST_HUMAN | gn20g05.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1898840 3' |
| 12911 | 25490 | | 2.91 | 1.2E-01 | L10187.1 | NT | Xenopus laevis integrin alpha 3 subunit mRNA, partial cds |
| 12917 | 25862 | | 9.28 | 1.2E-01 | O96433 | SWISSPROT | CYCLIN T |
| 12946 | 25525 | 31712 | 1.76 | 1.2E-01 | AE004428.1 | NT | Vibrio cholerae chromosome II, section 85 of 93 of the complete chromosome |
| 13092 | 16538 | | 2.08 | 1.2E-01 | Z99118.1 | NT | Bacillus subtilis complete genome (section 15 of 21): from 2795131 to 3013540 |
| 13098 | 25623 | | 1.5 | 1.2E-01 | BF314481.1 | EST_HUMAN | 601900763F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5' |
| 568 | 13636 | 26552 | 1.01 | 1.1E-01 | AI561003.1 | EST_HUMAN | tr18408.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2167983 3' |
| 617 | 13682 | 26599 | 1.84 | 1.1E-01 | AA569006.1 | EST_HUMAN | nm03911.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1058620 3' similar to gb:X06985_mn1 |
| 1057 | 14103 | 27054 | 1.55 | 1.1E-01 | BF697308.1 | EST_HUMAN | 602128847F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286771 5' |
| 1087 | 14131 | | 1.48 | 1.1E-01 | AL161560.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60 |
| 1163 | 15860 | 27158 | 4.8 | 1.1E-01 | AW972158.1 | EST_HUMAN | EST384142 IMAGE resequences, MAGL Homo sapiens cDNA |
| 1254 | 14280 | 27255 | 2.03 | 1.1E-01 | D64004.1 | NT | Synechocystis sp. PC C8803 complete genome, 23/27, 2668767-3002965 |
| 1524 | 14556 | 27527 | 2.46 | 1.1E-01 | AU140363.1 | EST_HUMAN | AU140363 PLACE2 Homo sapiens cDNA clone PLACE2000403 5' |
| 2322 | 15333 | | 2.72 | 1.1E-01 | 6755215 | NT | Mus musculus pre T-cell antigen receptor alpha (Ptra), mRNA |
| 2545 | 15926 | | 0.93 | 1.1E-01 | 6978676 | NT | Rattus norvegicus Procollagen II alpha 1 (Col2a1), mRNA |
| 2574 | 15575 | | 0.93 | 1.1E-01 | AW821909.1 | EST_HUMAN | RC0-ST0379-210100-032-g04 ST0379 Homo sapiens cDNA |
| 3046 | 16103 | 28017 | 0.95 | 1.1E-01 | F03265.1 | EST_HUMAN | HSC1RF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1rf02 3' |
| 3352 | 16403 | | 1.66 | 1.1E-01 | 6753231 | NT | Mus musculus calcium channel, voltage-dependent, T type, alpha 1G subunit (Cacna1g), mRNA |
| 3432 | 16480 | 28369 | 2.18 | 1.1E-01 | BE93186.1 | EST_HUMAN | 601308679F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3627066 5' |
| 3466 | 16512 | 28493 | 1.3 | 1.1E-01 | X62135.1 | NT | C.reinhardtii nuclear gene on linkage group XIX |
| 3566 | 16941 | 29560 | 0.8 | 1.1E-01 | Y07695.1 | NT | A.immersus gene for transposase |
| 3715 | 16758 | | 0.86 | 1.1E-01 | P67384 | SWISSPROT | ANNEXIN XI (CALCYCLIN-ASSOCIATED ANNEXIN 50) (CAP-50) |
| 3722 | 16765 | 29676 | 1.23 | 1.1E-01 | X52708.1 | NT | G.gallus gene encoding non-histone chromosomal protein HMG-14b, exons 4 and 5 |
| 4137 | 17169 | 30054 | 1.14 | 1.1E-01 | AW819412.1 | EST_HUMAN | MR3-ST0290-280100-025-g07 ST0290 Homo sapiens cDNA |
| 4137 | 17169 | 30055 | 1.14 | 1.1E-01 | AW819412.1 | EST_HUMAN | MR3-ST0290-280100-025-g07 ST0290 Homo sapiens cDNA |
| 4281 | 17310 | | 9.36 | 1.1E-01 | AF157066.1 | NT | Drosophila melanogaster klarsicht protein (klar) mRNA, complete cds |

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|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 4316 | 17345 | 30229 | 0.69 | 1.1E-01 | AW802056.1 | EST_HUMAN | IL5-UM0070-020500-068-a08 UM0070 Homo sapiens cDNA |
| 4670 | 17691 | 30577 | 1.02 | 1.1E-01 | S44957.1 | NT | Tapa-1=Integral membrane protein TAPA-1 [mice, B cell lymphoma line 38C13, Genomic, 1973 nt, segment 1 of 7] |
| 4869 | 17886 | 30774 | 0.98 | 1.1E-01 | Y07695.1 | NT | A.immersus gene for transposase |
| 5058 | 17174 | | 0.76 | 1.1E-01 | AF030001.1 | NT | Mus musculus major histocompatibility locus class III region:butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PP12), CREB-RP, and tenascin X (TNX) genes, complete> |
| 5753 | 18847 | | 1.36 | 1.1E-01 | AA747216.1 | EST_HUMAN | nx76a03 s1 NCI_CGAP_Ewt Homo sapiens cDNA clone IMAGE:1268140 similar to contains Alu repetitive element; contains element MER35 repetitive element; |
| 5829 | 18919 | 32102 | 1.16 | 1.1E-01 | AF020927.1 | NT | 6 Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 6 |
| 5888 | 18957 | 32145 | 0.95 | 1.1E-01 | AL110985.1 | NT | Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation |
| 5904 | 18990 | 32180 | 0.73 | 1.1E-01 | BF339519.1 | EST_HUMAN | 602039176F1 NCI_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4186818 5' |
| 5904 | 18990 | 32181 | 0.73 | 1.1E-01 | BF339519.1 | EST_HUMAN | 602039176F1 NCI_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4186818 5' |
| 5935 | 19021 | 32215 | 1.67 | 1.1E-01 | X68851.1 | NT | S.pombe ste8 gene encoding protein kinase |
| 5971 | 19056 | 32256 | 4.98 | 1.1E-01 | M86533.1 | NT | Providencia rettgeri penicillin G amidase gene |
| 6142 | 19217 | 32446 | 1.63 | 1.1E-01 | AJ007973.1 | NT | Homo sapiens LGMD2B gene |
| 6164 | 19239 | 32470 | 1.54 | 1.1E-01 | BE769152.1 | EST_HUMAN | PM3-FT0024-130800-004-f12 FT0024 Homo sapiens cDNA |
| 6184 | 19259 | 32493 | 8 | 1.1E-01 | AW853699.1 | EST_HUMAN | RC3-C10264-280999-011-e01 C10264 Homo sapiens cDNA |
| 6564 | 19624 | 32889 | 0.5 | 1.1E-01 | AL183282.2 | NT | Homo sapiens chromosome 21 segment HS21C082 |
| 6571 | 19631 | 32898 | 1.26 | 1.1E-01 | AF035746.1 | EST_HUMAN | AF035746 Human salivary gland cell line HSG Homo sapiens cDNA clone RL43 |
| 6617 | 19675 | 32953 | 0.84 | 1.1E-01 | AI216307.1 | EST_HUMAN | gg76d06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1841098 3' |
| 6762 | 19816 | 33096 | 6.18 | 1.1E-01 | O69835 | SWISSPROT | ACETYL-COENZYME A SYNTHETASE (ACETATE-COA LIGASE) (ACYL-ACTIVATING ENZYME) |
| 6862 | 19915 | | 2.81 | 1.1E-01 | AF032922.1 | NT | Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds |
| 6962 | 20187 | 33512 | 2.23 | 1.1E-01 | 11432372 | NT | Homo sapiens phosphatidylinositol glycan, class B (PIGB), mRNA |
| 7249 | 19984 | 33281 | 0.65 | 1.1E-01 | AE002155.1 | NT | Ureaplasma urealyticum section 56 of 59 of the complete genome |
| 7249 | 19984 | 33282 | 0.65 | 1.1E-01 | AE002155.1 | NT | Ureaplasma urealyticum section 56 of 59 of the complete genome |
| 7393 | 25999 | | 0.94 | 1.1E-01 | BF382758.1 | EST_HUMAN | 601816524F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050863 5' |
| 7523 | 25683 | 33850 | 1.59 | 1.1E-01 | AF000006.1 | NT | Pyrococcus horikoshii O13 genomic DNA, 1166001-1485000 nt, position (617) |
| 7781 | 20734 | 34105 | 7.99 | 1.1E-01 | BF684628.1 | EST_HUMAN | 602140976F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019 5' |
| 7781 | 20734 | 34106 | 7.99 | 1.1E-01 | BF684628.1 | EST_HUMAN | 602140976F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019 5' |
| 7839 | 20766 | 34161 | 0.54 | 1.1E-01 | AA959908.1 | EST_HUMAN | ou44g03 s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1629172 3' |
| 7917 | 20860 | 34249 | 1.77 | 1.1E-01 | P41067 | SWISSPROT | TRAB PROTEIN |
| 7959 | 20900 | | 0.79 | 1.1E-01 | Z14098.1 | NT | B.subtilis gene encoding hypothetical polyketide synthase |

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|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 7961 | 20902 | 34294 | 2.99 | 1.1E-01 | AA788784.1 | EST_HUMAN | ah31506.s1 Soares_perathyroid_tumor_NbHPA Homo sapiens cDNA clone 1240403 3' similar to gb.J03483 |
| 8111 | 21048 | 34448 | 0.65 | 1.1E-01 | BE782290.1 | EST_HUMAN | CHROMOGHRANIN A PRECURSOR (HUMAN); |
| 8301 | 21270 | 34882 | 0.48 | 1.1E-01 | U67492.1 | NT | 601470055F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873229 5' |
| 8501 | 21518 | 34936 | 1.61 | 1.1E-01 | AA495574.1 | EST_HUMAN | Methanococcus jannaschii section 34 of 150 of the complete genome |
| 8550 | 21518 | 34937 | 1.61 | 1.1E-01 | AA495574.1 | EST_HUMAN | nh04g10.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943362 |
| 8598 | 21566 | 34982 | 1.1 | 1.1E-01 | X91233.1 | NT | nh04g10.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943362 |
| 8637 | 21605 | | 1.05 | 1.1E-01 | AW817918.1 | EST_HUMAN | H.sapiens IL15 gene |
| 8694 | 21662 | 35088 | 1.59 | 1.1E-01 | AL134348.1 | EST_HUMAN | PM1-ST0270-Q80200-001-109 ST0270 Homo sapiens cDNA |
| 9170 | 22136 | 35562 | 1.82 | 1.1E-01 | U02482.1 | NT | DKFZp547P194.1 547 (synonym: hfb1) Homo sapiens cDNA clone DKFZp547P194 5' |
| 9263 | 22229 | 35660 | 0.96 | 1.1E-01 | AB07474.1 | EST_HUMAN | Pedococcus acidilactici H plasmid pSMB74 pediocin ACh production (pap) gene cluster papA, papB, papC and papO genes, complete cds |
| 9362 | 22327 | 35758 | 0.56 | 1.1E-01 | AF050081.1 | NT | wf48c01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358816 3' similar to contains Alu repetitive element |
| 9398 | 22363 | 35794 | 2.27 | 1.1E-01 | AA192153.1 | EST_HUMAN | Homo sapiens C16orf3 large protein mRNA, complete cds |
| 9398 | 22363 | 35795 | 2.27 | 1.1E-01 | AA192153.1 | EST_HUMAN | zp93b12.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:627743 5' |
| 9490 | 22454 | 35894 | 0.77 | 1.1E-01 | Y12727.1 | NT | zp93b12.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:627743 5' |
| 9520 | 22483 | 35929 | 2.1 | 1.1E-01 | T72875.1 | EST_HUMAN | P.furiosus partial dph5 gene and argF gene |
| 9546 | 22509 | | 0.62 | 1.1E-01 | BE893280.1 | EST_HUMAN | yd19h03.s1 Soares_fetal liver spleen (NFLS) Homo sapiens cDNA clone IMAGE:108725 3' similar to gb:M81181 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-2 (HUMAN); |
| 9777 | 22718 | | 0.89 | 1.1E-01 | BE142305.1 | EST_HUMAN | 601436972F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922048 5' |
| 9853 | 22789 | | 2.05 | 1.1E-01 | BF085149.1 | EST_HUMAN | CM3-HT0142-27-1089-026-g11 HT0142 Homo sapiens cDNA |
| 10270 | 23185 | | 0.68 | 1.1E-01 | AL161543.2 | NT | MR2-GN0027-040900-005-a08 GN0027 Homo sapiens cDNA |
| 10478 | 23398 | | 0.45 | 1.1E-01 | BE315509.1 | EST_HUMAN | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 43 |
| 10568 | 23488 | | 1.01 | 1.1E-01 | R80590.1 | EST_HUMAN | 601140231F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049543 5' |
| 10701 | 23623 | 37119 | 1.05 | 1.1E-01 | U60528.1 | NT | y95a09.s1 Soares_placenta_Nb2HP Homo sapiens cDNA clone IMAGE:147064 3' |
| 11156 | 18103 | 29017 | 1.7 | 1.1E-01 | F03265.1 | EST_HUMAN | Ceratitis capitata yoyo retrotransposon gag-like, pol-like and env-like genes, complete cds |
| 11267 | 24219 | | 3.13 | 1.1E-01 | AF169032.1 | NT | HSCIRF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1f02 3' |
| | | | | | | | Carassius auratus actvln beta A precursor, mRNA, complete cds |
| | | | | | | | y35f12.r1 Soares_placenta_Nb2HP Homo sapiens cDNA clone IMAGE:131759 5' similar to contains Alu repetitive element; contains TAR1 repetitive element; |
| 11384 | 24331 | 37850 | 3.51 | 1.1E-01 | R23708.1 | EST_HUMAN | Rattus norvegicus Phosphofructokinase, liver, B-type (Pfkf), mRNA |
| 11392 | 24338 | 37868 | 1.54 | 1.1E-01 | 6981351 | NT | |
| 11542 | 24483 | 38035 | 2.18 | 1.1E-01 | Z11910.1 | NT | Z.mobilis tgt and lig genes encoding RNA guanine transglycosylase and DNA ligase |
| 11542 | 24483 | 38036 | 2.18 | 1.1E-01 | Z11910.1 | NT | Z.mobilis tgt and lig genes encoding RNA guanine transglycosylase and DNA ligase |
| 11636 | 24573 | 38137 | 3.66 | 1.1E-01 | P17437 | SWISSPROT | SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN) |

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|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 12260 | 25084 | | 2.03 | 1.1E-01 | AA192153.1 | EST_HUMAN | z93b12.1 Stratigene muscle 937209 Homo sapiens cDNA clone IMAGE:627743 5' |
| 12379 | 25161 | | 3.66 | 1.1E-01 | BE767023.1 | EST_HUMAN | RC2-NT0112-120600-014-f03 NT0112 Homo sapiens cDNA |
| 12625 | 25732 | | 2.18 | 1.1E-01 | BE974596.1 | EST_HUMAN | 601680551R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950604 3' |
| 13038 | 25580 | 31699 | 1.89 | 1.1E-01 | BF239753.1 | EST_HUMAN | 601906350F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134085 5' |
| 13098 | 25912 | | 1.32 | 1.1E-01 | P14400 | SWISSPROT | ELECTROMOTOR NEURON-ASSOCIATED PROTEIN 1 |
| 1206 | 14245 | | 2.05 | 1.0E-01 | O62855 | SWISSPROT | DEOXYRIBONUCLEASE II PRECURSOR (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II) |
| 1277 | 14312 | 27273 | 1.95 | 1.0E-01 | A1985499.1 | EST_HUMAN | wa08401.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2496577 3' similar to contains MER7.3 |
| 1393 | 14427 | 27396 | 2.25 | 1.0E-01 | AL161504.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16 |
| 2497 | 15500 | 28526 | 1.16 | 1.0E-01 | AW451365.1 | EST_HUMAN | U1-H-B13-alc-d-07-0-U1.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2738420 3' |
| 3524 | 16570 | 29493 | 1.32 | 1.0E-01 | BF033991.1 | EST_HUMAN | 601455301F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3859849 5' |
| 3732 | 16774 | 29686 | 0.68 | 1.0E-01 | BF239818.1 | EST_HUMAN | 601906489F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134071 5' |
| 3849 | 16889 | 29792 | 2.49 | 1.0E-01 | AF297081.1 | NT | Escherichia coli enterotoxin EspC (espC) gene, complete cds; and unknown genes |
| 3849 | 16889 | 29783 | 2.49 | 1.0E-01 | AF297081.1 | NT | Escherichia coli enterotoxin EspC (espC) gene, complete cds; and unknown genes |
| 3976 | 17016 | 29830 | 2.66 | 1.0E-01 | BF365703.1 | EST_HUMAN | QV2-NT0048-160800-316-e05 NT0048 Homo sapiens cDNA |
| 4585 | 17607 | | 0.86 | 1.0E-01 | AI792349.1 | EST_HUMAN | an32c04.y6 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700358 5' |
| 4741 | 17761 | 30655 | 1.32 | 1.0E-01 | U50450.1 | NT | Drosophila melanogaster tyrosine kinase p45 isoform (fer) mRNA, complete cds |
| 4957 | 17972 | 30863 | 2.34 | 1.0E-01 | AW952344.1 | EST_HUMAN | EST384414 IMAGE resequences, MAGB Homo sapiens cDNA |
| 5267 | 18274 | 31138 | 0.97 | 1.0E-01 | AV721471.1 | EST_HUMAN | AV721471 HTB Homo sapiens cDNA clone HTBBQ10 5' |
| 5273 | 18279 | | 1.04 | 1.0E-01 | AV763980.1 | EST_HUMAN | AV763980 MDS Homo sapiens cDNA clone MDSBQB11 5' |
| 5394 | 18497 | | 8.1 | 1.0E-01 | W86490.1 | EST_HUMAN | zh62h04.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416695 3' |
| 5492 | 18592 | | 0.59 | 1.0E-01 | X54015.1 | NT | X.campestris genes for sensor and regulator protein |
| 5980 | 19065 | | 0.87 | 1.0E-01 | AK024472.1 | NT | Homo sapiens mRNA for FLJ00065 protein, partial cds |
| 6140 | 19216 | 32445 | 12.15 | 1.0E-01 | AF274875.1 | NT | Homo sapiens growth factor receptor-bound protein 7 (GRB7) gene, complete cds |
| 6469 | 19534 | 32782 | 0.9 | 1.0E-01 | AA481878.1 | EST_HUMAN | zv41g10.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:756258 3' similar to contains L1.3 L1 repetitive element |
| 6483 | 19548 | 32797 | 0.95 | 1.0E-01 | AA406039.1 | EST_HUMAN | zu67c12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743062 3' |
| 7220 | 20242 | | 1.62 | 1.0E-01 | R23821.1 | EST_HUMAN | va34h06.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:131676 5' similar to contains Alu repetitive element |
| 8009 | 20947 | | 2.16 | 1.0E-01 | Y12488.1 | NT | M.musculus wln gene |
| 8108 | 21045 | 34444 | 0.65 | 1.0E-01 | AJ011400.1 | NT | Bos taurus mRNA for b17.2 subunit of NADH:ubiquinone oxidoreductase complex (complex I) |
| 8108 | 21045 | 34445 | 0.65 | 1.0E-01 | AJ011400.1 | NT | Bos taurus mRNA for b17.2 subunit of NADH:ubiquinone oxidoreductase complex (complex I) |
| 8265 | 21234 | 34845 | 0.63 | 1.0E-01 | AA861091.1 | EST_HUMAN | ak32g01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1407698 3' similar to gb.M34182 CAMP-DEPENDENT PROTEIN KINASE, GAMMA-CATALYTIC SUBUNIT (HUMAN); |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 8287 | 21256 | 34665 | 0.45 | 1.0E-01 | AF260225.1 | NT | Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced |
| 8287 | 21256 | 34666 | 0.45 | 1.0E-01 | AF260225.1 | NT | Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced |
| 8506 | 21474 | | 0.68 | 1.0E-01 | 4758365 | NT | Homo sapiens fibroblast growth factor 13 (FGF13) mRNA |
| 8837 | 21804 | | 0.94 | 1.0E-01 | AW189797.1 | EST_HUMAN | x09b01.x1 NCL CGAP_U14 Homo sapiens cDNA clone IMAGE:2675689 3' similar to gb.X17206 40S |
| 9540 | 22503 | 35952 | 1.19 | 1.0E-01 | AF102855.2 | NT | RIBOSOMAL PROTEIN S4 (HUMAN); contains TAR1 t3 TAR1 repetitive element ; |
| 9852 | 22788 | 36241 | 0.54 | 1.0E-01 | R44893.1 | EST_HUMAN | Rattus norvegicus synaptic SAPAP-interacting protein Synanon mRNA, complete cds |
| 9865 | 22801 | | 2.05 | 1.0E-01 | M76728.1 | NT | Y033H04.s1 Soares infant brain INIB Homo sapiens cDNA clone IMAGE:34549 3' |
| 9908 | 22729 | | 2.65 | 1.0E-01 | AE001501.1 | NT | Human pro-alpha-1 (V) collagen mRNA, complete cds |
| 9922 | 22806 | 36259 | 0.61 | 1.0E-01 | W01955.1 | EST_HUMAN | Helicobacter pylori, strain J99 section 62 of 132 of the complete genome |
| 10180 | 23105 | 36588 | 1.83 | 1.0E-01 | BF240154.1 | EST_HUMAN | z066c10.s1 Soares fetal heart NBH19W Homo sapiens cDNA clone IMAGE:327282 3' |
| 10285 | 23220 | 36703 | 9.1 | 1.0E-01 | AB046769.1 | NT | 601905661F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133487 5' |
| 10295 | 23220 | 36704 | 9.1 | 1.0E-01 | AB046769.1 | NT | Homo sapiens mRNA for KIAA1579 protein, partial cds |
| 10502 | 23424 | | 0.95 | 1.0E-01 | AW957425.1 | EST_HUMAN | Homo sapiens mRNA for KIAA1579 protein, partial cds |
| 10507 | 23428 | 36926 | 0.55 | 1.0E-01 | T51952.1 | EST_HUMAN | EST1369615 IMAGE resequences, IMAGE Homo sapiens cDNA |
| 10604 | 23616 | 37110 | 0.89 | 1.0E-01 | BE792750.1 | EST_HUMAN | Y028a06.s1 Stralagene fetal spleen (#637205) Homo sapiens cDNA clone IMAGE:72562 3' similar to contains Alu repetitive element |
| 11018 | 23983 | | 1.65 | 1.0E-01 | AU159127.1 | EST_HUMAN | 601584604F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3939096 5' |
| 11370 | 24317 | 37844 | 2.25 | 1.0E-01 | BF242946.1 | EST_HUMAN | AU159127 THYROT1 Homo sapiens cDNA clone THYROT100895 3' |
| 11370 | 24317 | 37845 | 2.25 | 1.0E-01 | BF242946.1 | EST_HUMAN | 601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5' |
| 11728 | 24614 | 38191 | 3.16 | 1.0E-01 | BE790543.1 | EST_HUMAN | 601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5' |
| 12365 | 25481 | | 4.11 | 1.0E-01 | BE37719.1 | EST_HUMAN | 601582556F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936734 5' |
| 12588 | 25292 | | 2.18 | 1.0E-01 | 7662165 | NT | 601065554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451833 5' |
| 12804 | 25305 | | 2.58 | 1.0E-01 | X00854.1 | NT | Homo sapiens KIAA0514 gene product (KIAA0514), mRNA |
| 12798 | 25425 | | 1.45 | 1.0E-01 | AA737961.1 | EST_HUMAN | Drosophila melanogaster fiz gene |
| 12895 | 25481 | | 4.47 | 1.0E-01 | BE37719.1 | EST_HUMAN | inx11c08.s1 NCL CGAP_GC3 Homo sapiens cDNA clone IMAGE:1255780 3' |
| 12943 | 25522 | | 1.32 | 1.0E-01 | BE158905.1 | EST_HUMAN | 601065554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451833 5' |
| 12959 | 25891 | | 6.14 | 1.0E-01 | U66834.1 | NT | QV4-HT0401-211299-064-gp3 HT0401 Homo sapiens cDNA |
| 13016 | 25566 | | 7.59 | 1.0E-01 | AP001507.1 | NT | Saccharomyces cerevisiae suppressor of ABF1 (SAB2) gene, complete cds |
| 2789 | 15781 | 28797 | 1.74 | 9.9E-02 | AF274008.1 | NT | Bacillus halodurans genomic DNA, section 1/14 |
| 2798 | 15790 | 28808 | 1.71 | 9.9E-02 | BE545554.1 | EST_HUMAN | Drosophila melanogaster cAMP-dependent protein kinase type II regulatory subunit (pke-R11) mRNA, complete cds |
| 2798 | 15790 | 28809 | 1.71 | 9.9E-02 | BE545554.1 | EST_HUMAN | 601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5' |
| 3280 | 16334 | 29254 | 1.48 | 9.9E-02 | AF09810.1 | NT | 601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5' |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 3974 | 17014 | 29928 | 0.67 | 9.9E-02 | AB21637.1 | EST_HUMAN | z145c03.x5 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740932 3' |
| 4707 | 17728 | 30622 | 1.02 | 9.8E-02 | BE674249.1 | EST_HUMAN | 7d77c12.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3278988 3' |
| 7044 | 20096 | 33373 | 2.69 | 9.8E-02 | BE613498.1 | EST_HUMAN | 601504252F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906084 5' |
| 7163 | 18394 | 31239 | 7.77 | 9.8E-02 | D83710.1 | NT | Aspergillus terreus BSD mRNA for blasticidin S deaminase, complete cds |
| 8247 | 21216 | 34624 | 0.65 | 9.9E-02 | AW103088.1 | EST_HUMAN | xd43c09.x1 NCL_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2596528 3' similar to contains Alu repetitive element; contains element MIR MIR repetitive element ; |
| 8247 | 21216 | 34625 | 0.65 | 9.9E-02 | AW103088.1 | EST_HUMAN | xd43c09.x1 NCL_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2596528 3' similar to contains Alu repetitive element; contains element MIR MIR repetitive element ; |
| 9612 | 22616 | 36068 | 1.23 | 9.9E-02 | 6755111 | NT | Mus musculus phospholipid transfer protein (Pltp), mRNA |
| 665 | 13635 | | 1.88 | 9.8E-02 | X56338.1 | NT | O. sativa RAMP3C gene for alpha-amyase |
| 3160 | 16216 | 28130 | 4.25 | 9.8E-02 | AF184274.1 | NT | Daucus carota leucoanthocyanidin dioxygenase 2 (LDOX) mRNA, LDOX-2 allele, complete cds |
| 4251 | 17280 | 30160 | 6.93 | 9.8E-02 | AF257329.1 | NT | Leptospira maculans beta-tubulin mRNA, complete cds |
| 4251 | 17280 | 30161 | 6.93 | 9.8E-02 | AF257329.1 | NT | Leptospira maculans beta-tubulin mRNA, complete cds |
| 7723 | 20879 | | 0.94 | 9.8E-02 | X54133.1 | NT | Human HPTP delta mRNA for protein tyrosine phosphatase delta |
| 9609 | 22613 | | 1.21 | 9.8E-02 | M61943.1 | NT | Human laminin B1 chain gene, exon 26 |
| 11798 | 23943 | 37465 | 1.83 | 9.8E-02 | BF037421.1 | EST_HUMAN | 601460793F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3864287 5' |
| 12330 | 25131 | | 1.84 | 9.8E-02 | 8393751 | NT | Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA |
| 1352 | 14387 | 27357 | 1.75 | 9.7E-02 | AB005808.1 | NT | Aloe arborescens mRNA for NADP-malic enzyme, complete cds |
| 1589 | 14621 | | 1.33 | 9.7E-02 | 4503710 | NT | Homo sapiens fibroblast growth factor receptor 3 (echondroplasia, thanatophoric dwarfism) (FGFR3) mRNA |
| 2270 | 15283 | 28309 | 2.78 | 9.7E-02 | BE168660.1 | EST_HUMAN | QV1-HT0516-070300-085-a04 HT0516 Homo sapiens cDNA |
| 4008 | 17047 | | 4.89 | 9.7E-02 | Q99795 | SWISSPROT | CELL SURFACE A33 ANTIGEN PRECURSOR (GLYCOPROTEIN A33) |
| 5418 | 18521 | 31398 | 0.88 | 9.7E-02 | AF099189.1 | NT | Caulobacter crescentus thymidylate kinase (tnk) and DNA polymerase III delta prime subunit (dnaC) genes, complete cds |
| 5418 | 18521 | 31399 | 0.88 | 9.7E-02 | AF099189.1 | NT | Caulobacter crescentus thymidylate kinase (tnk) and DNA polymerase III delta prime subunit (dnaC) genes, complete cds |
| 6130 | 19207 | 32432 | 1.48 | 9.7E-02 | AW0954476.1 | EST_HUMAN | EST366546 MAGC resequences, MAGC Homo sapiens cDNA |
| 7617 | 20482 | 33843 | 3.36 | 9.7E-02 | Z99119.1 | NT | Bacillus subtilis complete genome (section 18 of 21): from 2997771 to 3213410 |
| 8315 | 21284 | 34697 | 1.09 | 9.7E-02 | N22798.1 | EST_HUMAN | yw41c03.s1 Weizmann Offactory Epithelium Homo sapiens cDNA clone IMAGE:254788 3' |
| 8315 | 21284 | 34698 | 1.09 | 9.7E-02 | N22798.1 | EST_HUMAN | yw41c03.s1 Weizmann Offactory Epithelium Homo sapiens cDNA clone IMAGE:254788 3' |
| 9201 | 22187 | 35597 | 1.52 | 9.7E-02 | AI955984.1 | EST_HUMAN | yw41c03.s1 Weizmann Offactory Epithelium Homo sapiens cDNA clone IMAGE:254788 3' |
| 11529 | 24470 | | 2.01 | 9.7E-02 | U58337.1 | NT | PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (HUMAN); |
| 2032 | 15051 | 28066 | 1.27 | 9.6E-02 | AI080721.1 | EST_HUMAN | wk78b06.x1 NCL_CGAP_Ov38 Homo sapiens cDNA clone IMAGE:2549747 3' similar to gb:X52851_rna1 |
| | | | | | | | Mus musculus ligatin (Lgtin) mRNA, partial cds |
| | | | | | | | oz47d11.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1678495 3' |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 2032 | 15051 | 28067 | 1.27 | 9.6E-02 | AI080721.1 | EST_HUMAN | 0247d11.x1 Soares_NhMPu_S1 Homo sapiens cDNA clone IMAGE:1678485 3' |
| 4372 | 17399 | 30279 | 6.7 | 9.6E-02 | Z32686.2 | NT | Proteus mirabilis fimbrial operon, strain HI4320 |
| 5037 | 18050 | 30830 | 1.16 | 9.6E-02 | AW066230.1 | EST_HUMAN | EST378303 IMAGE resequences, MAGI Homo sapiens cDNA |
| 6225 | 19299 | | 2.63 | 9.6E-02 | BE910039.1 | EST_HUMAN | 607498088F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3900165 5' |
| 8719 | 21687 | | 0.85 | 9.6E-02 | AU137084.1 | EST_HUMAN | AU137084 PLACE1 Homo sapiens cDNA clone PLACE1005740 5' |
| 9902 | 22854 | 36315 | 1.35 | 9.6E-02 | AV687898.1 | EST_HUMAN | AV687898 GKC Homo sapiens cDNA clone GKCAAH02 5' |
| 10231 | 23156 | | 1.29 | 9.6E-02 | BE894895.1 | EST_HUMAN | 607434080F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918363 5' |
| 10399 | 23321 | 36805 | 1.27 | 9.6E-02 | AJ243211.1 | NT | Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55 |
| 10399 | 23321 | 36806 | 1.27 | 9.6E-02 | AJ243211.1 | NT | Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55 |
| 10479 | 23401 | 36898 | 0.44 | 9.6E-02 | BF677270.1 | EST_HUMAN | 602086798F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4280969 5' |
| 10511 | 23433 | 36930 | 1.37 | 9.6E-02 | AB013985.1 | NT | Anthrimum majus transposon Tam3 pseudogene for transposase (in S-6 copy) |
| 10511 | 23433 | 36931 | 1.37 | 9.6E-02 | AB013985.1 | NT | Anthrimum majus transposon Tam3 pseudogene for transposase (in S-6 copy) |
| 10621 | 23543 | 37043 | 3.5 | 9.6E-02 | P08174 | SWISSPROT | COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR (CD55) |
| 11094 | 24054 | 37577 | 5.31 | 9.6E-02 | Z78702.1 | NT | Mycobacterium tuberculosis H37Rv complete genome, segment 102/162 |
| 12028 | 24904 | 38498 | 1.53 | 9.6E-02 | AA625755.1 | EST_HUMAN | zu91g01.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:745392 3' |
| 12933 | 25515 | | 1.81 | 9.6E-02 | H14599.1 | EST_HUMAN | ym19h03.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:48653 3' |
| 12995 | 25553 | 31719 | 1.51 | 9.6E-02 | BE728219.1 | EST_HUMAN | 607583355F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3832908 5' |
| 4128 | 17181 | 30050 | 2.66 | 9.5E-02 | AW992395.1 | EST_HUMAN | CM2-BN0023-050200-087-f12 BN0023 Homo sapiens cDNA |
| 5748 | 18942 | 32025 | 0.81 | 9.5E-02 | P51854 | SWISSPROT | TRANSKETOLASE 2 (TK 2) (TRANSKETOLASE RELATED PROTEIN) |
| 7294 | 20266 | 33601 | 0.51 | 9.5E-02 | AA780728.1 | EST_HUMAN | ac88a09.s1 Stragene fetal retina 937202 Homo sapiens cDNA clone IMAGE:867736 3' |
| 7522 | 20487 | 33849 | 4.14 | 9.5E-02 | AB003473.1 | NT | Trimeresurus flavoviridis DNA for phospholipase A2 inhibitor, complete cds |
| 7818 | 20767 | 34144 | 7.16 | 9.5E-02 | AL161538.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38 |
| 7963 | 18942 | 32025 | 0.89 | 9.5E-02 | P51854 | SWISSPROT | TRANSKETOLASE 2 (TK 2) (TRANSKETOLASE RELATED PROTEIN) |
| 8212 | 21181 | 34591 | 2.85 | 9.5E-02 | BF035961.1 | EST_HUMAN | 607453642F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3857243 5' |
| 8212 | 21181 | 34592 | 2.85 | 9.5E-02 | BF035961.1 | EST_HUMAN | 607453642F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3857243 5' |
| 11039 | 24003 | 37628 | 2.31 | 9.5E-02 | BF035861.1 | EST_HUMAN | 607453642F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3857243 5' |
| 11039 | 24003 | 37628 | 2.31 | 9.5E-02 | BF035861.1 | EST_HUMAN | 607453642F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3857243 5' |
| 1850 | 14876 | 27871 | 4.07 | 9.4E-02 | BF671063.1 | EST_HUMAN | 602150882F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4281917 5' |
| 3894 | 16334 | 29844 | 4.91 | 9.4E-02 | Z33039.1 | NT | M.capricolum DNA for CONTIG MC073 |
| 5240 | 18248 | | 0.96 | 9.4E-02 | X98106.1 | NT | Lactobacillus bacteriophage phi1e complete genomic DNA |
| 6450 | 19515 | 32766 | 1.21 | 9.4E-02 | AF097363.1 | NT | Triticum aestivum heat shock protein 101 (Hsp101a) mRNA, complete cds |
| 7851 | 20797 | 34173 | 0.54 | 9.4E-02 | L78833.1 | NT | Human BRCA1, Rho7 and val genes, complete cds, and lpf35 gene, partial cds |
| 8947 | 21913 | | 2.5 | 9.4E-02 | Z46883.1 | NT | Acinetobacter sp. cysD, cobQ, cobQ, sodM, lysS, rubA, rubB, estB, oxyR, ppk, mtgA, ORF2 and ORF3 genes |

Table 4

Single Exon Probes Expressed In Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 11280 | 20797 | 34173 | 2.22 | 9.4E-02 | L78833.1 | NT | Human BRCA1, Rho7 and vcl genes, complete cds, and p135 gene, partial cds |
| 12212 | 25826 | | 10.73 | 9.4E-02 | U31815.1 | NT | Rattus norvegicus calcium channel alpha-1C subunit (ROB2) mRNA, partial cds |
| 13087 | 25817 | 31692 | 1.37 | 9.4E-02 | U27699.1 | NT | Human pectin-BGT-1 betaine-GABA transporter mRNA, complete cds |
| 3002 | 16060 | | 1.71 | 9.3E-02 | 4809280 | NT | Homo sapiens BAI1-associated protein 3 (BAIAP3) mRNA |
| 3041 | 16099 | | 7.39 | 9.3E-02 | 6912525 | NT | Homo sapiens nasopharyngeal epithelium specific protein 1 (NESG1), mRNA |
| 3270 | 16324 | 29247 | 2.01 | 9.3E-02 | BF575511.1 | EST_HUMAN | 602133086F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288269 5' |
| 4179 | 17210 | 30096 | 3.73 | 9.3E-02 | BE391943.1 | EST_HUMAN | 601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5' |
| 4179 | 17210 | 30097 | 3.73 | 9.3E-02 | BE391943.1 | EST_HUMAN | 601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5' |
| 4768 | 17798 | | 2.29 | 9.3E-02 | AV732224.1 | EST_HUMAN | AV732224 HTF Homo sapiens cDNA clone HTFAUA06 5' |
| 6745 | 18839 | | 0.68 | 9.3E-02 | AP001507.1 | NT | Bacillus halodurans genomic DNA, section 1/14 |
| 8153 | 21091 | 34490 | 0.59 | 9.3E-02 | AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C010 |
| 8591 | 21559 | 34875 | 0.6 | 9.3E-02 | AW566007.1 | EST_HUMAN | EST169 Human Fetal Brain MATCHMAKER cDNA Library Homo sapiens cDNA |
| 9480 | 22444 | | 0.42 | 9.3E-02 | AL113179.1 | NT | Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation |
| 10088 | 22995 | 36484 | 2.32 | 9.3E-02 | BE92831.2 | EST_HUMAN | 601655888F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855581 3' |
| 10551 | 23473 | 36987 | 3.65 | 9.3E-02 | Q15034 | SWISSPROT | HYPOTHETICAL PROTEIN KIAA0032 |
| 10551 | 23473 | 36988 | 3.65 | 9.3E-02 | Q15034 | SWISSPROT | HYPOTHETICAL PROTEIN KIAA0032 |
| 10883 | 23605 | | 3.59 | 9.3E-02 | AW206117.1 | EST_HUMAN | U1-H-B11-afx-h-05-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2723553 3' |
| 12482 | 25750 | | 2.55 | 9.3E-02 | AJ249850.1 | NT | Photobacterium damsela subsp. damsela partial gyrB gene for DNA gyrase B subunit |
| 12831 | 25778 | | 9.12 | 9.3E-02 | AW468850.1 | EST_HUMAN | hd28h12.x1 Soares_NFL_T_OBC_S1 Homo sapiens cDNA clone IMAGE:2910887 3' |
| | | | | | | | Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; BING1 (BING1), tapasin (tapasin), RalGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3-galactosyl transferase (beta1, 3-galactosyl tr> |
| 13040 | 25824 | | 2.24 | 9.3E-02 | AF100956.1 | NT | galactosyl transferase (beta1, 3-galactosyl tr> |
| 231 | 13331 | 26252 | 7.81 | 9.2E-02 | U60315.1 | NT | Molluscum contagiosum virus subtype 1, complete genome |
| 231 | 13331 | 26253 | 7.81 | 9.2E-02 | U60315.1 | NT | Molluscum contagiosum virus subtype 1, complete genome |
| 231 | 13331 | 26254 | 7.81 | 9.2E-02 | U60315.1 | NT | Molluscum contagiosum virus subtype 1, complete genome |
| 2236 | 15250 | | 2.72 | 9.2E-02 | R54156.1 | EST_HUMAN | y9807.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:41618 5' |
| 3194 | 16249 | 29167 | 3.72 | 9.2E-02 | Q28631 | SWISSPROT | MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20) |
| 3316 | 16369 | 29289 | 0.99 | 9.2E-02 | AA534354.1 | EST_HUMAN | nt79e01.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:926136 3' |
| 3599 | 16844 | | 1.27 | 9.2E-02 | 6755215 | NT | Mus musculus pre T-cell antigen receptor alpha (Pctra), mRNA |
| 4266 | 17295 | | 1.24 | 9.2E-02 | U92048.1 | NT | Human herpesvirus 1 strain KOS-63, latency-associated transcript, promoter region |
| 4337 | 17364 | | 0.94 | 9.2E-02 | BE29722.1 | EST_HUMAN | 600944365F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960176 5' |
| 4668 | 17689 | 30575 | 1.4 | 9.2E-02 | X96402.1 | NT | G. gallus Mia-CK gene |
| | | | | | | | y99c09.r1 Stralagene placenta (#937225) Homo sapiens cDNA clone IMAGE:69808 5' similar to similar to |
| 8342 | 21311 | 34725 | 1.87 | 9.2E-02 | T49920.1 | EST_HUMAN | gb:X56009 GUANINE NUCLEOTIDE-BINDING PROTEIN G(S), ALPHA SUBUNIT (HUMAN) |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 8517 | 21485 | 34899 | 2.19 | 9.2E-02 | X95256.1 | NT | H.vulgaris xylose isomerase gene |
| 12002 | 24879 | 38475 | 1.74 | 9.2E-02 | AF026552.3 | NT | Mesocricetus auratus oviductin precursor (OVI) gene, complete cds |
| 13019 | 25986 | | 1.31 | 9.2E-02 | 11468872 | NT | Podiceps arseinina mitochondrion, complete genome |
| 423 | 13118 | 26017 | 7.62 | 9.1E-02 | X77665.1 | NT | O. cuniculus K12 keratin gene |
| 3694 | 16727 | | 0.96 | 9.1E-02 | AW372569.1 | EST_HUMAN | PM2-BT0349-161296-001-02 BT0349 Homo sapiens cDNA |
| 4510 | 17535 | 30419 | 1.5 | 9.1E-02 | AL161554.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 54 |
| 5304 | 18307 | | 0.98 | 9.1E-02 | AB010896.1 | NT | Giona intestinalis endostyle-specific mRNA, complete cds |
| 5819 | 18909 | 32093 | 1.27 | 9.1E-02 | AF129756.1 | NT | Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G5b, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, 1C7, TNF, and LTA genes, complete cds |
| 7528 | 26000 | | 0.52 | 9.1E-02 | AF029308.1 | NT | Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families |
| 7616 | 20576 | 33939 | 12.92 | 9.1E-02 | AW160658.1 | EST_HUMAN | au74e05.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781968 5' |
| 7937 | 20879 | 34269 | 0.74 | 9.1E-02 | AP000091.1 | NT | Aeropyrum pernix genomic DNA, section 4/7 |
| 7977 | 20916 | 34307 | 0.87 | 9.1E-02 | U39073.1 | NT | Mus musculus thymopoietin zeta mRNA, complete cds |
| 9276 | 22242 | 35671 | 0.95 | 9.1E-02 | Y14379.1 | NT | Homo sapiens gamma adducin gene, exon 9 |
| 10793 | 23714 | | 1.84 | 9.1E-02 | T02984.1 | EST_HUMAN | FB19F10 Fetal brain, Strategene Homo sapiens cDNA clone FB19F10 3' end |
| 10823 | 23744 | 37245 | 1.24 | 9.1E-02 | S74059.1 | NT | Tg916=Cyl actin [Tripneustes gratilla=sea urchins, embryos, Genomic, 5275 nt] |
| 10852 | 23772 | 37271 | 0.8 | 9.1E-02 | Y11187.1 | NT | A.thaliana RH1, TC1, G14587-5, G14587-6, and PRL1 genes |
| 12151 | 25009 | | 3.53 | 9.1E-02 | 9633494 | NT | Bacteriophage Mu, complete genome |
| 12393 | 25919 | | 2.15 | 9.1E-02 | AA179901.1 | EST_HUMAN | zp38h12.s1 Strategene muscle 937209 Homo sapiens cDNA clone IMAGE:611783 3' similar to |
| 12468 | 25217 | | 1.82 | 9.1E-02 | AF052695.1 | NT | SW:TRT3_HUMAN P45378 TROPONIN T, FAST SKELETAL MUSCLE, ISOFORM BETA ; |
| 12916 | 25771 | | 1.78 | 9.1E-02 | AJ291390.1 | NT | Rattus norvegicus cell cycle protein p55CDC gene, complete cds |
| 746 | 13807 | 26747 | 6.38 | 9.0E-02 | P16328 | SWISSPROT | Homo sapiens partial MUC3B gene for MUC3B much, exons 1-11 |
| 1640 | 14672 | 27645 | 6.7 | 9.0E-02 | BE220482.1 | EST_HUMAN | FOLATE RECEPTOR ALPHA PRECURSOR (FR-ALPHA) (FOLATE RECEPTOR 1) (FOLATE RECEPTOR, ADULT) (ADULT FOLATE-BINDING PROTEIN) (FBP) (OVARIAN TUMOR-ASSOCIATED ANTIGEN MOV18) (KB CELLS FBP) |
| 2815 | 15807 | 28826 | 6.5 | 9.0E-02 | AF138522.1 | NT | h3ag10.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175842 3' similar to contains Alu repetitive element |
| 2815 | 15807 | 28827 | 6.5 | 9.0E-02 | AF138522.1 | NT | HIV-1 p8c095-06 from USA envelope glycoprotein (env) gene, partial cds |
| 3347 | 16398 | 29321 | 1.11 | 9.0E-02 | AF279135.1 | NT | HIV-1 p8c095-06 from USA envelope glycoprotein (env) gene, partial cds |
| 4328 | 17356 | 30243 | 0.83 | 9.0E-02 | S68757.1 | NT | Dicystostium discoidum spore coat structural protein SP65 (cotE) gene, complete cds |
| 4328 | 17356 | 30244 | 0.83 | 9.0E-02 | S68757.1 | NT | corticosteroid-binding globulin [Saimiri sciureus=squirrel monkeys, liver, mRNA, 1474 nt] |
| 4328 | 17356 | 30244 | 0.83 | 9.0E-02 | S68757.1 | NT | corticosteroid-binding globulin [Saimiri sciureus=squirrel monkeys, liver, mRNA, 1474 nt] |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|-----------------------------|-------------------------------|---|
| 4448 | 17474 | 30363 | 1.25 | 9.0E-02 | P55268 | SWISSPROT | LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) |
| 4695 | 17716 | 30611 | 2.37 | 9.0E-02 | X65740.2 | NT | Plasmodium falciparum P-type ATPase 3 gene |
| 5281 | 18289 | 31137 | 0.93 | 9.0E-02 | Q24597 | SWISSPROT | REGULATORY PROTEIN ZESTE |
| 6110 | 19189 | 32409 | 14.12 | 9.0E-02 | W56037.1 | EST_HUMAN | za68a12.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:297694 5' similar to PIR:S52171 S52171 small G protein - human ; |
| 6880 | 19932 | | 1.14 | 9.0E-02 | BF062651.1 | EST_HUMAN | 7h63d03.x1 NCI_CGAP_C016 Homo sapiens cDNA clone IMAGE:3320845 3' similar to contains Alu repetitive element; |
| 6931 | 20155 | 33473 | 0.88 | 9.0E-02 | R82805.1 | EST_HUMAN | y11b08.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138903 3' |
| 12762 | 25404 | | 2.03 | 9.0E-02 | AF022236.1 | NT | Escherichia coli strain E2348/69 pathogenicity island, rOrf1 (rOrf1), rOrf2 (rOrf2), EscR (escR), EscS (escS), EscT (escT), EscU (escU), CsdD (cesD), EscC (escC), EscJ (escJ), SepZ (sepZ), EscV (escV), EscN (escN), SepQ (sepQ), Tir (tir), OrfU (orfU), > |
| 1432 | 14466 | 27442 | 2.04 | 8.9E-02 | BF701593.1 | EST_HUMAN | 602128030F2 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4285951 5' |
| 1432 | 14466 | 27443 | 2.04 | 8.9E-02 | BF701593.1 | EST_HUMAN | 602128030F2 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4285951 5' |
| 2396 | 15403 | 28429 | 1.1 | 8.9E-02 | BE153572.1 | EST_HUMAN | PMO-HT0339-251199-003-d01 HT0339 Homo sapiens cDNA |
| 4227 | 17258 | | 2 | 8.9E-02 | AF280655.1 | NT | Atrichum angustatum AvranFlo2 protein (AtranFlo2) gene, partial cds |
| 5950 | 19036 | 32230 | 2.64 | 8.9E-02 | AW452122.1 | EST_HUMAN | UI-H-B13-alo-f-08-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3088294 3' |
| 5950 | 19036 | 32231 | 2.64 | 8.9E-02 | AW452122.1 | EST_HUMAN | UI-H-B13-alo-f-08-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3088294 3' |
| 5968 | 19051 | 32252 | 3.5 | 8.9E-02 | 11433478 | NT | Homo sapiens similar to endoglycan (H. sapiens) (LOC83107), mRNA |
| 7399 | 20367 | 33720 | 1.49 | 8.9E-02 | P47259 | SWISSPROT | FOLD BIFUNCTIONAL PROTEIN [INCLUDES: METHYLENETETRAHYDROFOLATE DEHYDROGENASE; METHENYL-TETRAHYDROFOLATE CYCLOHYDROLASE] |
| 7807 | 20757 | | 2.02 | 8.9E-02 | Z79021.1 | NT | H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA20F8 |
| 8385 | 21354 | 34762 | 0.77 | 8.9E-02 | P29475 | SWISSPROT | NITRIC-OXIDE SYNTHASE, BRAIN (NOS, TYPE I) (NEURONAL NOS) (N-NOS) (NNOS) |
| 8468 | 21437 | 34855 | 0.7 | 8.9E-02 | BF701665.1 | EST_HUMAN | (CONSTITUTIVE NOS) (NC-NOS) (BNOS) |
| 8468 | 21437 | 34856 | 0.7 | 8.9E-02 | BF701665.1 | EST_HUMAN | 60212911F2 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4285827 5' |
| 8845 | 21911 | 35336 | 5.01 | 8.9E-02 | AA309319.1 | EST_HUMAN | 60212911F2 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4285827 5' |
| 9978 | 22905 | 36369 | 0.62 | 8.9E-02 | A1285827.1 | EST_HUMAN | EST180167 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end |
| 9978 | 22905 | 36370 | 0.62 | 8.9E-02 | A1285827.1 | EST_HUMAN | qu55c05.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1988680 3' similar to contains MER10.b1 MER10 repetitive element ; |
| 10090 | 23018 | 36492 | 0.67 | 8.9E-02 | AA339358.1 | EST_HUMAN | qu55c05.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1988680 3' similar to contains MER10.b1 MER10 repetitive element ; |
| 12150 | 25743 | | 1.3 | 8.9E-02 | P30143 | SWISSPROT | EST44454 Fetal brain I Homo sapiens cDNA 5' end |
| 12211 | 25778 | | 1.91 | 8.9E-02 | P19524 | SWISSPROT | HYPOTHETICAL 51.7 KD PROTEIN IN THRC-TALB INTERGENIC REGION (ORF8) |
| 12367 | 25154 | | 9.08 | 8.9E-02 | BF695918.1 | EST_HUMAN | MYOSIN-2 ISOFORM |
| | | | | | | | 602129682F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286180 5' |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 12530 | 25258 | | 1.81 | 8.9E-02 | 6680220 | NT | Mus musculus hippocampus abundant gene transcript 1 (Hiat1), mRNA |
| 12571 | 25282 | | 1.5 | 8.9E-02 | U28895.1 | NT | Human 4-hydroxyphenylpyruvate-dioxygenase gene, complete cds |
| 1374 | 14408 | 27378 | 1.25 | 8.8E-02 | Q27474 | SWISSPROT | PROBABLE DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE (ATP)) |
| 3921 | 16961 | 28874 | 1.03 | 8.8E-02 | AA299128.1 | EST_HUMAN | EST11695 Uterus Homo sapiens cDNA 5' end |
| 4065 | 17101 | | 3.7 | 8.8E-02 | O00268 | SWISSPROT | TRANSCRIPTION INITIATION FACTOR TFIIID 135 KDA SUBUNIT (TAFII135) (TAFII-130) (TAFII130) |
| 4267 | 17296 | | 1.26 | 8.8E-02 | 4502804 | NT | Homo sapiens chromogranin A (parathyroid secretory protein 1) (CHGA) mRNA |
| 4331 | 17359 | | 2.3 | 8.8E-02 | 4580423 | NT | Homo sapiens paired box gene 6 (entitidia, keratitidis) (PAX6), isoform b, mRNA |
| 7792 | 20744 | | 0.86 | 8.8E-02 | D17520.1 | NT | Sheep mRNA for angiotensinogen, complete cds |
| 9339 | 22304 | 35732 | 1.32 | 8.8E-02 | AA151872.1 | EST_HUMAN | z198a05.s1 Stratagene colon (#837204) Homo sapiens cDNA clone IMAGE:566288 3' |
| 11453 | 24396 | 37941 | 3.43 | 8.8E-02 | BE264455.1 | EST_HUMAN | 601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5' |
| 11453 | 24396 | 37942 | 3.43 | 8.8E-02 | BE264455.1 | EST_HUMAN | 601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5' |
| 11593 | 24531 | 38088 | 5.78 | 8.8E-02 | AL040129.1 | EST_HUMAN | DKFZp434D1313_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434D1313 5' |
| 12441 | 25204 | 31827 | 2.4 | 8.8E-02 | Z71561.1 | NT | S.cerevisiae chromosome XIV reading frame ORF YNL285w |
| 1654 | 14686 | 27661 | 1.55 | 8.7E-02 | AI167281.1 | EST_HUMAN | α65k01.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1661161 3' |
| 3707 | 16750 | 29665 | 3.84 | 8.7E-02 | U82695.2 | NT | Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds |
| 3707 | 16750 | 29666 | 3.84 | 8.7E-02 | U82695.2 | NT | Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds |
| 4736 | 17756 | 30650 | 1.2 | 8.7E-02 | AF178636.1 | NT | Mus musculus JNK interacting protein-3a (Jip3) mRNA, complete cds |
| 5138 | 18147 | | 1.02 | 8.7E-02 | AE000895.1 | NT | Methanobacterium thermoautotrophicum from bases 1176181 to 1189406 (section 101 of 148) of the complete genome |
| 5166 | 18175 | 31053 | 0.97 | 8.7E-02 | 6563384 | NT | Homo sapiens protein kinase C, nu (PRKCN), mRNA |
| 5387 | 18490 | 31365 | 6.04 | 8.7E-02 | AA286875.1 | EST_HUMAN | zs55g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3' |
| 5387 | 18490 | 31366 | 6.04 | 8.7E-02 | AA286875.1 | EST_HUMAN | zs55g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3' |
| 7022 | 20147 | 33466 | 0.81 | 8.7E-02 | AJ271885.2 | NT | Mus musculus partial Kcnq1 gene for potassium channel protein, exons 10-14 |
| 7022 | 20147 | 33467 | 0.81 | 8.7E-02 | AJ271885.2 | NT | Mus musculus partial Kcnq1 gene for potassium channel protein, exons 10-14 |
| 7243 | 19978 | 33275 | 0.83 | 8.7E-02 | AF281342.1 | NT | Oncorhynchus mykiss TAT-binding protein 1 mRNA, partial cds |
| 8860 | 21827 | 35250 | 0.71 | 8.7E-02 | AE004787.1 | NT | Pseudomonas aeruginosa PAO1, section 348 of 529 of the complete genome |
| 8860 | 21827 | 35251 | 0.71 | 8.7E-02 | AE004787.1 | NT | Pseudomonas aeruginosa PAO1, section 348 of 529 of the complete genome |
| 11067 | 24030 | | 2.15 | 8.7E-02 | L04758.1 | NT | Oryctolagus cuniculus cytochrome P-450 (CYP4A4) gene, 5' end |
| 11641 | 24578 | 38144 | 1.79 | 8.7E-02 | AJ007763.1 | NT | Gluconobacter oxydans tRNA-Ile and tRNA-Ala genes |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 12123 | 24992 | 38593 | 1.89 | 8.7E-02 | Z74060.1 | NT | S.cerevisiae chromosome IV reading frame ORF YDL012c |
| 12123 | 24992 | 38594 | 1.89 | 8.7E-02 | Z74060.1 | NT | S.cerevisiae chromosome IV reading frame ORF YDL012c |
| 12428 | 25196 | | 1.6 | 8.7E-02 | X17116.1 | NT | Human DNA for immunoglobulin alpha heavy chain from a case of alpha heavy chain disease |
| 1257 | 14292 | 27256 | 6.2 | 8.6E-02 | A1271736.1 | NT | Human sapiens Xq pseudautosomal region; segment 2/2 |
| 2256 | 15270 | 28295 | 1.96 | 8.6E-02 | BE408667.1 | EST_HUMAN | 601304076F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638843 5' |
| 3202 | 16257 | 29176 | 4.47 | 8.6E-02 | L05468.1 | NT | Trichomonas vaginalis beta-tubulin (btub1) gene, complete cds |
| 3658 | 18701 | | 4.37 | 8.6E-02 | AF153362.1 | NT | Dictyostelium discoideum adenyl cyclase (acrA) gene, complete cds |
| 3793 | 18834 | | 0.66 | 8.6E-02 | U29187.1 | NT | Mus musculus long incubation prion protein (Prnpb) and prion-like protein (Prnd) genes, complete cds |
| 4512 | 17537 | 30421 | 0.87 | 8.6E-02 | U68179.1 | NT | Oryctolagus cuniculus galectin-3 gene, untranslated exon and 5' flanking region |
| 5170 | 18179 | | 1.09 | 8.6E-02 | L13419.1 | NT | Chromatium vinosum tetraheme cytochrome c gene, 3' end, bacterial ankyrin homologue, flavocytochrome c heme subunit fccA (complete cds), and flavin subunit, fccB (3' end) |
| 5276 | 19282 | | 1.09 | 8.6E-02 | AB011163.1 | NT | Homo sapiens mRNA for KIAA0591 protein, partial cds |
| 6213 | 19287 | 32520 | 4.24 | 8.6E-02 | Y10826.1 | NT | Homo sapiens LCN1b gene |
| 6510 | 19574 | 32828 | 1.48 | 8.6E-02 | J00440.1 | NT | Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a) |
| 6510 | 19574 | 32829 | 1.48 | 8.6E-02 | J00440.1 | NT | Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a) |
| 7834 | 20781 | 34159 | 1.01 | 8.6E-02 | P14616 | SWISSPROT | INSULIN RECEPTOR-RELATED PROTEIN PRECURSOR (IRR) (IR-RELATED RECEPTOR) |
| 8262 | 21231 | 34640 | 1.33 | 8.6E-02 | 5730066 | NT | Homo sapiens Snf2-related CBP activator protein (SRCAP) mRNA |
| 8405 | 21374 | 34782 | 0.66 | 8.6E-02 | 5730066 | NT | Homo sapiens Snf2-related CBP activator protein (SRCAP) mRNA |
| 8469 | 21438 | | 0.81 | 8.6E-02 | U60168.1 | NT | Homo sapiens hypothetical protein FLJ11006 (FLJ11006), mRNA |
| 10094 | 23020 | 36495 | 1.04 | 8.6E-02 | AF11170.3 | NT | Dictyostelium discoideum proteasome subunit C2 homolog PrtC (prtC) gene, complete cds |
| 10131 | 23057 | | 1.57 | 8.6E-02 | AW662153.1 | EST_HUMAN | Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene |
| 10513 | 23435 | 36933 | 0.97 | 8.6E-02 | AF026504.1 | NT | hi20c08.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972846 3' |
| 11579 | 24517 | 38072 | 2.47 | 8.6E-02 | BF305606.1 | EST_HUMAN | Rattus norvegicus SPA-1 like protein p1294 mRNA, complete cds |
| 11579 | 24517 | 38073 | 2.47 | 8.6E-02 | BF305606.1 | EST_HUMAN | 601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5' |
| 11767 | 23922 | 37441 | 9.23 | 8.6E-02 | AE001073.1 | NT | 601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5' |
| | | | | | | | Archaeoglobus fulgidus section 34 of 172 of the complete genome |
| | | | | | | | Bacillus stearothermophilus BsrFI methylase (Flm) and BsrFI restriction endonuclease (FIR) genes, complete cds |
| 11901 | 24782 | 38370 | 1.57 | 8.6E-02 | AF283680.1 | NT | Helicobacter pylori 26695 section 130 of 134 of the complete genome |
| 2406 | 15413 | 28437 | 2.86 | 8.6E-02 | AE000652.1 | NT | Helicobacter pylori 26695 section 130 of 134 of the complete genome |
| 5752 | 18848 | 32028 | 0.71 | 8.5E-02 | AA985491.1 | EST_HUMAN | q93b07.s1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:1692917 3' similar to gb:K01144 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, GAMMA CHAIN PRECURSOR (HUMAN); |
| 5793 | 18885 | | 1.92 | 8.5E-02 | P08089 | SWISSPROT | M PROTEIN, SEROTYPE 6 PRECURSOR |
| 6127 | 19205 | 32428 | 6.34 | 8.5E-02 | AF233885.1 | NT | Mus musculus phospholipase C-like protein mRNA, partial cds |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 8953 | 21919 | 35345 | 1.92 | 8.5E-02 | 6754779 | NT | Mus musculus myosin XV (Myo15), mRNA |
| 10198 | 23121 | 36807 | 3.17 | 8.5E-02 | BE833054.1 | EST_HUMAN | RC4-O10037-200700-014-e05 OT0037 Homo sapiens cDNA |
| 10196 | 23121 | 36808 | 3.17 | 8.5E-02 | BE833054.1 | EST_HUMAN | RC4-O10037-200700-014-e05 OT0037 Homo sapiens cDNA |
| 10338 | 23262 | 36742 | 0.44 | 8.5E-02 | AI140618.1 | EST_HUMAN | qs05g05.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1738136 3' |
| 10728 | 23650 | 37143 | 0.56 | 8.5E-02 | X76731.1 | NT | V. ammodontes gene for ammodontin C |
| 10851 | 23771 | 37270 | 1 | 8.5E-02 | 11418108 | NT | Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA |
| 11480 | 24433 | | 8.1 | 8.5E-02 | AF155510.1 | NT | Homo sapiens heparanase precursor, mRNA, complete cds |
| 11507 | 24449 | 37899 | 4.05 | 8.5E-02 | AB001562.1 | NT | Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds |
| 12985 | 25547 | | 5.18 | 8.5E-02 | AA362934.1 | EST_HUMAN | EST72736 Ovary II Homo sapiens cDNA 5' end |
| 2675 | 15901 | 28690 | 3.69 | 8.4E-02 | W69330.1 | EST_HUMAN | z044e11.1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:343532 5' |
| 4381 | 17409 | 30290 | 1.02 | 8.4E-02 | AF257213.1 | NT | Cavia porcellus glycoprotein alpha-subunit mRNA, complete cds |
| 4381 | 17409 | 30291 | 1.02 | 8.4E-02 | AF257213.1 | NT | Cavia porcellus glycoprotein alpha-subunit mRNA, complete cds |
| 5235 | 18243 | 31115 | 0.98 | 8.4E-02 | 5453817 | NT | Homo sapiens nucleobindin 1 (NUCB1), mRNA |
| 5385 | 18488 | 31363 | 8.74 | 8.4E-02 | BE267153.1 | EST_HUMAN | 601190436F1 NIH_MGC.7 Homo sapiens cDNA clone IMAGE:3534383 5' |
| 6847 | 19900 | 33194 | 1.86 | 8.4E-02 | AK024458.1 | NT | Homo sapiens mRNA for FLJ00050 protein, partial cds |
| 8363 | 21332 | 34744 | 7.84 | 8.4E-02 | BE095074.1 | EST_HUMAN | CM3-B T0790-260400-162-d05 B T0790 Homo sapiens cDNA |
| 9194 | 22160 | 35588 | 1.02 | 8.4E-02 | AF218890.1 | NT | Homo sapiens attractin precursor (ATRIN) gene, exon 2 |
| 10727 | 23649 | 37142 | 1.9 | 8.4E-02 | AI735184.1 | EST_HUMAN | as88g10.x1 Barstead codon HPLRB7 Homo sapiens cDNA clone IMAGE:2335842 3' similar to TR:O88312 |
| 12351 | 25146 | 31853 | 1.46 | 8.4E-02 | R79408.1 | EST_HUMAN | O88312 GOB-4; |
| 2027 | 15047 | 28060 | 0.97 | 8.3E-02 | 5835680 | NT | y83h12.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145895 5' |
| 2027 | 15047 | 28061 | 0.97 | 8.3E-02 | 5835680 | NT | Ixodes hexagonus mitochondrion, complete genome |
| 3608 | 16651 | 29568 | 6.11 | 8.3E-02 | P75334 | SWISSPROT | Ixodes hexagonus mitochondrion, complete genome |
| 3634 | 16677 | 29590 | 0.66 | 8.3E-02 | AI436797.1 | EST_HUMAN | HYPOTHETICAL LIPOPROTEIN MG309 HOMOLOG PRECURSOR |
| 3634 | 16677 | 29591 | 0.66 | 8.3E-02 | AI436797.1 | EST_HUMAN | th82g06.x1 Soares_NhtIMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3' |
| 6389 | 19487 | 32702 | 0.78 | 8.3E-02 | AI942338.1 | EST_HUMAN | th82g06.x1 Soares_NhtIMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3' |
| 6502 | 19566 | 32818 | 2.54 | 8.3E-02 | AF052683.1 | NT | wc78f11.x1 NCJ_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2461581 3' |
| 8313 | 21282 | 34694 | 3.61 | 8.3E-02 | AF195787.1 | NT | Homo sapiens protocadherin 43 gene, exon 1 |
| 8346 | 21315 | | 1.19 | 8.3E-02 | AA865285.1 | EST_HUMAN | Rattus norvegicus dystrophin-related protein 2 A-form splice variant (Dnp2) mRNA, complete cds |
| 8642 | 21610 | | 1.54 | 8.3E-02 | AA987873.1 | EST_HUMAN | cg88g08.s1 NCJ_CGAP_Kids Homo sapiens cDNA clone IMAGE:1455422 3' similar to contains L1.t1 L1 L1 |
| 9896 | 22849 | 36306 | 1.58 | 8.3E-02 | AW583503.1 | EST_HUMAN | cg81f10.s1 NCJ_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1592779 3' |
| 9909 | 22730 | | 2.19 | 8.3E-02 | AL161595.2 | NT | la05h10.x1 Human Pancreatic islets Homo sapiens cDNA 3' similar to TR:Q15332 Q15332 GAMMA |
| | | | | | | | SUBUNIT OF SODIUM POTASSIUM ATPASE LIKE. ; |
| | | | | | | | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91 |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 10706 | 23628 | | 0.5 | 8.3E-02 | AF020409.1 | NT | Dichystellium discoidium DocA (docA) mRNA, complete cds |
| 12444 | 25924 | | 1.48 | 8.3E-02 | BE958458.1 | EST_HUMAN | 601644770F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3929893 5' |
| 1378 | 14413 | | 7.44 | 8.2E-02 | Y08170.2 | NT | Gallus gallus mRNA for OBCAM protein gamma isoform |
| 1494 | 14527 | 27498 | 1.77 | 8.2E-02 | AF167077.2 | NT | Canis familiaris glutamate transporter (EAA14) mRNA, complete cds |
| 3089 | 16147 | | 2.24 | 8.2E-02 | AL163206.2 | NT | Homo sapiens chromosome 21 segment HS21C006 |
| 3815 | 16855 | | 1.61 | 8.2E-02 | AL161498.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10 |
| 4033 | 17071 | 28972 | 1.22 | 8.2E-02 | AL163206.2 | NT | Homo sapiens chromosome 21 segment HS21C006 |
| 4313 | 17342 | 30222 | 5.83 | 8.2E-02 | P48960 | SWISSPROT | LEUCOCYTE ANTIGEN CD97 PRECURSOR |
| 4313 | 17342 | 30223 | 5.83 | 8.2E-02 | P48960 | SWISSPROT | LEUCOCYTE ANTIGEN CD97 PRECURSOR |
| 4313 | 17342 | 30224 | 5.83 | 8.2E-02 | P48960 | SWISSPROT | LEUCOCYTE ANTIGEN CD97 PRECURSOR |
| 5108 | 18118 | 30992 | 1.29 | 8.2E-02 | AF240776.1 | NT | Mus musculus pepsinogen F (Pepf) mRNA, complete cds |
| 5118 | 18128 | 31004 | 4.13 | 8.2E-02 | U76009.1 | NT | Mus musculus zinc transporter (Znt-3) gene, complete cds |
| 5300 | 18128 | 31004 | 0.95 | 8.2E-02 | U76009.1 | NT | Mus musculus zinc transporter (Znt-3) gene, complete cds |
| 5408 | 18511 | 31389 | 1.47 | 8.2E-02 | BE897030.1 | EST_HUMAN | 601439576F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924523 5' |
| 7221 | 20243 | 33577 | 2.84 | 8.2E-02 | AF309555.1 | NT | Bos taurus connective tissue growth factor precursor (CTGF) gene, complete cds |
| 8005 | 20944 | | 0.6 | 8.2E-02 | AV743341.1 | EST_HUMAN | AV743341 CB Homo sapiens cDNA clone CBLANF07 5' |
| 9057 | 22023 | | 0.45 | 8.2E-02 | U29397.1 | NT | Rattus norvegicus plasma membrane Ca2+ ATPase isoform 3 (PMCA3) gene, 5' flanking region |
| 9124 | 22090 | 35518 | 2.75 | 8.2E-02 | AW875126.1 | EST_HUMAN | RC2-PT0004-031 299-011-005 PT0004 Homo sapiens cDNA |
| 9658 | 22885 | 36346 | 5.43 | 8.2E-02 | X04197.1 | NT | Beet necrotic yellow vein virus RNA-2 |
| 10121 | 23047 | 36526 | 2.38 | 8.2E-02 | BE254318.1 | EST_HUMAN | 601115055F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355596 5' |
| 12450 | 25209 | 31831 | 6.88 | 8.2E-02 | AE002246.2 | NT | Chlamydia pneumoniae AR39, section 73 of 94 of the complete genome |
| 12835 | 25710 | | 5.74 | 8.2E-02 | AF275366.1 | NT | Mus musculus epidermal growth factor receptor (Egfr) gene, exons 5 through 28, and complete cds, alternatively spliced |
| 1493 | 14526 | 27498 | 1.05 | 8.1E-02 | AB017138.1 | NT | Pseudomonas putida malonate decarboxylase gene cluster (mdcA, mdcB, mdcC, mdcD, mdcE, mdcG, mdcH, mdcI, and mdcM genes), complete cds |
| 5848 | 18938 | 32123 | 1.05 | 8.1E-02 | AE004006.1 | NT | Xylella fastidiosa, section 152 of 229 of the complete genome |
| 6516 | 19578 | 32836 | 1.38 | 8.1E-02 | T11532.1 | EST_HUMAN | A1484F Heart Homo sapiens cDNA clone A1484 |
| 7403 | 20371 | | 0.81 | 8.1E-02 | AL163279.2 | NT | Homo sapiens chromosome 21 segment HS21C079 |
| 7835 | 20782 | | 0.9 | 8.1E-02 | A1692681.1 | EST_HUMAN | wd86f08.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2338503 3' |
| 8683 | 21651 | 35072 | 0.53 | 8.1E-02 | 11426974 | NT | Homo sapiens hypothetical protein FLJ10060 (FLJ10060), mRNA |
| 8683 | 21651 | 35073 | 0.53 | 8.1E-02 | 11426974 | NT | Homo sapiens hypothetical protein FLJ10060 (FLJ10060), mRNA |
| 10272 | 23187 | | 1.58 | 8.1E-02 | AY005150.1 | NT | Homo sapiens extracellular glycoprotein lactrin precursor, gene, complete cds |
| 11827 | 24710 | 38294 | 1.53 | 8.1E-02 | AL163202.2 | NT | Homo sapiens chromosome 21 segment HS21C002 |
| 6 | 15830 | 28026 | 4.82 | 8.0E-02 | AW954653.1 | EST_HUMAN | EST365723 IMAGE resequences, MAGC Homo sapiens cDNA |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 1709 | 15875 | 27722 | 13.63 | 8.0E-02 | D26535.1 | NT | Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15) |
| 1709 | 15875 | 27723 | 13.63 | 8.0E-02 | D26535.1 | NT | Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15) |
| 1919 | 14943 | 27939 | 4.07 | 8.0E-02 | BE067219.1 | EST_HUMAN | PM3-BT0347-170200-001-508 BT0347 Homo sapiens cDNA |
| 2384 | 15392 | 28417 | 1.05 | 8.0E-02 | D90915.1 | EST | Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2267259 |
| 2384 | 15392 | 28418 | 1.05 | 8.0E-02 | D90915.1 | NT | Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2267259 |
| 2478 | 15482 | | 4.69 | 8.0E-02 | BF246744.1 | EST_HUMAN | 601855548F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075619 5' |
| 2831 | 14137 | 27088 | 0.99 | 8.0E-02 | M23449.1 | NT | Dictyosellum discoideum cyclic nucleotide phosphodiesterase gene, complete cds |
| 2911 | 15969 | 28892 | 0.76 | 8.0E-02 | AL445097.1 | NT | Thermoplasma acidophilum complete genome, segment 5/6 |
| 3830 | 16870 | 29772 | 5.64 | 8.0E-02 | AW96618.1 | EST_HUMAN | EST378191 IMAGE resequences, MAGI Homo sapiens cDNA |
| 4810 | 17827 | 30724 | 1.7 | 8.0E-02 | AI434202.1 | EST_HUMAN | 631902.X1 NCJ_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132114 3' |
| 4818 | 17835 | 30733 | 0.99 | 8.0E-02 | AF116586.1 | NT | Arabidopsis thaliana putative transcription factor (HUA2) mRNA, complete cds |
| 4852 | 17869 | | 7.57 | 8.0E-02 | X72794.1 | NT | M.musculus gene for gelatinase B |
| 5832 | 18922 | 32105 | 0.71 | 8.0E-02 | AW951139.1 | EST_HUMAN | EST3693209 IMAGE resequences, MAGA Homo sapiens cDNA |
| 5993 | 19077 | 32274 | 3.28 | 8.0E-02 | AF275948.1 | NT | Homo sapiens ABCA1 (ABCA1) gene, complete cds |
| 7386 | 19077 | 32274 | 1.44 | 8.0E-02 | AF275948.1 | NT | Homo sapiens ABCA1 (ABCA1) gene, complete cds |
| 8485 | 21434 | 34851 | 3.74 | 8.0E-02 | AL114693.1 | NT | Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation |
| 9744 | 22685 | 36139 | 1.21 | 8.0E-02 | X74208.1 | NT | H. sapiens AGT gene, intron 4 |
| 9744 | 22685 | 36140 | 1.21 | 8.0E-02 | X74208.1 | NT | H. sapiens AGT gene, intron 4 |
| 10519 | 23441 | | 0.6 | 8.0E-02 | AL163209.2 | NT | Homo sapiens chromosome 21 segment HS21C009 |
| 11145 | 24105 | 37632 | 2.18 | 8.0E-02 | AF217798.1 | NT | Homo sapiens SCG10 like-protein, helicase-like protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARFRP-1) genes, complete cds |
| 12483 | 25230 | 31798 | 6.54 | 8.0E-02 | AJ005375.1 | NT | Drosophila arena hunchback region |
| 13036 | 18342 | | 2.06 | 8.0E-02 | 4503034 | NT | Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA |
| 2184 | 15199 | 28219 | 4.36 | 7.9E-02 | BE250008.1 | EST_HUMAN | 600943191F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959510 5' |
| 2992 | 16050 | 28971 | 8.43 | 7.9E-02 | AI582029.1 | EST_HUMAN | ar68c08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2959510 5' |
| 3864 | 16903 | 29808 | 5.68 | 7.9E-02 | 6681044 | NT | Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA |
| 3864 | 16903 | 29809 | 5.68 | 7.9E-02 | 6681044 | NT | Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA |
| 4722 | 17742 | 30633 | 1.08 | 7.9E-02 | BF348454.1 | EST_HUMAN | 602019770F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4155401 5' |
| 4849 | 17866 | | 1.49 | 7.9E-02 | AB0098019.1 | NT | Arabidopsis thaliana RXW24L, mRNA, partial cds |
| 6855 | 19908 | | 1.06 | 7.9E-02 | BF368016.1 | EST_HUMAN | RC3-GN0042-310800-024-411 GN0042 Homo sapiens cDNA |
| 8366 | 21335 | 34747 | 3.26 | 7.9E-02 | U27832.1 | NT | Saccharomyces cerevisiae suppressor of Mif2 Smt4p (SMT4) gene, complete cds |
| 10388 | 23310 | 38788 | 4.89 | 7.9E-02 | AI081644.1 | EST_HUMAN | ou63105.x1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2 CE08811 |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|-----------------------------|-------------------------------|---|
| 10388 | 23310 | 36789 | 4.89 | 7.9E-02 | A1081644.1 | EST_HUMAN | ou63b05.s1 NCL_CGAP_BR2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2 CE08611; |
| 1215 | 14253 | 27210 | 1.69 | 7.8E-02 | A1793275.1 | EST_HUMAN | cc59d02.y6 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1670467 5' similar to contains L1.13 L1 repetitive element; |
| 1215 | 14253 | 27211 | 1.69 | 7.8E-02 | A1793275.1 | EST_HUMAN | cc59d02.y6 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1670467 5' similar to contains L1.13 L1 repetitive element; |
| 5123 | 16804 | | 3.25 | 7.8E-02 | BE260048.1 | EST_HUMAN | 600943055F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2956693 5' |
| 7279 | 20013 | 33317 | 1.29 | 7.8E-02 | U82695.2 | NT | Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds |
| 7279 | 20013 | 33318 | 1.29 | 7.8E-02 | U82695.2 | NT | Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds |
| 9137 | 22103 | 35529 | 1.26 | 7.8E-02 | BE97947.1 | EST_HUMAN | 601440439F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925449 5' |
| 9232 | 22198 | 35626 | 0.6 | 7.8E-02 | X78344.1 | NT | S. cerevisiae CAT8 gene |
| 9408 | 22373 | 35808 | 0.66 | 7.8E-02 | AF233437.1 | NT | Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds |
| 9408 | 22373 | 35809 | 0.66 | 7.8E-02 | AF233437.1 | NT | Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds |
| 9716 | 22744 | 36195 | 1.23 | 7.8E-02 | AA469354.1 | EST_HUMAN | nc88b06.r1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:771731 |
| 10161 | 23086 | 36593 | 0.65 | 7.8E-02 | Z99124.1 | NT | Bacillus subtilis complete genome (section 21 of 21); from 3999281 to 4214814 |
| 12114 | 24984 | 38585 | 1.64 | 7.8E-02 | BF025981.1 | EST_HUMAN | 601669379F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3953083 5' |
| 1399 | 15867 | 27402 | 0.93 | 7.7E-02 | AF181897.1 | NT | Homo sapiens WRN (WRN) gene, complete cds |
| 3600 | 16845 | | 2.05 | 7.7E-02 | AJ238093.1 | NT | Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements |
| 5622 | 18718 | 31877 | 0.61 | 7.7E-02 | AF062636.1 | NT | Gallus gallus collagen type XII alpha-1 (COL12A1) gene, promoter region and partial cds |
| 8241 | 21210 | 34615 | 7.34 | 7.7E-02 | AA402949.1 | EST_HUMAN | zu53d11.1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:741717 5' similar to TR:G1173905 G1173905 SPLICEOSOME ASSOCIATED PROTEIN.; |
| 10195 | 23120 | 36606 | 3.76 | 7.7E-02 | P38080 | SWISSPROT | PROBABLE SERINE/THREONINE-PROTEIN KINASE YBR059C |
| 10490 | 23412 | 36909 | 0.76 | 7.7E-02 | A1318662.1 | EST_HUMAN | ta80b08.x1 NCL_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050359 3' similar to gb:Z26876 60S RIBOSOMAL PROTEIN L38 (HUMAN); |
| 10490 | 23412 | 36910 | 0.76 | 7.7E-02 | A1318662.1 | EST_HUMAN | ta80b08.x1 NCL_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050359 3' similar to gb:Z26876 60S RIBOSOMAL PROTEIN L38 (HUMAN); |
| 11352 | 24302 | 37829 | 4.65 | 7.7E-02 | 11422757 | NT | Homo sapiens KIAA0628 gene product (KIAA0628), mRNA |
| 12671 | 25785 | | 1.91 | 7.7E-02 | 11436859 | NT | Homo sapiens interferon regulatory factor 7 (IRF7), mRNA |

Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 3398 | 16447 | 29373 | 2.43 | 7.6E-02 | BE514432.1 | EST_HUMAN | 601316426F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634903 5' |
| 3419 | 16467 | 29387 | 1 | 7.6E-02 | AA296447.1 | EST_HUMAN | EST112214 Cerebellum II Homo sapiens cDNA 5' end similar to similar to protocadherin 43 |
| 6216 | 19280 | 32523 | 0.72 | 7.6E-02 | AI061275.1 | EST_HUMAN | an25g02.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1699730 3' |
| 6491 | 19556 | 32806 | 0.87 | 7.6E-02 | BE379328.1 | EST_HUMAN | 601236402F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608401 5' |
| 9725 | 22753 | 36206 | 1.35 | 7.6E-02 | AJ131016.1 | NT | Homo sapiens SCL gene locus |
| 10257 | 23182 | | 1.42 | 7.6E-02 | AL139078.2 | NT | Campylobacter jejuni NCTC11168 complete genome; segment 5/6 |
| 10580 | 23502 | 36994 | 0.47 | 7.6E-02 | BE708002.1 | EST_HUMAN | RC1-HIT0545-020800-017-d06 HT0545 Homo sapiens cDNA |
| 10714 | 23636 | | 0.56 | 7.6E-02 | BE959638.2 | EST_HUMAN | 601654915R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839810 3' |
| 10952 | 23872 | 37384 | 0.67 | 7.6E-02 | X92656.1 | NT | L. esculentum mRNA for those phosphate translocator |
| 10952 | 23872 | 37385 | 0.67 | 7.6E-02 | X92656.1 | NT | L. esculentum mRNA for those phosphate translocator |
| 11986 | 24863 | 38459 | 1.9 | 7.6E-02 | AW996645.1 | EST_HUMAN | QV3-BN0046-150400-151-e04 BN0046 Homo sapiens cDNA |
| 785 | 13845 | 26790 | 2.89 | 7.5E-02 | 5902093 | NT | Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA |
| 785 | 13845 | 26791 | 2.89 | 7.5E-02 | 5902093 | NT | Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA |
| 1935 | 14959 | 27955 | 0.93 | 7.5E-02 | AL163278.2 | NT | Homo sapiens chromosome 21 segment HS21C078 |
| 4536 | 17559 | 30447 | 0.63 | 7.5E-02 | AB015661.1 | NT | Homo sapiens IL-18 gene for interleukin-18, intron 1 and exon 2 |
| 5952 | 19037 | 32233 | 0.71 | 7.5E-02 | AI948714.1 | EST_HUMAN | wg24h09.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2472257 3' |
| 8681 | 21649 | 35071 | 1.01 | 7.5E-02 | AI864367.1 | EST_HUMAN | w52b02.x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2428491 3' similar to gb:M14328 ALPHA |
| 8852 | 21819 | 35239 | 1.29 | 7.5E-02 | AU116913.1 | EST_HUMAN | ENOLASE (HUMAN); |
| 10392 | 23314 | | 0.45 | 7.5E-02 | BF221730.1 | EST_HUMAN | AUT116913 HEMBA1 Homo sapiens cDNA clone HEMBA1000264 5' |
| 10859 | 23779 | 37279 | 0.9 | 7.5E-02 | BF206909.1 | EST_HUMAN | 7o61c05.x1 NCI CGAP_P28 Homo sapiens cDNA clone IMAGE:3578504 3' similar to contains element |
| 10953 | 23873 | 37386 | 0.68 | 7.5E-02 | X70460.1 | NT | MER27 repetitive element |
| 478 | 13550 | 26478 | 1.24 | 7.4E-02 | AW838547.1 | EST_HUMAN | 601870205F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100449 5' |
| 1456 | 14489 | | 1.08 | 7.4E-02 | AF030027.1 | NT | C.fiml DSM 20113 16S rDNA |
| 2565 | 15596 | | 0.99 | 7.4E-02 | 6755069 | NT | RCS-LT0054-280100-011-H09 LT0054 Homo sapiens cDNA |
| 3608 | 16653 | 29571 | 0.78 | 7.4E-02 | AI807885.1 | EST_HUMAN | Equine herpesvirus 4 strain NS80567, complete genome |
| 4733 | 17793 | 30646 | 1.09 | 7.4E-02 | L78810.1 | NT | Mus musculus paired-like homeodomain transcription factor 1 (Pitx1), mRNA |
| 4833 | 17850 | 30750 | 3.24 | 7.4E-02 | 6978442 | NT | wf43h01.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356385 3' |
| 4979 | 17894 | 30883 | 2.52 | 7.4E-02 | 6678492 | NT | Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds |
| 6643 | 19701 | | 1.8 | 7.4E-02 | R17477.1 | EST_HUMAN | Rattus norvegicus Activin receptor like kinase 1 (Acvrl1), mRNA |
| 7707 | 20664 | 34031 | 0.79 | 7.4E-02 | AA605132.1 | EST_HUMAN | Mus musculus ubiquitin c-terminal hydrolase related polypeptide (Uchrp), mRNA |
| | | | | | | | y914g06.l1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:32339 5' |
| | | | | | | | nc01d02.s1 NCI CGAP_AA1 Homo sapiens cDNA clone IMAGE:1112259 3' |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 8233 | 21202 | 34608 | 1.2 | 7.4E-02 | BE880112.1 | EST_HUMAN | 601493366F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3895264 5' |
| 8846 | 21813 | 35233 | 1.01 | 7.4E-02 | U56089.1 | NT | Human periodic tyrophan protein 2 (PWP2) gene, exons 15 to 21, and complete cds |
| 9521 | 22484 | 35930 | 1.02 | 7.4E-02 | AW629605.1 | EST_HUMAN | hh67d11.1 y1 NCI_CGAP_GUT1 Homo sapiens cDNA clone IMAGE:2967861 5' similar to SW:SCA2_HUMAN |
| 9521 | 22484 | 35931 | 1.02 | 7.4E-02 | AW629605.1 | EST_HUMAN | O15127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2 ; |
| 9794 | 21117 | 34516 | 0.48 | 7.4E-02 | AI672939.1 | EST_HUMAN | hh67d11.1 y1 NCI_CGAP_GUT1 Homo sapiens cDNA clone IMAGE:2967861 5' similar to SW:SCA2_HUMAN |
| 9794 | 21117 | 34517 | 0.48 | 7.4E-02 | AI672939.1 | EST_HUMAN | O15127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2 ; |
| 10173 | 23098 | 36578 | 1.07 | 7.4E-02 | U62293.1 | NT | we74d02.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2346819 3' |
| 10301 | 23226 | 36708 | 0.53 | 7.4E-02 | BF512678.1 | EST_HUMAN | we74d02.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2346819 3' |
| 12408 | 25181 | | 1.47 | 7.4E-02 | 11525893 | NT | Human LIM-kinase1 and alternatively spliced LIM-kinase1 (LIMK1) gene, complete cds |
| 12865 | 25903 | | 2.51 | 7.4E-02 | AW379431.1 | EST_HUMAN | UI-H-BW1-emg-g-06-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3069898 3' |
| 469 | 13542 | 26468 | 1.3 | 7.3E-02 | BE964961.2 | EST_HUMAN | Homo sapiens histone deacetylase 5 (NY-CO-9), mRNA |
| 469 | 13542 | 26469 | 1.3 | 7.3E-02 | BE964961.2 | EST_HUMAN | CM4-HT0243-081199-037-d11 HT0243 Homo sapiens cDNA |
| 686 | 13748 | 26674 | 5.48 | 7.3E-02 | AE001789.1 | NT | 601688738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3' |
| 1477 | 15869 | 27486 | 3.94 | 7.3E-02 | AW900281.1 | EST_HUMAN | 601688738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3' |
| 1862 | 15879 | | 15.78 | 7.3E-02 | AL163302.2 | NT | Thermotoga maritima section 101 of 136 of the complete genome |
| 3785 | 16826 | | 0.72 | 7.3E-02 | U66059.1 | NT | CM0-NN1004-130300-284-g08 NN1004 Homo sapiens cDNA |
| 5032 | 18046 | | 1.06 | 7.3E-02 | U12283.1 | NT | Homo sapiens chromosome 21 segment HS21C102 |
| 6595 | 19655 | 32827 | 1.04 | 7.3E-02 | AA778977.1 | EST_HUMAN | Human gemline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2P, TCRBV7S2A1N4T, TCRBV13S9/13S> |
| 7706 | 20683 | 34029 | 2.47 | 7.3E-02 | P05143 | SWISSPROT | Mus musculus transcription factor USF2 (USF2) gene, exons 8-10 and complete cds |
| 7706 | 20683 | 34030 | 2.47 | 7.3E-02 | P05143 | SWISSPROT | z24d02.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to gb:L02426 26S PROTEASE SUBUNIT 4 (HUMAN); |
| 8508 | 21476 | | 1.2 | 7.3E-02 | 7862107 | NT | PROLINE-RICH PROTEIN MP-3 |
| 9565 | 22527 | | 1.39 | 7.3E-02 | AB011090.1 | NT | PROLINE-RICH PROTEIN MP-3 |
| 11552 | 19655 | 32827 | 1.89 | 7.3E-02 | AA778977.1 | EST_HUMAN | Homo sapiens mRNA for KIAA0518 protein, partial cds |
| 12925 | 25510 | | 1.33 | 7.3E-02 | Z73597.1 | NT | z24d02.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to gb:L02426 26S PROTEASE SUBUNIT 4 (HUMAN); |
| 120 | 13229 | 26156 | 0.7 | 7.2E-02 | AE000882.1 | NT | S. cerevisiae chromosome XVI reading frame ORF YPL241c Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete genome |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 120 | 13229 | 26157 | 0.7 | 7.2E-02 | AE000882.1 | NT | Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete genome |
| 1472 | 14505 | 27478 | 2.77 | 7.2E-02 | AL163301.2 | NT | Homo sapiens chromosome 21 segment HS21C101 |
| 1472 | 14505 | 27479 | 2.77 | 7.2E-02 | AL163301.2 | NT | Homo sapiens chromosome 21 segment HS21C101 |
| 2556 | 15558 | | 2.98 | 7.2E-02 | U14794.1 | NT | Human immunodeficiency virus type 1 isolate 26 reverse transcriptase (pol) gene, internal fragment, partial cds |
| 3900 | 16940 | 29851 | 0.74 | 7.2E-02 | AW298322.1 | EST_HUMAN | UI-H-BW0-aj-e-05-Q-U1s1 NCL CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732049 3' |
| 4373 | 17400 | 30280 | 4.97 | 7.2E-02 | BF572307.1 | EST_HUMAN | 602077757F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4251950 5' |
| 5360 | 18485 | 31336 | 2.81 | 7.2E-02 | U67531.1 | NT | Methanococcus jannaschii section 73 of 150 of the complete genome |
| 5361 | 18486 | 31337 | 9.14 | 7.2E-02 | P11120 | SWISSPROT | CALMODULIN |
| 6239 | 18312 | | 0.73 | 7.2E-02 | BF217596.1 | EST_HUMAN | 601863905F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4096224 5' |
| 7374 | 20344 | 33696 | 1.76 | 7.2E-02 | BF216086.1 | EST_HUMAN | 601863558F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095710 5' |
| 7391 | 20380 | 33712 | 0.6 | 7.2E-02 | AF221126.1 | NT | Streptococcus pneumoniae putative response regulator (zmpR), putative histidine kinase (zmpS), and putative zinc metalloprotease (zmpB) genes, complete cds |
| 7417 | 20394 | | 1.74 | 7.2E-02 | 5834897 | NT | Strongyloides purpuratus mitochondrion, complete genome |
| 8529 | 21497 | 34912 | 0.89 | 7.2E-02 | P05143 | SWISSPROT | PROLINE-RICH PROTEIN MP-3 |
| 8529 | 21497 | 34913 | 0.89 | 7.2E-02 | P05143 | SWISSPROT | PROLINE-RICH PROTEIN MP-3 |
| 9419 | 22384 | | 0.92 | 7.2E-02 | Y17217.1 | NT | Lactobacillus lactis cspE gene |
| 9934 | 22861 | | 0.63 | 7.2E-02 | X16349.1 | NT | Human gene for sex hormone-binding globulin (SHBG) |
| 9970 | 22897 | 36360 | 1.98 | 7.2E-02 | AV712452.1 | EST_HUMAN | AV712452 DCA Homo sapiens cDNA clone DCAUUG01 5' |
| 10117 | 23043 | 36523 | 3.63 | 7.2E-02 | L14561.1 | NT | Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds |
| 10274 | 23199 | 36683 | 1.17 | 7.2E-02 | BF125399.1 | EST_HUMAN | 601763523F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026436 5' |
| 10362 | 23285 | 36762 | 2.26 | 7.2E-02 | AW873187.1 | EST_HUMAN | hq24f11.x1 NCL CGAP_Adr1 Homo sapiens cDNA clone IMAGE:3120333 3' similar to TR:Q9Z340 Q9Z340 ATYPICAL PKC SPECIFIC BINDING PROTEIN. |
| 10552 | 23474 | 36669 | 0.54 | 7.2E-02 | AA768204.1 | EST_HUMAN | ca62c07.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1316844 3' |
| 10717 | 23639 | 37132 | 2.17 | 7.2E-02 | U82895.2 | NT | Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds |
| 10840 | 23760 | 37260 | 5.41 | 7.2E-02 | BE565003.1 | EST_HUMAN | 601343926F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3686951 5' |
| 10864 | 23784 | | 3.24 | 7.2E-02 | BE539214.1 | EST_HUMAN | 601065104F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451559 5' |
| 11258 | 24210 | 37733 | 4.17 | 7.2E-02 | AF049874.1 | NT | Rattus norvegicus HLH transcription factor Mist1 (Mist1) gene, complete cds |
| 12311 | 25119 | 31842 | 1.58 | 7.2E-02 | AA773696.1 | EST_HUMAN | af81a04.r1 Soares_NH-IMPu_S1 Homo sapiens cDNA clone IMAGE:1048398 5' |
| 12350 | 25145 | | 5.13 | 7.2E-02 | AJ230796.1 | EST_HUMAN | AJ230796 Homo sapiens library (Seranski P) Homo sapiens cDNA clone PS13D5 3' |

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Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 12469 | 25218 | | 3.99 | 7.2E-02 | U82828.1 | NT | Homo sapiens ataxia telangiectasia (ATM) gene, complete cds |
| 12484 | 25754 | | 8.41 | 7.2E-02 | AW900982.1 | EST_HUMAN | CM4-NN1009-200300-116-c11 NN1009 Homo sapiens cDNA |
| 12880 | 25933 | | 1.45 | 7.2E-02 | AF020439.1 | NT | Homo sapiens ATP-citrate lyase gene, intron 3 |
| 12964 | 25533 | | 1.85 | 7.2E-02 | AA401779.1 | EST_HUMAN | z157c12.1 Soares_NHT Homo sapiens cDNA clone IMAGE:728454 5' |
| 1920 | 14944 | 27940 | 1.83 | 7.1E-02 | L02290.1 | NT | Human immunodeficiency virus type 1 (D9) proviral structural capsid protein (gag) gene, partial cds |
| 2300 | 15312 | 28332 | 6.39 | 7.1E-02 | BF209802.1 | EST_HUMAN | 601872281F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4092981 5' |
| 8239 | 21208 | 34812 | 0.87 | 7.1E-02 | A1125284.1 | EST_HUMAN | q092a10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1736922 3' |
| 12193 | 25038 | | 8.33 | 7.1E-02 | BE304764.1 | EST_HUMAN | 601143974F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051234 5' |
| 529 | 13600 | 26518 | 1.42 | 7.0E-02 | Q07092 | SWISSPROT | COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR |
| 1499 | 14532 | | 1.82 | 7.0E-02 | X98877.1 | NT | Martellia Mcut-1 gene |
| 1778 | 14805 | 27791 | 1.18 | 7.0E-02 | AA056343.1 | EST_HUMAN | z166104.s1 Sitratogene colon (#937204) Homo sapiens cDNA clone IMAGE:509599 3' |
| 3042 | 16100 | 29015 | 1.78 | 7.0E-02 | AW138152.1 | EST_HUMAN | U1-H-B1-acy-c-07-0-U1.s1 NC1 CGAP Sub3 Homo sapiens cDNA clone IMAGE:2716020 3' |
| 3913 | 16953 | 28864 | 0.98 | 7.0E-02 | AA815438.1 | EST_HUMAN | ai65a12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1375678 3' similar to gb:K03002 60S |
| 4074 | 17110 | 30004 | 1.05 | 7.0E-02 | BE070264.1 | EST_HUMAN | RIBOSOMAL PROTEIN L32 (HUMAN); |
| 4164 | 17195 | | 1.24 | 7.0E-02 | AW792962.1 | EST_HUMAN | QV4-BT0407-280100-090-e10 BT0407 Homo sapiens cDNA |
| 4242 | 17271 | 30158 | 1.28 | 7.0E-02 | AF077821.1 | NT | CM0-UJ0001-060300-270-e12 UM0001 Homo sapiens cDNA |
| 4968 | 17981 | 30871 | 8.41 | 7.0E-02 | BF381987.1 | EST_HUMAN | Canis familiaris inducible nitric oxide synthase mRNA, complete cds |
| 5451 | 18553 | | 1.03 | 7.0E-02 | Y09143.2 | NT | 601816291F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4050071 5' |
| 7630 | 20590 | 33953 | 0.9 | 7.0E-02 | AV689285.1 | EST_HUMAN | Lumbricus rubellus mRNA for cyclophilin B |
| 7864 | 20808 | 34186 | 0.6 | 7.0E-02 | Y19187.1 | NT | AY688285 GK Homo sapiens cDNA clone GKCCAE08 5' |
| 9454 | 22418 | 35856 | 1.2 | 7.0E-02 | K02901.1 | NT | Gallus gallus mRNA for partial ezonin, XL spliced variant (ecz gene) |
| 9958 | 22883 | 36345 | 1.21 | 7.0E-02 | K02901.1 | NT | African swine fever virus, complete genome |
| 10312 | 23238 | 36718 | 0.76 | 7.0E-02 | U27266.1 | NT | Rat Ig gamma epsilon H-chain gene C-region, 3' end |
| 11700 | 24965 | 38242 | 2.23 | 7.0E-02 | AA724265.1 | EST_HUMAN | Human myosin binding protein H (MyBP-H) gene, complete cds |
| 12839 | 25519 | 31710 | 1.68 | 7.0E-02 | 11421638 | NT | ah99a05.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1327184 3' similar to gb:U14837 |
| 515 | 13586 | 28504 | 11.2 | 6.9E-02 | AL163210.2 | NT | TIGHT JUNCTION PROTEIN ZO-1 (HUMAN); |
| 515 | 13586 | 26505 | 11.2 | 6.9E-02 | AL163210.2 | NT | Homo sapiens hypothetical protein FLJ20116 (FLJ20116), mRNA |
| | | | | | | NT | Homo sapiens chromosome 21 segment HS21C010 |
| | | | | | | NT | Homo sapiens chromosome 21 segment HS21C010 |
| 1336 | 14370 | | 1.68 | 6.9E-02 | 4507968 | NT | Homo sapiens regulator of Gz-selective protein signaling (ZGAP1) mRNA, and translated products |
| 3807 | 18947 | 29754 | 1.37 | 6.9E-02 | Q06364 | SWISSPROT | 26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7) |
| 3807 | 18947 | 29755 | 1.37 | 6.9E-02 | Q06364 | SWISSPROT | 26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7) |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 5151 | 18161 | 31041 | 0.97 | 6.9E-02 | AA670269.1 | EST_HUMAN | af256a08.s1 Soares total_fetus Nb2HF8 9w Homo sapiens cDNA clone IMAGE:1032710 3' |
| 6026 | 19109 | | 0.57 | 6.9E-02 | AF161364.1 | NT | Homo sapiens HSPC101 mRNA, partial cds |
| 7876 | 20820 | | 0.67 | 6.9E-02 | AF164967.1 | NT | Canine distemper virus strain A75/17, complete genome |
| 8387 | 21356 | | 1.18 | 6.9E-02 | U12022.1 | NT | Human calmodulin (CALM1) gene, exons 2,3,4,5 and 6, and complete cds |
| 8899 | 21865 | 35287 | 1.08 | 6.9E-02 | BE567435.1 | EST_HUMAN | 601340661F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5' |
| 8899 | 21865 | 35288 | 1.08 | 6.9E-02 | BE567435.1 | EST_HUMAN | 601340661F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5' |
| 9475 | 22439 | 35879 | 0.55 | 6.9E-02 | U22967.1 | NT | Barbarie duck parvovirus REP protein (rep) and three capsid protein VP (vp) genes, complete cds |
| 12343 | 25141 | | 2.17 | 6.9E-02 | X74315.1 | NT | Xlaevis XFD2 mRNA for fork head protein |
| 12519 | 25250 | | 1.75 | 6.9E-02 | P44621 | SWISSPROT | PROTEIN TRANSPORT PROTEIN HOFc HOMOLOG |
| 13112 | 25631 | 31648 | 3.69 | 6.9E-02 | BF352899.1 | EST_HUMAN | IL3-HT0619-110700-210-C04 HT0619 Homo sapiens cDNA |
| 1899 | 14924 | 27918 | 1.18 | 6.8E-02 | AA496759.1 | EST_HUMAN | ae30f02.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:887339 5' similar to gb:M22382 MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN); |
| 1899 | 14924 | 27919 | 1.18 | 6.8E-02 | AA496759.1 | EST_HUMAN | ae30f02.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:887339 5' similar to gb:M22382 MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN); |
| 1922 | 14946 | 27942 | 4.7 | 6.8E-02 | AF156873.1 | NT | Homo sapiens putative hepatic transcription factor (WBSR14) gene, complete cds |
| 3117 | 16174 | 29084 | 1.05 | 6.8E-02 | AA781996.1 | EST_HUMAN | ai75a06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1376628 3' |
| 3117 | 16174 | 29085 | 1.05 | 6.8E-02 | AA781996.1 | EST_HUMAN | ai75a06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1376628 3' |
| 3117 | 16174 | 29086 | 1.05 | 6.8E-02 | AA781996.1 | EST_HUMAN | ai75a06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1376628 3' |
| 4583 | 17605 | | 0.71 | 6.8E-02 | BE141076.1 | EST_HUMAN | MRO-HT0069-071099-001-c05 HT0069 Homo sapiens cDNA |
| 5283 | 18289 | | 0.76 | 6.8E-02 | T03013.1 | EST_HUMAN | FB20A6 Fetal brain, Strabagene Homo sapiens cDNA clone FB20A6 3' and |
| 6776 | 19831 | | 0.66 | 6.8E-02 | P20792 | SWISSPROT | GELL-SURFACE RECEPTOR DAF-1 PRECURSOR |
| 7084 | 20018 | | 1.05 | 6.8E-02 | BE061890.1 | EST_HUMAN | RC1-BT0254-090300-017-409 BT0254 Homo sapiens cDNA |
| 7497 | 20462 | 33822 | 7.18 | 6.8E-02 | AL163268.2 | NT | Homo sapiens chromosome 21 segment HS21C068 |
| 7948 | 20889 | 34280 | 0.64 | 6.8E-02 | U16856.1 | NT | Dicotyledon discoidium myosin heavy chain kinase A (MHCK A) mRNA, complete cds |
| 8031 | 21599 | 35020 | 5.44 | 6.8E-02 | AJ248287.1 | NT | Pyrococcus abyssi complete genome; segment 5/6 |
| 8031 | 21599 | 35021 | 5.44 | 6.8E-02 | AJ248287.1 | NT | Pyrococcus abyssi complete genome; segment 5/6 |
| 12140 | 25949 | | 3.73 | 6.8E-02 | T03214.1 | EST_HUMAN | FB4A8 Fetal brain, Strabagene Homo sapiens cDNA clone FB4A8 3' end similar to LINE-1 |
| 12274 | 25094 | | 2.52 | 6.8E-02 | AA758014.1 | EST_HUMAN | ah6705.s1 Soares_testis_NHT Homo sapiens cDNA clone 1320705 3' |
| 12832 | 25449 | | 1.68 | 6.8E-02 | AW975839.1 | EST_HUMAN | EST3B7B48 MAGe resequences, MAGN Homo sapiens cDNA |
| 12894 | 25480 | | 2.35 | 6.8E-02 | 9910585 | NT | Mus musculus latent TGF beta binding protein (Tgfb), mRNA |
| 1531 | 14564 | | 1.93 | 6.7E-02 | AF115536.1 | NT | Oncorhynchus mykiss TAP1 protein (OnmyTAP1) mRNA, OnmyTAP1*01 allele, complete cds |
| 1910 | 14934 | 27930 | 1.99 | 6.7E-02 | AJ20285.1 | EST_HUMAN | ag79e04.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1841406 3' |
| 3730 | 16772 | 29683 | 4.34 | 6.7E-02 | P17278 | SWISSPROT | HOMEOBOX PROTEIN HOX-D4 (CHOX-A) |
| 8183 | 21153 | 34560 | 1.01 | 6.7E-02 | X62695.1 | NT | H.sapiens DNA for cGMP phosphodiesterase (exons 4-22) |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 8183 | 21153 | 34561 | 1.01 | 6.7E-02 | X62695.1 | NT | H. sapiens DNA for cGMP phosphodiesterase (exons 4-22) |
| 8781 | 21748 | 35170 | 0.45 | 6.7E-02 | AW082688.1 | EST_HUMAN | xb61c11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2580788 3' |
| 9959 | 22886 | 36347 | 0.73 | 6.7E-02 | AW137359.1 | EST_HUMAN | UI-H-B11-act-g-01-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715433 3' |
| 9959 | 22886 | 36348 | 0.73 | 6.7E-02 | AW137359.1 | EST_HUMAN | UI-H-B11-act-g-01-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715433 3' |
| 1371 | 14405 | 27375 | 0.9 | 6.6E-02 | AF245118.1 | NT | Drosophila melanogaster cactin mRNA, complete cds |
| 2192 | 15207 | 28228 | 2.66 | 6.6E-02 | AJ289241.1 | NT | Mus musculus Capn12 gene for calpain 12, exons 1-21, three alternative transcripts |
| 3477 | 16523 | 29447 | 11.07 | 6.6E-02 | R64306.1 | EST_HUMAN | y18b10.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:139579 3' |
| 3491 | 16537 | 29462 | 2.1 | 6.6E-02 | 7108357 | NT | Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA |
| 3491 | 16537 | 29463 | 2.1 | 6.6E-02 | 7108357 | NT | Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA |
| 4107 | 17141 | 30036 | 1.45 | 6.6E-02 | AF260225.1 | NT | Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced |
| 5015 | 18029 | 30913 | 9.23 | 6.6E-02 | Q61703 | SWISSPROT | INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2) |
| 5015 | 18029 | 30914 | 9.23 | 6.6E-02 | Q61703 | SWISSPROT | INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2) |
| 6736 | 19792 | 33073 | 3.97 | 6.6E-02 | X06411.1 | NT | P. vulgaris mRNA for chalcone synthase |
| 6967 | 19823 | 33105 | 0.55 | 6.6E-02 | P25189 | SWISSPROT | MATERNAL EFFECT PROTEIN STAUFIN |
| 6967 | 19823 | 33106 | 0.55 | 6.6E-02 | P25189 | SWISSPROT | MATERNAL EFFECT PROTEIN STAUFIN |
| 8162 | 21090 | | 0.57 | 6.6E-02 | D14567.1 | NT | Penicillium urticae mitochondrial l-rRNA (large rRNA) gene and its flanking region |
| 8279 | 21248 | 34660 | 1.6 | 6.6E-02 | AF052572.1 | NT | Homo sapiens chemokine receptor CXCR4 gene, promoter region and complete cds |
| 8517 | 21784 | 35209 | 0.67 | 6.6E-02 | AF006055.1 | NT | Dictyostellum discoideum darlin (darA) gene, complete cds |
| 9273 | 22239 | 35666 | 0.87 | 6.6E-02 | 9629198 | NT | Human respiratory syncytial virus, complete genome |
| 9273 | 22239 | 35667 | 0.87 | 6.6E-02 | 9629198 | NT | Human respiratory syncytial virus, complete genome |
| 10311 | 23235 | 36717 | 0.52 | 6.6E-02 | A1458752.1 | EST_HUMAN | ig97g06.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2149498 3' |
| 10447 | 23469 | 36860 | 1.65 | 6.6E-02 | Y07848.1 | NT | Homo sapiens EWS, gar22, rrp22 and bam22 genes |
| 10481 | 23403 | | 0.6 | 6.6E-02 | 11430559 | NT | Homo sapiens vinculin (VCL), mRNA |
| 11310 | 24260 | 37766 | 4.9 | 6.6E-02 | BF374248.1 | EST_HUMAN | MR1-SN0064-010600-006-a12 SN0064 Homo sapiens cDNA |
| 12063 | 24936 | | 1.73 | 6.6E-02 | C05789.1 | EST_HUMAN | C05789 Human pancreatic islet Homo sapiens cDNA clone hbc5156 |
| 12719 | 25373 | | 2.53 | 6.6E-02 | 9937991 | NT | Mus musculus DIPB gene (Dipb), mRNA |
| 13024 | 25572 | | 1.31 | 6.6E-02 | AF167430.1 | NT | Rattus norvegicus cytochrome P450 2E1 (CYP2E1) gene, 5' flanking region |
| 584 | 13652 | 26566 | 2.67 | 6.5E-02 | BF027639.1 | EST_HUMAN | 601671046F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954178 5' |
| 989 | 14041 | 26996 | 1.95 | 6.5E-02 | 7706068 | NT | Homo sapiens E2F-like protein (LOC51270), mRNA |
| 1392 | 14426 | 27395 | 3.5 | 6.5E-02 | U47624.1 | NT | Xenopus laevis alpha(E)-catenin mRNA, complete cds |
| 1749 | 14778 | 27763 | 2.08 | 6.5E-02 | AE000764.1 | NT | Aquifex aeolicus section 96 of 109 of the complete genome |
| 5638 | 18734 | 31896 | 1.71 | 6.5E-02 | AA443991.1 | EST_HUMAN | zv48h12.s1 Soares ovary tumor NBH0T Homo sapiens cDNA clone IMAGE:756743 3' similar to gb:M26038 |
| 6993 | 19750 | 33027 | 0.83 | 6.5E-02 | BF665340.1 | EST_HUMAN | HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-5 BETA CHAIN (HUMAN); 602118687F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4276029 5' |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 7165 | 18396 | 31241 | 1.17 | 6.5E-02 | U22661.1 | NT | Azobacter vinelandii ATCC 9046 negative regulator MucB (mucB) gene, partial cds |
| 10302 | 23227 | 36709 | 0.65 | 6.5E-02 | BE963200.2 | EST_HUMAN | 601656817R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3865637 3' |
| 10302 | 23227 | 36710 | 0.65 | 6.5E-02 | BE963200.2 | EST_HUMAN | 601656817R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3865637 3' |
| 10832 | 23753 | 37252 | 0.53 | 6.5E-02 | BF106300.1 | EST_HUMAN | 601823611F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4043138 5' |
| 11002 | 23958 | 37492 | 4.51 | 6.5E-02 | AA195848.1 | EST_HUMAN | z32g05.s1 Soares_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:665144 3' |
| 12164 | 25017 | | 4.16 | 6.5E-02 | M21496.1 | NT | Rabbit microsomal epoxide hydrolase |
| 12526 | 25255 | | 7.31 | 6.5E-02 | AF102993.1 | NT | Nectria haematococca kinesis related protein 2 (KRP2) gene, complete cds |
| 577 | 13646 | 26559 | 1.74 | 6.4E-02 | X94549.1 | NT | A. carterae precursor of peridinin-chlorophylla-protein (PCP) gene |
| 1746 | 14775 | 27760 | 0.93 | 6.4E-02 | AE001777.1 | NT | Thermotoga maritima section 89 of 138 of the complete genome |
| 1746 | 14775 | 27761 | 0.93 | 6.4E-02 | AE001777.1 | NT | Thermotoga maritima section 89 of 138 of the complete genome |
| 4933 | 15085 | 28007 | 1.16 | 6.4E-02 | 6596923 | NT | Mus musculus histone deacetylase 5 (Hdac5), mRNA |
| 5262 | 18270 | | 2.56 | 6.4E-02 | AA147572.1 | EST_HUMAN | z151e04.r1 Soares_pregnant_uterus_NBHPU Homo sapiens cDNA clone IMAGE:505470 5' similar to contains Alu repetitive element; |
| 5525 | 18624 | 31559 | 1.19 | 6.4E-02 | AI191956.1 | EST_HUMAN | q507b01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738249 3' similar to contains LTR8.b3 LTR8 repetitive element; |
| 5982 | 19067 | 32265 | 1.15 | 6.4E-02 | 7305186 | NT | Mus musculus IFN-response element binding factor 1 (IREBF-1), mRNA |
| 6234 | 19307 | 32539 | 4.16 | 6.4E-02 | AF052733.1 | NT | Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds |
| 6234 | 19307 | 32540 | 4.16 | 6.4E-02 | AF052733.1 | NT | Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds |
| 6542 | 19604 | 32866 | 0.72 | 6.4E-02 | AI672896.1 | EST_HUMAN | we73g12.x1 Soares_Dieckgraefe_colon_NHGD Homo sapiens cDNA clone IMAGE:2346790 3' |
| 6990 | 20213 | 33542 | 4.64 | 6.4E-02 | BE974448.1 | EST_HUMAN | 601690425R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950603 3' |
| 7683 | 20651 | 34015 | 0.52 | 6.4E-02 | AL162757.2 | NT | Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 6/7 |
| 8679 | 21647 | | 2.79 | 6.4E-02 | 6753323 | NT | Mus musculus chaperonin subunit 6a (zeta) (Cct6a), mRNA |
| 9012 | 21978 | 35397 | 4 | 6.4E-02 | AA083305.1 | EST_HUMAN | k1419.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5' |
| 9483 | 22447 | 35887 | 0.92 | 6.4E-02 | AF150195.1 | EST_HUMAN | AF150195 Human mRNA from cd34+ stem cells Homo sapiens cDNA clone CBDA/IA10 |
| 9944 | 22871 | | 0.51 | 6.4E-02 | BE834083.1 | EST_HUMAN | RC1-OT0083-150600-014-g06 OT0083 Homo sapiens cDNA |
| 10075 | 23002 | 38472 | 1.75 | 6.4E-02 | AB011126.1 | NT | Homo sapiens mRNA for KIAA0554 protein, partial cds |
| 10824 | 23546 | 37046 | 0.59 | 6.4E-02 | AF087150.1 | NT | Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18 |
| 10824 | 23546 | 37047 | 0.59 | 6.4E-02 | AF087150.1 | NT | Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18 |
| 12018 | 24895 | 38492 | 2.18 | 6.4E-02 | U91328.1 | NT | Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds |
| 12018 | 24895 | 38493 | 2.18 | 6.4E-02 | U91328.1 | NT | Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds |

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Table 4
Single Exon Probes Expressed In Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|-----------------------------|-------------------------------|---|
| 12424 | 25861 | | 5.38 | 6.4E-02 | AF107890.1 | NT | Homo sapiens mucin 5B (MUC5B) gene, partial cds |
| 12476 | 25224 | 31793 | 5.68 | 6.4E-02 | AJ277174.1 | NT | Drosophila melanogaster mRNA for mod(mdg4)51.4 protein |
| 1769 | 14798 | 27784 | 2.76 | 6.3E-02 | AF109905.1 | NT | Mus musculus major histocompatibility locus class III regions Hsc701 gene, partial cds; enRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes |
| 3618 | 16862 | | 2.77 | 6.3E-02 | P37092 | SWISSPROT | HEAT SHOCK PROTEIN 70 HOMOLOG |
| 6259 | 18332 | 32563 | 1.06 | 6.3E-02 | BF210736.1 | EST_HUMAN | 601873316F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097489 5' |
| 7453 | 20418 | | 1.39 | 6.3E-02 | X97869.1 | NT | H. sapiens gene encoding La autoantigen |
| 9646 | 22690 | 36039 | 1.01 | 6.3E-02 | AJ243916.1 | NT | Drosophila melanogaster Domin gene, exons 1-3 |
| 10374 | 23297 | 36773 | 2.98 | 6.3E-02 | AB010162.1 | NT | Hepatitis G virus RNA for polyprotein (NS5A region), partial cds, strain: CMR-162 |
| 10634 | 23556 | | 0.81 | 6.3E-02 | AV698070.1 | EST_HUMAN | AV698070 GKCO Homo sapiens cDNA clone GKCAHE01 5' |
| 11070 | 18332 | 32563 | 2.76 | 6.3E-02 | BF210736.1 | EST_HUMAN | 601873316F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097489 5' |
| 4278 | 17307 | 30186 | 2.48 | 6.2E-02 | AL161872.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68 |
| 4365 | 17392 | | 1.12 | 6.2E-02 | AF271235.1 | NT | Rattus norvegicus differentiation-associated Na-dependent inorganic phosphate cotransporter (DNP1) mRNA, complete cds |
| 4612 | 17833 | | 6.56 | 6.2E-02 | Q62191 | SWISSPROT | 52 KD RO PROTEIN (SJOEGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (RO52) |
| 6963 | 20188 | 33513 | 0.67 | 6.2E-02 | D49530.1 | NT | Spirulina platensis DNA for adenylate cyclase, complete cds |
| 7889 | 20833 | 34212 | 0.79 | 6.2E-02 | U41453.1 | NT | Rattus norvegicus PKC binding protein and substrate mRNA, complete cds |
| 8158 | 21086 | | 0.58 | 6.2E-02 | AL161845.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45 |
| 9299 | 26007 | | 0.63 | 6.2E-02 | M61101.1 | NT | Porcine group C rotavirus (strain Cowden) outer membrane protein (VP7) mRNA, complete cds |
| 9699 | 22652 | 38106 | 0.53 | 6.2E-02 | AA778450.1 | EST_HUMAN | af20a06.s1 Soares total_fetus Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1032178 3' |
| 9835 | 22771 | 38226 | 1.25 | 6.2E-02 | AE000750.1 | NT | Mus musculus stromal cell derived factor receptor 2 (Sdf2), mRNA |
| 12269 | 25979 | | 15.66 | 6.2E-02 | AE000750.1 | NT | Aquifex aeolicus section 82 of 109 of the complete genome |
| 12596 | 25289 | | 1.38 | 6.2E-02 | BE793085.1 | EST_HUMAN | 601583773F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3937842 5' |
| 12676 | 25346 | 31764 | 3.54 | 6.2E-02 | BF112039.1 | EST_HUMAN | 7137h08.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3523815 3' similar to |
| 256 | 13353 | 26278 | 3.09 | 6.1E-02 | D16471.1 | NT | Human mRNA, Xq terminal portion |
| 4017 | 17056 | | 15.65 | 6.1E-02 | U73325.1 | NT | Arabidopsis thaliana K+ inward rectifying channel protein (AKC1) gene, complete cds |
| 6043 | 19125 | 32330 | 0.62 | 6.1E-02 | 7662463 | NT | Homo sapiens KIAA1052 protein (KIAA1052), mRNA |
| 6043 | 19125 | 32331 | 0.62 | 6.1E-02 | 7662463 | NT | Homo sapiens KIAA1052 protein (KIAA1052), mRNA |
| 6235 | 19308 | | 1.64 | 6.1E-02 | 4507070 | NT | Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA |
| 8606 | 21574 | 34989 | 3.52 | 6.1E-02 | X99268.1 | NT | H. sapiens mRNA for B-HLH DNA binding protein |
| 9008 | 21974 | 35393 | 1.93 | 6.1E-02 | BE971853.1 | EST_HUMAN | 601651056R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934604 3' |

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Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 9008 | 21974 | 35394 | 1.93 | 6.1E-02 | BE971853.1 | EST_HUMAN | 601651086R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934604 3' |
| 11082 | 24044 | 37566 | 3.44 | 6.1E-02 | BE179543.1 | EST_HUMAN | IL3-HT0618-110500-136-C06 HT0618 Homo sapiens cDNA |
| 12216 | 25897 | | 2.42 | 6.1E-02 | X70969.1 | NT | S. japonicum mRNA for serine-enzyme |
| 12779 | 25774 | | 1.35 | 6.1E-02 | AI88661.1 | EST_HUMAN | ts59107.x1 NCI_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2292801 3' |
| 12912 | 25491 | | 7.44 | 6.1E-02 | AL163207.2 | NT | Homo sapiens chromosome 21 segment HS21C007 |
| 1267 | 14302 | 27263 | 1.25 | 6.0E-02 | AE001777.1 | NT | Thermotoga maritima section 89 of 136 of the complete genome |
| 2684 | 15690 | 28698 | 1.17 | 6.0E-02 | AW969848.1 | EST_HUMAN | EST380924 MAGE resequences, MAGJ Homo sapiens cDNA |
| 2783 | 15775 | | 1.98 | 6.0E-02 | AB031289.1 | NT | Mesocricetus corti mitochondrial DNA, NADH dehydrogenase subunit 4, tRNA-Phe, tRNA-Met, ATPase subunit 6, and NADH dehydrogenase subunit 2 |
| 2948 | 13213 | 26137 | 1.47 | 6.0E-02 | AA188730.1 | EST_HUMAN | zp78c04.r1 Stratagene HeLa cell s3 837216 Homo sapiens cDNA clone IMAGE:826310 5' |
| 2948 | 13213 | 26138 | 1.47 | 6.0E-02 | AA188730.1 | EST_HUMAN | zp78c04.r1 Stratagene HeLa cell s3 837216 Homo sapiens cDNA clone IMAGE:826310 5' |
| 3243 | 16298 | 29222 | 1.52 | 6.0E-02 | AA372376.1 | EST_HUMAN | EST84266 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein |
| 3243 | 16298 | 29223 | 1.52 | 6.0E-02 | AA372376.1 | EST_HUMAN | EST84266 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein |
| 5472 | 18573 | | 0.76 | 6.0E-02 | AW370211.1 | EST_HUMAN | RC3-BT0253-01189-013-b04 BT0253 Homo sapiens cDNA |
| 6341 | 19410 | 32651 | 0.98 | 6.0E-02 | AB07537.1 | EST_HUMAN | wf48n05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2368873 3' similar to contains |
| 7180 | 18411 | 31212 | 2.79 | 6.0E-02 | 5174698 | NT | L1.11 L1 L1 repetitive element ; |
| 7180 | 18411 | 31213 | 2.79 | 6.0E-02 | 5174698 | NT | Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA |
| 7394 | 20362 | 33714 | 2.08 | 6.0E-02 | BF382349.1 | EST_HUMAN | Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA |
| 7508 | 20473 | 33833 | 0.57 | 6.0E-02 | BF210498.1 | EST_HUMAN | 601815274F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4049228 5' |
| 7944 | 20886 | 34277 | 1.71 | 6.0E-02 | AI204275.1 | EST_HUMAN | 601874710F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4101074 5' |
| 8765 | 21732 | | 0.52 | 6.0E-02 | 11466495 | NT | qf58n08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1754199 3' |
| 9627 | 22571 | 36020 | 1.17 | 6.0E-02 | AI623167.1 | EST_HUMAN | Reclinomonas americana mitochondrion, complete genome |
| 9627 | 22571 | 36021 | 1.17 | 6.0E-02 | AI623167.1 | EST_HUMAN | ts78n06.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2237362 3' |
| 9761 | 22702 | 36159 | 2.03 | 6.0E-02 | AJ245365.1 | NT | ts78n06.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2237362 3' |
| 9761 | 22702 | 36160 | 2.03 | 6.0E-02 | AJ245365.1 | NT | Acipenser baeri partial GLV gene for immunoglobulin light chain variable region, exons 1-2 |
| 10265 | 23190 | 36675 | 0.66 | 6.0E-02 | AA309797.1 | EST_HUMAN | Acipenser baeri partial GLV gene for immunoglobulin light chain variable region, exons 1-2 |
| 10265 | 23190 | 36676 | 0.66 | 6.0E-02 | AA309797.1 | EST_HUMAN | EST180654 Jurkat T-cells V Homo sapiens cDNA 5' end similar to heat shock protein 1, 60 kDa-like |
| 12475 | 25223 | 31792 | 3.08 | 6.0E-02 | 11431702 | NT | EST180654 Jurkat T-cells V Homo sapiens cDNA 5' end similar to heat shock protein 1, 60 kDa-like |
| 12845 | 25455 | | 3.16 | 6.0E-02 | AI609273.1 | EST_HUMAN | Homo sapiens DNA-dependent protein kinase catalytic subunit-interacting protein 2 (KIP2), mRNA |
| 232 | 13332 | 28255 | 5.34 | 5.9E-02 | AW934719.1 | EST_HUMAN | wf69n03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360885 3' similar to TR:O60298 |
| | | | | | | | O60298 KIAA0551 PROTEIN ; |
| | | | | | | | RC1-DT0001-280100-012-410 DT0001 Homo sapiens cDNA |

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Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|-----------------------------|-------------------------------|--|
| 2998 | 16054 | 28975 | 3.42 | 5.9E-02 | AF190269.1 | NT | Mus musculus p53 tumor suppressor gene, exon 10 and 11, partial cds; alternatively spliced |
| 4905 | 17922 | 30814 | 0.94 | 5.9E-02 | AF006304.1 | NT | Saccharomyces cerevisiae protein tyrosine phosphatase (PTP3) gene, complete cds |
| 7077 | 25874 | 33409 | 0.62 | 5.9E-02 | AF145880.1 | NT | Drosophila melanogaster LD23107 sting (sting) mRNA, complete cds |
| 8964 | 21830 | 35355 | 1.92 | 5.9E-02 | 9055249 | NT | Mus musculus troloxol related homeobox 5 (Drosophila) (Irxf5), mRNA |
| 9808 | 21128 | | 0.82 | 5.9E-02 | BF242748.1 | EST_HUMAN | 601877609F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105994 5' |
| 11138 | 24098 | | 3.23 | 5.9E-02 | 6879870 | NT | Mus musculus follistatin-like (Fstl), mRNA |
| 933 | 13986 | | 6.03 | 5.8E-02 | D80110.1 | NT | Thiobacillus ferrooxidans merC, merA genes and URF-1 |
| 2872 | 15932 | | 0.99 | 5.8E-02 | AJ223821.1 | NT | Populus trichocarpa CC&AOMT1 gene, exon 1 to exon 5 |
| 3876 | 16719 | 28633 | 1.32 | 5.8E-02 | AE001775.1 | NT | Thermotoga maritima section 87 of 136 of the complete genome |
| 4382 | 17410 | 30292 | 5.33 | 5.8E-02 | AW051927.1 | EST_HUMAN | wx24c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3' |
| 4382 | 17410 | 30293 | 5.33 | 5.8E-02 | AW051927.1 | EST_HUMAN | wx24c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3' |
| 4578 | 17600 | 30495 | 4.73 | 5.8E-02 | A1247505.1 | EST_HUMAN | qhs6f01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to gb:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN); |
| 4578 | 17600 | 30496 | 4.73 | 5.8E-02 | A1247505.1 | EST_HUMAN | qhs6f01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to gb:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN); |
| 4604 | 17625 | 32298 | 2.93 | 5.8E-02 | AF096264.1 | NT | Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds |
| 6014 | 19097 | 32298 | 0.53 | 5.8E-02 | AA190994.1 | EST_HUMAN | zp80g11.s1 Stratisgene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627068 3' |
| 7941 | 20893 | 34273 | 2.52 | 5.8E-02 | M99150.1 | NT | Human polymorphic microsatellite DNA |
| 7941 | 20893 | 34274 | 2.52 | 5.8E-02 | M99150.1 | NT | Human polymorphic microsatellite DNA |
| 9014 | 21980 | 35399 | 0.59 | 5.8E-02 | AL163283.2 | NT | Homo sapiens chromosome 21 segment HS21C083 |
| 12655 | 25668 | | 10.6 | 5.8E-02 | AA604269.1 | EST_HUMAN | no75e11.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:1112584 3' |
| 3070 | 16127 | 29039 | 1.27 | 5.7E-02 | A1081644.1 | EST_HUMAN | ou63b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2 |
| 3086 | 16143 | 29055 | 1.51 | 5.7E-02 | AF119117.1 | NT | CE08811 ; |
| 3814 | 16854 | 29761 | 2.47 | 5.7E-02 | AW968791.1 | EST_HUMAN | Homo sapiens dopamine transporter (SLC6A3) gene, complete cds |
| 5199 | 18208 | 31082 | 0.91 | 5.7E-02 | AJ251973.1 | NT | EST1378865 MAGI resequences, MAGI Homo sapiens cDNA |
| 5306 | 18308 | | 1.18 | 5.7E-02 | 6754525 | NT | Homo sapiens partial steerin-1 gene |
| 5979 | 19084 | | 0.69 | 5.7E-02 | AF275948.1 | NT | Mus musculus low density lipoprotein receptor (Ldlr), mRNA |
| 7704 | 20661 | 34025 | 0.59 | 5.7E-02 | BE871811.1 | EST_HUMAN | Homo sapiens ABCA1 (ABCA1) gene, complete cds |
| 7704 | 20661 | 34026 | 0.59 | 5.7E-02 | BE871811.1 | EST_HUMAN | 601447937F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3851985 5' |
| 7766 | 20739 | 34111 | 0.68 | 5.7E-02 | D78003.1 | NT | 601447937F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3851985 5' |
| 7766 | 20739 | 34112 | 0.68 | 5.7E-02 | D78003.1 | NT | Xenopus laevis mRNA for fourth component of complement, complete cds |
| 8495 | 21483 | 34879 | 1.74 | 5.7E-02 | AJ286090.1 | NT | Xenopus laevis mRNA for fourth component of complement, complete cds |
| 10209 | 23134 | 35621 | 0.65 | 5.7E-02 | 6681260 | NT | Rattus norvegicus mRNA for potassium channel, alpha subunit (Kv9.2 gene) |
| | | | | | | | Mus musculus ec2 oncogene (Ec2), mRNA |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO. | Exon SEQ ID NO. | CRF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 10930 | 23850 | 37365 | 0.49 | 5.7E-02 | Z49963.1 | NT | L.mexicana cpb1 gene |
| 11521 | 24462 | 38013 | 3.22 | 5.7E-02 | A1752685.1 | EST_HUMAN | cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn18b09 random |
| 11521 | 24462 | 38014 | 3.22 | 5.7E-02 | A1752685.1 | EST_HUMAN | cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn18b09 random |
| 11676 | 24642 | | 1.89 | 5.7E-02 | AL163303.2 | NT | Homo sapiens chromosome 21 segment HS21C103 |
| 12573 | 25782 | | 8.27 | 5.7E-02 | D50320.1 | NT | Pig DNA for SPA1-2, complete cds |
| 12794 | 25855 | | 3.72 | 5.7E-02 | AF217490.1 | NT | Homo sapiens fragile 160 oxidoreductase (FOR) gene, exons 8, 9, and partial cds |
| 12930 | 25858 | | 5.65 | 5.7E-02 | AF261280.1 | NT | Pan troglodytes apolipoprotein-E gene, complete cds |
| 1529 | 14562 | 27533 | 1.85 | 5.6E-02 | AF094455.1 | NT | Hydrocotyle rotundifolia ribosomal protein L16 (pH16) gene, intron; chloroplast gene for chloroplast product |
| 4671 | 17692 | 30578 | 1.92 | 5.6E-02 | AB013100.1 | NT | Lycopodium esculentum LE-ACS6 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds |
| 4725 | 17745 | 30636 | 1.21 | 5.6E-02 | AA290599.1 | EST_HUMAN | zs45c01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700416 3' |
| 6817 | 19871 | 33160 | 5.93 | 5.6E-02 | AW172708.1 | EST_HUMAN | x102c10.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2666050 3' similar to TR:O94979 O94979 KIAA0905 PROTEIN. ; |
| 7075 | 20097 | 33407 | 0.77 | 5.6E-02 | AA866182.1 | EST_HUMAN | cd47f12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1371119 3' similar to contains Alu repetitive element; contains element L1 repetitive element ; |
| 7358 | 20328 | 33677 | 2.94 | 5.6E-02 | BE008001.1 | EST_HUMAN | QV0-BN0147-290400-214-g07 BN0147 Homo sapiens cDNA |
| 8141 | 21078 | 34479 | 0.91 | 5.6E-02 | A1183583.1 | EST_HUMAN | qd64g11.x1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:1734308 3' |
| 9154 | 22120 | 35548 | 2.47 | 5.6E-02 | BE542663.1 | EST_HUMAN | 601067158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453279 5' |
| 9154 | 22120 | 35549 | 2.47 | 5.6E-02 | BE542663.1 | EST_HUMAN | 601067158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453279 5' |
| 10171 | 23096 | 36576 | 1.06 | 5.6E-02 | AA482864.1 | EST_HUMAN | nf49d07.s1 NCI_CGAP_A161 Homo sapiens cDNA clone IMAGE:923245 similar to TR:G769859 G769859 LAMINA ASSOCIATED POLYPEPTIDE 1C. ; |
| 11891 | 24772 | | 1.87 | 5.6E-02 | AF260225.1 | NT | Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced |
| 2663 | 15660 | 28678 | 8.23 | 5.5E-02 | X97869.1 | NT | H.sapiens gene encoding La autoantigen |
| 3228 | 16283 | 29207 | 3.44 | 5.5E-02 | 6755501 | NT | Mus musculus SH3 domain protein 1B (SH3d1B), mRNA |
| 4244 | 17273 | 30157 | 1.13 | 5.5E-02 | L41561.1 | NT | Gallid herpesvirus mRNA fragment |
| 5742 | 18836 | 32017 | 3.09 | 5.5E-02 | Q01174 | SWISSPROT | TROPOMYOSIN ALPHA CHAIN, NON MUSCLE |
| 6141 | 18836 | 32017 | 3.81 | 5.5E-02 | Q01174 | SWISSPROT | TROPOMYOSIN ALPHA CHAIN, NON MUSCLE |
| 7603 | 20564 | 33925 | 1.85 | 5.5E-02 | 6755502 | NT | Mus musculus tufelin 1 (Tuf1), mRNA |
| 8457 | 21426 | 34842 | 0.69 | 5.5E-02 | AF170911.1 | NT | Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1) mRNA, complete cds |
| 8457 | 21426 | 34843 | 0.69 | 5.5E-02 | AF170911.1 | NT | Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1) mRNA, complete cds |
| 10013 | 22940 | 36405 | 0.63 | 5.5E-02 | 10947034 | NT | Homo sapiens eIF4E-transcript (4E-T), mRNA |

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Table 4
Single Exon Probes Expressed In Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 10013 | 22940 | 38408 | 0.63 | 5.5E-02 | 10947034 | NT | Homo sapiens eIF4E-transporter (4E-T), mRNA |
| 10107 | 23033 | 36510 | 1.45 | 5.5E-02 | U69492.1 | NT | Mus musculus second IL11 receptor alpha chain (IL-11Ra2) gene, exons 1 and 2 |
| 11360 | 24309 | 37895 | 6.48 | 5.5E-02 | U09771.1 | NT | Citrobacter freundii DSM 30040 cyclopropane fatty acid synthase (cfa) gene, partial cds, dihydroxyacetone kinase (dhaK), glycerol dehydrogenase (dhaD), transcriptional activator (dhaR), 1,3-propanediol dehydrogenase (dhaT), glycerol dehydratase (dhaB)> |
| 13089 | 25920 | 31303 | 1.99 | 5.5E-02 | 11421332 | NT | Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA |
| 3032 | 18090 | | 1.02 | 5.4E-02 | AJ277468.1 | NT | Oryza sativa rbb3-1 gene for putative Bowman Birk trypsin inhibitor |
| 3433 | 18223 | | 6.97 | 5.4E-02 | BE073468.1 | EST_HUMAN | RC5-BT0559-140200-012-C03 BT0559 Homo sapiens cDNA |
| 3931 | 16971 | 29885 | 0.7 | 5.4E-02 | U85806.1 | NT | Hirudo medicinalis SNAP-25 homolog mRNA, complete cds |
| 8462 | 21431 | | 1.05 | 5.4E-02 | Z99116.1 | NT | Bacillus subtilis complete genome (section 13 of 21): from 2395261 to 2613730 |
| 8426 | 22390 | 35828 | 0.53 | 5.4E-02 | AF260225.1 | NT | Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced |
| 11057 | 24020 | 37543 | 1.54 | 5.4E-02 | U20790.1 | NT | Neurospora crassa ubiquinol-cytochrome c oxidoreductase subunit VIII (QCR8) mRNA, complete cds |
| 1056 | 14102 | 27052 | 1.91 | 5.3E-02 | AW391248.1 | EST_HUMAN | QV0-ST0213-021289-062-a09 ST0213 Homo sapiens cDNA |
| 1058 | 14102 | 27053 | 1.91 | 5.3E-02 | AW391248.1 | EST_HUMAN | QV0-ST0213-021289-062-a09 ST0213 Homo sapiens cDNA |
| 1506 | 14539 | 27511 | 16.63 | 5.3E-02 | T94759.1 | EST_HUMAN | ye37f12.11 Stratiogene lung (#837210) Homo sapiens cDNA clone IMAGE:119951 5' similar to gb:K01506 |
| 2504 | 15507 | 28533 | 2.12 | 5.3E-02 | AJ276408.1 | NT | HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DP(1) ALPHA CHAIN (HUMAN): |
| 2953 | 16011 | 28937 | 0.95 | 5.3E-02 | M58417.1 | NT | Pseudomonas putida tggS gene |
| 2953 | 16011 | 28938 | 0.95 | 5.3E-02 | M58417.1 | NT | Drosophila melanogaster laminin B2 gene, complete cds |
| 3167 | 16222 | 29137 | 5.38 | 5.3E-02 | AJ276408.1 | NT | Drosophila melanogaster laminin B2 gene, complete cds |
| 4641 | 17662 | 30550 | 0.9 | 5.3E-02 | AJ011048.1 | NT | Pseudomonas putida tggS gene |
| 5125 | 18134 | 31011 | 8.41 | 5.3E-02 | M80463.1 | NT | Arabidopsis thaliana ell5 gene, exons 1-11 |
| 5392 | 18495 | 31372 | 1.8 | 5.3E-02 | AE000527.1 | NT | Mus musculus caudal type homeobox-1 (Cdx-1) gene, complete cds |
| 5392 | 18495 | 31373 | 1.8 | 5.3E-02 | AE000527.1 | NT | Helicobacter pylori 26695 section 5 of 134 of the complete genome |
| 6222 | 19296 | 32530 | 3.03 | 5.3E-02 | M85289.1 | NT | Helicobacter pylori 26695 section 5 of 134 of the complete genome |
| 7068 | 20090 | 33398 | 3.94 | 5.3E-02 | 9695413 | NT | Human heparan sulfate proteoglycan (HSPG2) mRNA, complete cds |
| 7289 | 20271 | 33606 | 1.23 | 5.3E-02 | U32832.1 | NT | Lymphocystis disease virus 1, complete genome |
| 7585 | 20546 | | 2.12 | 5.3E-02 | S78221.1 | NT | Haemophilus influenzae Rd section 147 of 163 of the complete genome |
| 8209 | 21108 | 34507 | 0.51 | 5.3E-02 | P38742 | SWISSPROT | nuclear protein TIF1 isoform [mouse, mRNA, 4053 nt] |
| 8748 | 21716 | | 0.5 | 5.3E-02 | U10098.1 | NT | HYPOTHETICAL 130.0 KD PROTEIN IN SNF6-SPO11 INTERGENIC REGION |
| 9481 | 22445 | 35886 | 2.05 | 5.3E-02 | X03127.1 | NT | Mus musculus 129/Sv cystatin C (cst3) gene, complete cds |
| 10491 | 23413 | 36911 | 0.61 | 5.3E-02 | AB022605.1 | NT | Podospore anserina mitochondrial epsilon-sen DNA |
| 10491 | 23413 | 36912 | 0.61 | 5.3E-02 | AB022605.1 | NT | Homo sapiens hCMT1b mRNA for mRNA (guanine-7-methyltransferase, complete cds) |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 10618 | 23540 | | 0.6 | 5.3E-02 | Y07907.1 | NT | D. rerio mRNA for zp-23 POU gene, splice variant (neurula, 9-18 hpf and postmitogenesis, 20-28 hpf) |
| 10695 | 23617 | 37111 | 0.69 | 5.3E-02 | X68432.1 | NT | B. rerio pou[c] mRNA for transcription factor |
| 12092 | 24963 | 38558 | 2.06 | 5.3E-02 | X68435.1 | NT | H. sapiens mRNA for HMG-CoA-synthase |
| 2293 | 15305 | | 89.73 | 5.2E-02 | 5031908 | NT | Homo sapiens mapin A, alpha (PABA peptide hydrolase) (MEP1A) mRNA |
| 3131 | 16198 | 28097 | 1.98 | 5.2E-02 | AJ277661.1 | NT | Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1 |
| 3131 | 16188 | 28098 | 1.98 | 5.2E-02 | AJ277661.1 | NT | Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1 |
| 3950 | 17000 | 25915 | 0.73 | 5.2E-02 | AF236101.1 | NT | Arabidopsis thaliana putative dicarboxylate diiron protein (Crd1) mRNA, complete cds |
| 3952 | 17002 | | 0.97 | 5.2E-02 | 6871757 | NT | Mus musculus cytokine inducible SH2-containing protein 3 (Cish3), mRNA |
| 4307 | 17336 | 30214 | 3.36 | 5.2E-02 | U07132.1 | NT | Human steroid hormone receptor Nsr-1 mRNA, complete cds |
| 6025 | 19108 | 32310 | 0.66 | 5.2E-02 | U14731.1 | NT | Saccharomyces cerevisiae Cdc54p (CDC54) gene, complete cds |
| 6228 | 19302 | | 1.22 | 5.2E-02 | AJ830965.1 | EST_HUMAN | w80e04.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2409150 3' similar to contains MER15.b1 MER15 repetitive element; |
| 7489 | 20454 | 33813 | 1.07 | 5.2E-02 | P36322 | SWISSPROT | DNA POLYMERASE PROCESSIVITY FACTOR (POLYMERASE ACCESSORY PROTEIN) (PAP) (DNA-BINDING GENE 18 PROTEIN) |
| 8537 | 21505 | | 2.15 | 5.2E-02 | AL163204.2 | NT | Homo sapiens chromosome 21 segment HS21C004 |
| 10087 | 23014 | 36487 | 1.77 | 5.2E-02 | D10927.1 | NT | Tumip mosaic virus genomic RNA for Capsid protein, complete cds |
| 10087 | 23014 | 36488 | 1.77 | 5.2E-02 | D10927.1 | NT | Tumip mosaic virus genomic RNA for Capsid protein, complete cds |
| 11888 | 24769 | 38357 | 5.42 | 5.2E-02 | F32386.1 | EST_HUMAN | HSPD25097 HM3 Homo sapiens cDNA clone s3000039A02 |
| 11888 | 24769 | 38358 | 5.42 | 5.2E-02 | F32386.1 | EST_HUMAN | HSPD25097 HM3 Homo sapiens cDNA clone s3000039A02 |
| 12593 | 25388 | | 1.55 | 5.2E-02 | Q03030 | SWISSPROT | OXALOACETATE DECARBOXYLASE ALPHA CHAIN |
| 2372 | 15380 | | 0.97 | 5.1E-02 | AL134071.1 | EST_HUMAN | DKFZp547D073_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D073 5' |
| 5041 | 18054 | | 0.94 | 5.1E-02 | AB031740.1 | NT | Homo sapiens PBII gene for salivary proline-rich protein P-B, complete cds |
| 6830 | 19884 | 33175 | 0.68 | 5.1E-02 | AF280369.1 | NT | HIV-1 patient 98 from Italy protease (pol) gene, complete cds |
| 7038 | 18371 | 31258 | 1.76 | 5.1E-02 | BF378625.1 | EST_HUMAN | QVQ-UM0051-250800-350-b08 UM0051 Homo sapiens cDNA |
| 8596 | 21564 | 34978 | 0.77 | 5.1E-02 | M28434.1 | NT | Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds |
| 8596 | 21564 | 34979 | 0.77 | 5.1E-02 | M28434.1 | NT | Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds |
| 8690 | 21658 | 35081 | 1.26 | 5.1E-02 | AJ131968.1 | NT | Spodoptera littoralis mRNA for 3-dehydrocyclohexone 3beta-reductase |
| 9237 | 22203 | 35634 | 0.61 | 5.1E-02 | P02533 | SWISSPROT | KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (OK 14) |
| 9237 | 22203 | 35635 | 0.61 | 5.1E-02 | P02533 | SWISSPROT | KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (OK 14) |
| 10168 | 23093 | 36571 | 7.1 | 5.1E-02 | AF012698.1 | NT | Candida albicans protein phosphatase Ssd1 homolog (SSD1) gene, complete cds |
| 10542 | 23484 | 36959 | 1.66 | 5.1E-02 | P40603 | SWISSPROT | ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX) |
| 11178 | 24135 | 37665 | 2.19 | 5.1E-02 | AF083930.1 | NT | Homo sapiens ES18 mRNA, partial cds |
| 11178 | 24135 | 37666 | 2.19 | 5.1E-02 | AF083930.1 | NT | Homo sapiens ES18 mRNA, partial cds |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 12699 | 25359 | | 1.75 | 5.1E-02 | AF082487.1 | NT | Cucumis melo polygalacturonase precursor (MPG3) mRNA, complete cds |
| 12861 | 25531 | | 1.6 | 5.1E-02 | AA534104.1 | EST_HUMAN | nt73f02.s1 NCI_CGAP_P10 Homo sapiens cDNA clone IMAGE:998139 |
| 483 | 13556 | 26481 | 2.16 | 5.0E-02 | AF098004.1 | NT | Mus musculus fatty acid amide hydrolase gene, exon 10 |
| 835 | 13988 | 28038 | 4.55 | 5.0E-02 | Z33896.1 | NT | O. virgatus (HEL37) microsatellite DNA |
| 1209 | 14247 | 27205 | 4.03 | 5.0E-02 | Z99104.1 | NT | Bacillus subtilis complete genome (section 1 of 21): from 1 to 213080 |
| 2007 | 15028 | 28036 | 4.94 | 5.0E-02 | P02810 | SWISSPROT | SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1/PRP-3) (PRP-2/PRP-4) (PIF-F/PIF-S) (PROTEIN A/PROTEIN C) [CONTAINS: PEPTIDE P-C] |
| 2829 | 14040 | 26995 | 1.62 | 5.0E-02 | U72742.1 | NT | Oryctolagus cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds |
| 3348 | 16399 | | 1.34 | 5.0E-02 | 7305610 | NT | Mus musculus Uro-51 like kinase 2 (C. elegans) (Ulk2), mRNA |
| 3809 | 16654 | | 1.01 | 5.0E-02 | U32782.1 | NT | Haemophilus influenzae Rd section 67 of 163 of the complete genome |
| 3896 | 16739 | 29652 | 13.52 | 5.0E-02 | U12769.2 | NT | Antheraea pernyi period clock protein homolog mRNA, complete cds |
| 6253 | 19326 | 32557 | 0.77 | 5.0E-02 | AF096264.1 | NT | Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds |
| 6441 | 19506 | | 1.25 | 5.0E-02 | AJ242625.1 | NT | Mus musculus Dmp-1 gene, exons 1-6 |
| 7181 | 18412 | 31214 | 0.6 | 5.0E-02 | P35618 | SWISSPROT | NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L) |
| 7785 | 20738 | 34110 | 12.03 | 5.0E-02 | P35618 | SWISSPROT | NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L) |
| 8008 | 20946 | | 0.52 | 5.0E-02 | AW082464.1 | EST_HUMAN | MR0-CT0084-100899-002-g10 CT0084 Homo sapiens cDNA |
| 10560 | 23482 | 36977 | 1.26 | 5.0E-02 | AF305238.1 | NT | Mus musculus Fas-interacting serine/threonine kinase 3 (Fist3) mRNA, complete cds |
| 11820 | 24703 | 38285 | 2.47 | 5.0E-02 | U67600.1 | NT | Methanococcus jannaschii section 142 of 150 of the complete genome |
| 12226 | 25818 | | 6.4 | 5.0E-02 | Q04047 | SWISSPROT | NO-ON-TRANSIENT A PROTEIN |
| 226 | 13325 | | 27.61 | 4.8E-02 | M14230.1 | NT | Chicken 28-kDa vitamin D-dependent calcium-binding protein (CaBP-28) mRNA, complete cds |
| 369 | 13455 | 26384 | 2.96 | 4.8E-02 | AF275948.1 | NT | Homo sapiens ABCA1 (ABCA1) gene, complete cds |
| 369 | 13455 | 26385 | 2.96 | 4.8E-02 | AF275948.1 | NT | Homo sapiens ABCA1 (ABCA1) gene, complete cds |
| 3302 | 16355 | 28274 | 1.64 | 4.9E-02 | P54258 | SWISSPROT | Homo sapiens ABCA1 (ABCA1) gene, complete cds |
| 3584 | 16629 | | 0.7 | 4.9E-02 | AA188940.1 | EST_HUMAN | ATROPHIN-1 (DENTATORUBRAL-PALLIDOLYSIAN ATROPHY PROTEIN) |
| 3605 | 16650 | 29566 | 0.96 | 4.9E-02 | AA400914.1 | EST_HUMAN | Zq48a12.s1 Stragene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632926 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element; |
| 3605 | 16650 | 29567 | 0.96 | 4.9E-02 | AA400914.1 | EST_HUMAN | Zf78a03.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:728428 3' |
| 4877 | 17894 | 30783 | 2.11 | 4.9E-02 | AW167821.1 | EST_HUMAN | Zf78a03.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:728428 3' |
| 4877 | 17894 | 30784 | 2.11 | 4.9E-02 | AW167821.1 | EST_HUMAN | Xg56g10.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2632366 3' |
| 5444 | 18546 | 31458 | 1.71 | 4.9E-02 | L00122.1 | NT | Xg56g10.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2632366 3' |
| 5444 | 18546 | 31459 | 1.71 | 4.9E-02 | L00122.1 | NT | Rat elastase II gene, exon 6 |
| 7349 | 20319 | 33666 | 2.83 | 4.9E-02 | AE000980.1 | NT | Rat elastase II gene, exon 6 |
| 8963 | 21929 | | 0.91 | 4.9E-02 | AE002309.1 | NT | Archaeoglobus fulgidus section 127 of 172 of the complete genome |
| 9107 | 22073 | 35500 | 0.8 | 4.9E-02 | AL161559.2 | NT | Chlamydia muridarum, section 40 of 85 of the complete genome |
| | | | | | | | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59 |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|-----------------------------|-------------------------------|--|
| 10656 | 23578 | 37075 | 0.53 | 4.9E-02 | P19532 | SWISSPROT | TRANSCRIPTION FACTOR E3 |
| 11730 | 24616 | 38193 | 3.44 | 4.9E-02 | AF008303.1 | NT | Homo sapiens prepro placental TGF-beta gene, complete cds |
| 12879 | 25473 | | 6.66 | 4.9E-02 | M19364.1 | NT | Human gamma-B-crystallin (gamma 1-2) and gamma-C-crystallin (gamma 2-1) genes, complete cds |
| 330 | 13420 | 26344 | 1.06 | 4.8E-02 | D16471.1 | NT | Human mRNA, Xq terminal portion |
| 331 | 13420 | 26344 | 2.41 | 4.8E-02 | D16471.1 | NT | Human mRNA, Xq terminal portion |
| 489 | 13562 | 26486 | 12.99 | 4.8E-02 | AF003100.1 | NT | Arabidopsis thaliana AP2 domain containing protein RAP2.7 mRNA, partial cds |
| 2281 | 15294 | 28318 | 2.24 | 4.8E-02 | W51983.1 | EST_HUMAN | zc49b02.s1 Soares senescent fibroblasts NBHSF Homo sapiens cDNA clone IMAGE:326611 3' similar to gb:M30838 LUPUS KU AUTOANTIGEN PROTEIN P86 (HUMAN); |
| 3222 | 16277 | 28202 | 1.93 | 4.8E-02 | X17144.1 | NT | Tetrahymena rostrata histone H3II and histone H4II intergenic DNA |
| 4688 | 17719 | | 1.24 | 4.8E-02 | Z54280.1 | NT | S. scrofa gene for skeletal muscle ryanodine receptor |
| 5174 | 18183 | 31060 | 0.63 | 4.8E-02 | U91914.1 | NT | Streptococcus constellatus D-alanine:D-alanine ligase gene, partial cds |
| 8477 | 21446 | 34863 | 1.55 | 4.8E-02 | AW388497.1 | EST_HUMAN | MR2-ST0129-221036-012-602 ST0129 Homo sapiens cDNA |
| 9485 | 22449 | 35889 | 0.76 | 4.8E-02 | AJ001398.1 | NT | Fugu rubripes rps24 gene |
| 9485 | 22449 | 35890 | 0.76 | 4.8E-02 | AJ001398.1 | NT | Fugu rubripes rps24 gene |
| 12505 | 25242 | | 1.35 | 4.8E-02 | 9632993 | NT | Streptococcus thermophilus bacteriophage Sfi19, complete genome |
| 7004 | 20130 | 33445 | 3.77 | 4.7E-02 | W01153.1 | EST_HUMAN | yz9709.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:291017 5' similar to contains Alu repetitive element; |
| 7089 | 20091 | 33399 | 0.88 | 4.7E-02 | BF686625.1 | EST_HUMAN | 602143554F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4304772 5' |
| 7089 | 20091 | 33400 | 0.88 | 4.7E-02 | BF686625.1 | EST_HUMAN | 602143554F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4304772 5' |
| 7103 | 20037 | 33340 | 1.56 | 4.7E-02 | M62752.1 | NT | Rat statin-related protein (s1) gene, complete CDS |
| 8584 | 21562 | 34976 | 8.56 | 4.7E-02 | X15543.1 | NT | B. taurus mRNA for RF-36-DNA-binding protein |
| 9305 | 22270 | 35701 | 1.65 | 4.7E-02 | X89211.1 | NT | H. sapiens DNA for endogenous retroviral like element |
| 9327 | 22292 | | 2.51 | 4.7E-02 | AB026678.1 | NT | Gallus gallus Wpki-8 gene, complete cds |
| 9582 | 22544 | 35995 | 7.94 | 4.7E-02 | X15543.1 | NT | B. taurus mRNA for RF-36-DNA-binding protein |
| 10005 | 22932 | 36395 | 0.55 | 4.7E-02 | BF305237.1 | EST_HUMAN | 601892692F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4138414 5' |
| 10092 | 23018 | | 0.56 | 4.7E-02 | A1873042.1 | EST_HUMAN | wet9c10.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347314 3' |
| 12783 | 25970 | | 1.97 | 4.7E-02 | P52951 | SWISSPROT | HOMEBOX PROTEIN GBX-2 (GASTRULATION AND BRAIN-SPECIFIC HOMEBOX PROTEIN 2) |
| 13022 | 25570 | | 1.56 | 4.7E-02 | AJ277662.1 | NT | Homo sapiens partial TUB gene for tubby (mouse) homolog and LMO1 gene for LIM domain only 1 protein |
| 270 | 13366 | 26292 | 1.08 | 4.6E-02 | BE153593.1 | EST_HUMAN | PM0-HT0339-251189-003-g05 HT0339 Homo sapiens cDNA |
| 741 | 13802 | 26741 | 3.47 | 4.6E-02 | AE000445.1 | NT | Escherichia coli K-12 MG1655 section 335 of 400 of the complete genome |
| 1361 | 14365 | 27366 | 3.62 | 4.6E-02 | AV727059.1 | EST_HUMAN | AV727059 HTC Homo sapiens cDNA clone HTC8W01 5' |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 2496 | 15499 | 28525 | 4.32 | 4.6E-02 | AW236023.1 | EST_HUMAN | xn24f03.x1 NCI CGAP_Kid111 Homo sapiens cDNA clone IMAGE:2694653 3' similar to SW:GRF1_HUMAN |
| 2819 | 13366 | 26292 | 1.03 | 4.6E-02 | BE153583.1 | EST_HUMAN | Q12849 G-RICH SEQUENCE FACTOR-1 ; |
| 3020 | 16078 | 28999 | 0.67 | 4.6E-02 | BE153583.1 | EST_HUMAN | PMO-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA |
| 3342 | 16078 | 28999 | 0.67 | 4.6E-02 | BE153583.1 | EST_HUMAN | PMO-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA |
| 3507 | 16078 | 28999 | 0.91 | 4.6E-02 | BE153583.1 | EST_HUMAN | PMO-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA |
| 4149 | 17180 | | 1.24 | 4.6E-02 | AF220365.1 | NT | Mus musculus nucleolar RNA helicase II/Gu (ddx21) gene, complete cds |
| 5252 | 18260 | 31129 | 0.84 | 4.6E-02 | AA079157.1 | EST_HUMAN | zn92c10.s1 Stralagene ovarian cancer (#837219) Homo sapiens cDNA clone IMAGE:545394 3' similar to gb:X03212 KERALATIN, TYPE II CYTOSKELETAL 7 (HUMAN); |
| 5823 | 18913 | 32096 | 1.42 | 4.6E-02 | AF076962.1 | NT | Heplochromis burtoni gonadotropin-releasing hormone and GnRH-associated peptide precursor (GnRH2) gene, complete cds |
| 6357 | 19426 | 32668 | 4.48 | 4.6E-02 | X61624.1 | NT | C.reinhardtii alp2 (alpB) mRNA |
| 6357 | 19426 | 32669 | 4.48 | 4.6E-02 | X61624.1 | NT | C.reinhardtii alp2 (alpB) mRNA |
| 6968 | 20191 | 33518 | 1.51 | 4.6E-02 | A1149574.1 | EST_HUMAN | qc60b06.x1 Soares_placenta_8to9weeks_2NbrHP8to9W Homo sapiens cDNA clone IMAGE:1713871 3' similar to contains L1.13 L1 repetitive element ; |
| 8134 | 21071 | 34470 | 0.66 | 4.6E-02 | 6978720 | NT | Rattus norvegicus Cathepsin H (Ctsh), mRNA |
| 9003 | 21969 | 35391 | 2.89 | 4.6E-02 | BE154006.1 | EST_HUMAN | PMO-HT0339-060400-009-G12 HT0339 Homo sapiens cDNA |
| 11731 | 24617 | 38194 | 5.31 | 4.6E-02 | AA913328.1 | EST_HUMAN | cd27h09.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1524737 3' |
| 12761 | 25967 | | 1.99 | 4.6E-02 | L11692.1 | NT | Oryctolagus cuniculus macrophage scavenger receptor type II mRNA, complete cds |
| 12992 | 25552 | | 8.41 | 4.6E-02 | X57608.1 | NT | Human germline immunoglobulin lambda light chain gene |
| 447 | 13520 | 26453 | 1.9 | 4.5E-02 | P22448 | SWISSPROT | RETINOIC ACID RECEPTOR BETA (RAR-BETA) |
| 1222 | 14260 | 27217 | 0.78 | 4.5E-02 | AF005730.1 | NT | Marburg Virus strain M/S.Africa/Johannesburg/1975/Ozolin VP35 gene, complete cds |
| 1222 | 14260 | 27218 | 0.78 | 4.5E-02 | AF005730.1 | NT | Marburg virus strain M/S.Africa/Johannesburg/1975/Ozolin VP35 gene, complete cds |
| 1821 | 14848 | 27841 | 4.23 | 4.5E-02 | P32182 | SWISSPROT | HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B) |
| 2119 | 15136 | 28156 | 3.34 | 4.5E-02 | AE003964.1 | NT | Xylella fastidiosa, section 110 of 229 of the complete genome |
| 3736 | 16778 | 29691 | 4.42 | 4.5E-02 | AL163278.2 | NT | Homo sapiens chromosome 21 segment HS21C078 |
| 6358 | 19427 | 32670 | 1.63 | 4.5E-02 | AJ400877.1 | NT | Homo sapiens chromosome 21 segment HS21C080 |
| 6656 | 19713 | 32990 | 0.94 | 4.5E-02 | AL163280.2 | NT | Methanosarcina frisia carbon monoxide dehydrogenase large subunit (cdh1A) gene, carbon monoxide dehydrogenase small subunit (cdh1B) gene, complete cds |
| 7062 | 20084 | 33392 | 0.96 | 4.5E-02 | L26487.1 | NT | Methanosarcina frisia carbon monoxide dehydrogenase large subunit (cdh1A) gene, carbon monoxide dehydrogenase small subunit (cdh1B) gene, complete cds |
| 7062 | 20084 | 33393 | 0.96 | 4.5E-02 | L26487.1 | NT | dehydrogenase small subunit (cdh1B) gene, complete cds |
| 8736 | 21704 | 35128 | 2.34 | 4.5E-02 | AF036694.1 | NT | Arabidopsis thaliana CCAAT-box binding factor HAP3 homolog gene, complete cds |

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Table 4
Single Exon Probes Expressed In Bone Marrow

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 10309 | 23233 | 38715 | 4.58 | 4.5E-02 | AA325216.1 | EST_HUMAN | EST28167 Cerebellum II Homo sapiens cDNA 5' end similar to neuro-D4 protein |
| 10460 | 23382 | 38875 | 0.43 | 4.5E-02 | X95508.1 | NT | A. europaeum mRNA for legumin-like protein |
| 10577 | 23499 | 38991 | 0.81 | 4.5E-02 | AB000470.1 | NT | Gallus gallus mRNA for alpha1 integrin, complete cds |
| 12440 | 25203 | 31826 | 2.95 | 4.5E-02 | 11418013 | NT | Homo sapiens ret finger protein-like 3 (RFLP3), mRNA |
| 12823 | 25863 | 31440 | 7.3 | 4.5E-02 | AA191097.1 | EST_HUMAN | zq4311.1 Stratagene HNT neuron (#837233) Homo sapiens cDNA clone IMAGE:332493 5' |
| 222 | 13322 | | 4.84 | 4.4E-02 | BE972733.1 | EST_HUMAN | 601662154F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935388 5' |
| 2107 | 15124 | | 6.38 | 4.4E-02 | P31568 | SWISSPROT | HYPOTHETICAL PROTEIN (ORF 2280) |
| 2498 | 15501 | 28527 | 2.11 | 4.4E-02 | AW875475.1 | EST_HUMAN | QV2-PT0012-010300-070-g02 PT0012 Homo sapiens cDNA |
| 3654 | 16697 | 29612 | 2.01 | 4.4E-02 | AF159160.1 | NT | Myxococcus xanthus serine/threonine kinase Pkn10 (pkn10) gene, complete cds |
| 4657 | 17678 | 30563 | 1.25 | 4.4E-02 | AF109607.1 | NT | Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds |
| 4657 | 17678 | 30564 | 1.25 | 4.4E-02 | AF109607.1 | NT | Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds |
| 4771 | 17791 | | 0.94 | 4.4E-02 | AI222689.1 | NT | Ovis aries CCAAT-enhancer binding protein epsilon gene |
| 7325 | 20296 | 33639 | 0.59 | 4.4E-02 | AF095824.1 | NT | Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds |
| 7325 | 20296 | 33640 | 0.59 | 4.4E-02 | AF095824.1 | NT | Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds |
| 9105 | 22071 | 35497 | 2.17 | 4.4E-02 | AA736966.1 | EST_HUMAN | nm13h03.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1239221 3' |
| 11409 | 24353 | 37886 | 3.75 | 4.4E-02 | AF060669.1 | NT | Hepatitis E virus strain HEV-US2 polyprotein (ORF1), (ORF3), and capsid protein (ORF2) genes, complete cds |
| 11533 | 24474 | 38025 | 2.56 | 4.4E-02 | AA496739.1 | EST_HUMAN | aa33104.1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:887631 5' |
| 12159 | 25014 | | 2.22 | 4.4E-02 | AB040928.1 | NT | Homo sapiens mRNA for KIAA1463 protein, partial cds |
| 12346 | 25980 | | 1.83 | 4.4E-02 | BF241245.1 | EST_HUMAN | 601878746F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4107418 5' |
| 781 | 13841 | 26786 | 5.93 | 4.3E-02 | AF003249.1 | NT | McCrone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds |
| 2575 | 15576 | 28595 | 1.4 | 4.3E-02 | AV704878.1 | EST_HUMAN | AV704878 ADB Homo sapiens cDNA clone ADBACH08 5' |
| 3443 | 16490 | 29409 | 8.93 | 4.3E-02 | AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C010 |
| 3671 | 16714 | | 1.25 | 4.3E-02 | AF080588.1 | NT | Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds |
| 6644 | 19702 | 32977 | 4.62 | 4.3E-02 | P30427 | SWISSPROT | PLECTIN |
| 6644 | 19702 | 32978 | 4.62 | 4.3E-02 | P30427 | SWISSPROT | PLECTIN |
| 6866 | 19948 | 33245 | 0.73 | 4.3E-02 | AA652266.1 | EST_HUMAN | ns68c12.s1 NCI_CGAP_P2 Homo sapiens cDNA clone IMAGE:1188866 |
| 8858 | 21825 | 35248 | 0.9 | 4.3E-02 | AF283359.1 | NT | Homo sapiens desmocollin 3 (DSC3) gene, complete cds, alternatively spliced |
| 9153 | 22119 | 35546 | 0.95 | 4.3E-02 | X55322.1 | NT | H. sapiens NCAM mRNA for neural cell adhesion molecule |
| 9153 | 22119 | 35547 | 0.95 | 4.3E-02 | X55322.1 | NT | H. sapiens NCAM mRNA for neural cell adhesion molecule |
| 823 | 13891 | 26832 | 1.85 | 4.2E-02 | AU123327.1 | EST_HUMAN | AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5' |
| 867 | 13923 | | 2.58 | 4.2E-02 | AU123327.1 | EST_HUMAN | AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5' |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 897 | 13952 | 26910 | 0.83 | 4.2E-02 | AW003645.1 | EST_HUMAN | w34g01.x1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:2545584 3' similar to TR:Q63291 Q63291 |
| 1733 | 14763 | | 1.54 | 4.2E-02 | AL445066.1 | NT | L1 RETROPOSON, ORF2 MRNA ; contains L1.13 L1 repetitive element ; |
| 1793 | 14822 | 27806 | 1.02 | 4.2E-02 | P23091 | SWISSPROT | Thermoplasma acidophilum complete genome; segment 4/5 |
| 3677 | 16720 | 29634 | 2.18 | 4.2E-02 | P23091 | SWISSPROT | TRANSFORMING PROTEIN MAF |
| 4774 | 17794 | 30686 | 0.73 | 4.2E-02 | BF342995.1 | EST_HUMAN | TRANSFORMING PROTEIN MAF |
| | | | | | | | 602017105F1 NCI_CGAP_Bn64 Homo sapiens cDNA clone IMAGE:4152672 5' |
| 5699 | 18794 | 31957 | 0.85 | 4.2E-02 | AF280107.1 | NT | Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds |
| | | | | | | | Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds |
| 5699 | 18794 | 31957 | 0.85 | 4.2E-02 | AF280107.1 | NT | 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds |
| 7175 | 18406 | 31205 | 0.73 | 4.2E-02 | BE268285.1 | EST_HUMAN | 601124596F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:2989319 5' |
| 7769 | 20722 | 34094 | 4.52 | 4.2E-02 | AF276752.1 | NT | Legionella pneumophila catalase-peroxidase (katA) gene, complete cds |
| 7783 | 20745 | 34118 | 0.61 | 4.2E-02 | AV730347.1 | EST_HUMAN | AV730347 HTF Homo sapiens cDNA clone HTFAVH04 5' |
| 9162 | 22128 | 35556 | 3.74 | 4.2E-02 | P05095 | SWISSPROT | ALPHA-ACTININ 3, NON MUSCULAR (F-ACTIN CROSS LINKING PROTEIN) |
| 10525 | 23447 | 36945 | 1.19 | 4.2E-02 | Q19650 | SWISSPROT | T-BRAIN-1 PROTEIN (T-BOX BRAIN PROTEIN 1) (TBR-1) (TES-56) |
| 11379 | 24326 | 37655 | 1.58 | 4.2E-02 | AA976118.1 | EST_HUMAN | on33b11.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1558461 3' similar to gb:M65280 |
| 11637 | 24574 | 38138 | 2.65 | 4.2E-02 | BE815822.1 | EST_HUMAN | INTERLEUKIN-12 BETA CHAIN PRECURSOR (HUMAN); |
| 11637 | 24574 | 38139 | 2.65 | 4.2E-02 | BE815822.1 | EST_HUMAN | PM3-BN0174-250500-009-d10 BN0174 Homo sapiens cDNA |
| 12694 | 25908 | | 5.62 | 4.2E-02 | A1963494.1 | EST_HUMAN | PM3-BN0174-250500-009-d10 BN0174 Homo sapiens cDNA |
| 12990 | 25550 | | 1.69 | 4.2E-02 | D14711.1 | NT | wf49g10.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510850 3' |
| 511 | 13582 | 26503 | 0.75 | 4.1E-02 | AF200629.1 | NT | Staphylococcus aureus HSP10 and HSP60 genes |
| 2685 | 15681 | 28698 | 1.16 | 4.1E-02 | AE002330.2 | NT | Homo sapiens HPS1 gene, intron 5 |
| 4489 | 17524 | | 7.84 | 4.1E-02 | AW893484.1 | EST_HUMAN | Chlamydia muridarum, section 60 of 85 of the complete genome |
| 5302 | 18305 | 31168 | 0.62 | 4.1E-02 | 5602103 | NT | QV1-NN0012-180400-164-068 NN0012 Homo sapiens cDNA |
| 5726 | 18820 | 31999 | 1.08 | 4.1E-02 | BE251894.1 | EST_HUMAN | Homo sapiens SRY (sex-determining region Y)-box 10 (SOX10), mRNA |
| 5726 | 18820 | 32000 | 1.08 | 4.1E-02 | BE251894.1 | EST_HUMAN | 601107535F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343856 5' |
| 7066 | 20098 | | 0.9 | 4.1E-02 | X75881.1 | NT | 601107535F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343856 5' |
| 7306 | 20277 | 33615 | 1.19 | 4.1E-02 | AE002132.1 | NT | A.thaliana mRNA for plasma membrane intrinsic protein 1a |
| 7756 | 20709 | 34078 | 2 | 4.1E-02 | 7662347 | NT | Ureaplasma urealyticum section 33 of 59 of the complete genome |
| | | | | | | | Homo sapiens KIAA0867 protein (KIAA0867), mRNA |
| | | | | | | | Mus musculus proviral insertion in the cGMP-phosphodiesterase (rd beta PDE) gene, intron 1, with the proviral insert encompassing the env pseudogene (3' end) and 3' LTR |
| 7860 | 20804 | 34180 | 0.7 | 4.1E-02 | L02110.1 | NT | |

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Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 8042 | 20978 | 34375 | 2.63 | 4.1E-02 | AF026198.1 | NT | Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit |
| 8549 | 21517 | 34935 | 0.58 | 4.1E-02 | P97857 | SWISSPROT | ADAM-TS 1 PRECURSOR (ADAMTS-1) (ADAM-TS1) |
| 8990 | 21956 | 35381 | 0.57 | 4.1E-02 | P34687 | SWISSPROT | CUTICLE COLLAGEN 34 |
| 9509 | 22472 | 35916 | 0.83 | 4.1E-02 | AA372398.1 | EST_HUMAN | EST84287 Colon adenocarcinoma IV Homo sapiens cDNA 5' end |
| 13013 | 25909 | 31423 | 4.48 | 4.1E-02 | AJ271908.1 | NT | Brassica napus glin gene for plastid glutamine synthetase, exons 1-12 |
| 13102 | 25625 | 31879 | 1.33 | 4.1E-02 | AF254822.1 | NT | Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced |
| 1649 | 14681 | 27854 | 1.21 | 4.0E-02 | AI675392.1 | EST_HUMAN | wb98h01.x1 NCI CGAP Pr28 Homo sapiens cDNA clone IMAGE:2313745 3' |
| 3258 | 16312 | 29233 | 2.57 | 4.0E-02 | AB040904.1 | NT | Homo sapiens mRNA for KIAA1471 protein, partial cds |
| 5453 | 18555 | 31466 | 5.39 | 4.0E-02 | AF280107.1 | NT | Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds |
| 6339 | 19408 | 32849 | 1.43 | 4.0E-02 | BF110434.1 | EST_HUMAN | 7n52h07.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3568380 3' similar to TR:O75296 O75296 R28124.1.; |
| 7954 | 20895 | 34288 | 8.1 | 4.0E-02 | L23838.1 | NT | Strongylocentrotus purpuratus homolog of human bone morphogenetic protein 1 (submp) mRNA, complete cds |
| 8026 | 20963 | | 0.68 | 4.0E-02 | AL161535.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 35 |
| 8043 | 20980 | 34376 | 0.85 | 4.0E-02 | AB000381.1 | NT | Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds |
| 8043 | 20980 | 34377 | 0.85 | 4.0E-02 | AB000381.1 | NT | Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds |
| 9087 | 22033 | 35458 | 2.78 | 4.0E-02 | P08840 | SWISSPROT | GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE)(1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE) |
| 10002 | 22929 | | 0.71 | 4.0E-02 | BF676376.1 | EST_HUMAN | 502153884F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294724 5' |
| 10027 | 22954 | 36423 | 2.95 | 4.0E-02 | AJ000941.1 | NT | Methanobacterium thermoautotrophicum strain Marburg, Thiol:fumarate reductase subunit A |
| 10344 | 23268 | | 0.92 | 4.0E-02 | D43949.1 | NT | Human mRNA for KIAA0082 gene, partial cds |
| 12068 | 24941 | | 1.48 | 4.0E-02 | AJ001018.1 | NT | Kluyveromyces fragilis gene for Car+ ATPase |
| 12331 | 25730 | 31614 | 3.52 | 4.0E-02 | AJ001056.1 | NT | Ovis aries mRNA for acetyl-coA carboxylase |
| 1122 | 14166 | 27118 | 3.13 | 3.9E-02 | BF516149.1 | EST_HUMAN | U1-H-BW1-enx-t-08-Q-U1.st NCI CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084134 3' |
| 1348 | 14383 | 27351 | 1.9 | 3.9E-02 | P41047 | SWISSPROT | FAS ANTIGEN LIGAND |
| 1978 | 14999 | 28001 | 2.82 | 3.9E-02 | AJ403386.1 | NT | Musculus DNA for desmin-binding fragment DesD7 |
| 2715 | 15709 | | 2.12 | 3.9E-02 | 4506862 | NT | Homo sapiens succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD (SDHC) mRNA |
| 5191 | 18200 | 31072 | 0.65 | 3.9E-02 | AW392417.1 | EST_HUMAN | RC6-ST0258-171199-021-C09 ST0258 Homo sapiens cDNA |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 5573 | 18669 | 31630 | 0.74 | 3.9E-02 | D50608.1 | NT | Rat gene for cholecystokinin type-A receptor (CCKAR), complete cds |
| 5573 | 18669 | 31631 | 0.74 | 3.9E-02 | D50608.1 | NT | Rat gene for cholecystokinin type-A receptor (CCKAR), complete cds |
| 5820 | 18910 | 32094 | 1.08 | 3.8E-02 | BE98841.1 | EST_HUMAN | 601649874F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933642 5' |
| 5957 | 19042 | 32241 | 0.71 | 3.9E-02 | BF675203.1 | EST_HUMAN | 602138132F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274910 5' |
| 7259 | 19994 | 33291 | 1.1 | 3.9E-02 | BE271437.1 | EST_HUMAN | 601140729F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049830 5' |
| 8167 | 21105 | 34504 | 0.53 | 3.9E-02 | P48778 | SWISSPROT | ANTIGEN GOR |
| 8172 | 21142 | 34548 | 1.07 | 3.9E-02 | BF239613.1 | EST_HUMAN | 601906848F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134779 5' |
| 8395 | 21364 | 34772 | 0.63 | 3.9E-02 | AJ229041.1 | NT | Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3 |
| 8395 | 21364 | 34773 | 0.63 | 3.9E-02 | AJ229041.1 | NT | Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3 |
| 11737 | 21105 | 34504 | 1.61 | 3.9E-02 | P48778 | SWISSPROT | ANTIGEN GOR |
| 12184 | 25972 | | 14.17 | 3.9E-02 | AB042553.1 | NT | Felis catus G-CSF gene for granulocyte colony-stimulating factor, complete cds |
| 12949 | 25794 | | 5.15 | 3.9E-02 | AL049866.2 | NT | Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mnxq28orf |
| 1969 | 14990 | 27993 | 1.13 | 3.8E-02 | BE885137.1 | EST_HUMAN | 601510891F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912215 5' |
| 2129 | 15146 | | 1.1 | 3.8E-02 | AJ251973.1 | NT | Homo sapiens partial sterih-1 gene |
| 4906 | 17923 | 30815 | 0.92 | 3.8E-02 | BE393275.1 | EST_HUMAN | 601308488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3626757 5' |
| 4906 | 17923 | 30816 | 0.92 | 3.8E-02 | BE393275.1 | EST_HUMAN | 601308488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3626757 5' |
| 4965 | 17980 | 30870 | 1.4 | 3.8E-02 | AJ124122.1 | EST_HUMAN | AJ124122 NT2RM2 Homo sapiens cDNA clone NT2RM2001698 5' |
| 5515 | 18615 | 31548 | 1.2 | 3.8E-02 | M11228.1 | NT | Human protein C gene, complete cds |
| 6206 | 19280 | 32513 | 1.04 | 3.8E-02 | P10284 | SWISSPROT | HOMEOBOX PROTEIN HOX-B4 (HOX-2.6) |
| 7540 | 20503 | 33862 | 1.43 | 3.8E-02 | 6005700 | NT | Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA |
| 9011 | 21977 | | 1.26 | 3.8E-02 | M60675.1 | NT | Human von Willebrand factor gene, exons 23 through 34 |
| 11014 | 23979 | 37505 | 2.04 | 3.8E-02 | AF143952.2 | NT | Homo sapiens PELOTA (PELOTA) gene, complete cds |
| 12009 | 24886 | 38481 | 1.53 | 3.8E-02 | P01641 | SWISSPROT | IG KAPPA CHAIN V-V REGION MOPC 173B PRECURSOR |
| 12009 | 24886 | 38482 | 1.53 | 3.8E-02 | P01641 | SWISSPROT | IG KAPPA CHAIN V-V REGION MOPC 173B PRECURSOR |
| 994 | 14045 | 26999 | 4.78 | 3.7E-02 | P19137 | SWISSPROT | LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN) |
| 1389 | 14423 | 27392 | 0.96 | 3.7E-02 | L14561.1 | NT | Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds |
| 2246 | 15260 | 28287 | 4.98 | 3.7E-02 | A1984806.1 | EST_HUMAN | wf85e03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2484502 3' |
| 3063 | 16120 | 29034 | 1.27 | 3.7E-02 | P79944 | SWISSPROT | ECM5/ODERMIN |
| 3065 | 16122 | 29035 | 4.14 | 3.7E-02 | BF312963.1 | EST_HUMAN | 601986233F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125584 5' |
| 3468 | 16514 | | 1.03 | 3.7E-02 | 6680541 | NT | Mus musculus potassium large conductance pH-sensitive channel, subfamily M, alpha member 3 (Kcnma3), mRNA |
| 5279 | 18285 | 31148 | 0.76 | 3.7E-02 | AF168106.1 | NT | Bubo virginianus cytochrome b gene, partial cds; mitochondrial gene for mitochondrial product |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 7281 | 25988 | | 0.79 | 3.7E-02 | AP000063.1 | NT | Aeropyrum pernix genomic DNA, section 6/7 |
| 7956 | 20897 | 34290 | 0.64 | 3.7E-02 | AE003975.1 | NT | Xylella fastidiosa, section 121 of 229 of the complete genome |
| 10375 | 23298 | | 0.99 | 3.7E-02 | AA782516.1 | EST_HUMAN | ai55c09.s1 Soares parathyroid tumor_NbHPA Homo sapiens cDNA clone 1360912 3' |
| 12225 | 25061 | 38628 | 5.94 | 3.7E-02 | BF124974.1 | EST_HUMAN | 601762117F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4024973 5' |
| 12883 | 25762 | 31520 | 2.34 | 3.7E-02 | 11418392 | NT | Homo sapiens salivary carrier family 22 (organic cation transporter), member 1 (SLC22A1), mRNA |
| 3667 | 16710 | 29625 | 1.04 | 3.6E-02 | X73221.1 | NT | H. vulgare Sst1 gene for sucrose synthase |
| 3674 | 16717 | 29631 | 0.75 | 3.6E-02 | AL096806.1 | NT | Homo sapiens genomic region containing hypervariable minisatellites chromosome 10[10q26.3] of Homo sapiens |
| 5253 | 18261 | 31130 | 2.27 | 3.6E-02 | AL096810.1 | NT | Homo sapiens genomic region containing hypervariable minisatellites chromosome 10[10q26.3] of Homo sapiens |
| 5501 | 18601 | 31514 | 0.8 | 3.6E-02 | X59403.1 | NT | C. glutamicum gap, pdk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase |
| 5501 | 18601 | 31530 | 0.8 | 3.6E-02 | X59403.1 | NT | C. glutamicum gap, pdk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase |
| 5578 | 18674 | 31638 | 0.68 | 3.6E-02 | AF181722.1 | NT | Homo sapiens RU2AS (RU2) mRNA, complete cds |
| 6865 | 19918 | 33212 | 4.97 | 3.6E-02 | AW945516.1 | EST_HUMAN | CM2-EN0013-110500-192-b10 EN0013 Homo sapiens cDNA |
| 6865 | 19918 | 33213 | 4.97 | 3.6E-02 | AW945516.1 | EST_HUMAN | CM2-EN0013-110500-192-b10 EN0013 Homo sapiens cDNA |
| 7150 | 18382 | 31270 | 0.5 | 3.6E-02 | U67575.1 | NT | Methanococcus jannaschii section 117 of 150 of the complete genome |
| 7291 | 20263 | 33597 | 1.7 | 3.6E-02 | AF025952.1 | NT | Chromatium vinosum sulfur globule protein Cx2 precursor (sgp2) gene, complete cds |
| 7527 | 20491 | 33853 | 2.75 | 3.6E-02 | AA714521.1 | EST_HUMAN | nm20e05.s1 NCL_CGAP_GCBO Homo sapiens cDNA clone IMAGE:1241024 3' similar to gb:J00314_ma2 |
| 7895 | 20838 | 34218 | 1.08 | 3.6E-02 | BE143078.1 | EST_HUMAN | TUBULIN BETA-1 CHAIN (HUMAN); |
| 9746 | 22687 | 36142 | 1.85 | 3.6E-02 | U20808.1 | NT | MR0-HT0158-030200-003-b08 HT0158 Homo sapiens cDNA |
| 9746 | 22687 | 36142 | 1.85 | 3.6E-02 | U20808.1 | NT | complete cds |
| 9746 | 22687 | 36142 | 1.85 | 3.6E-02 | U20808.1 | NT | complete cds |
| 9746 | 22687 | 36142 | 1.85 | 3.6E-02 | U20808.1 | NT | complete cds |
| 9971 | 22898 | 36361 | 0.68 | 3.6E-02 | BF347586.1 | EST_HUMAN | 602020453F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4156116 5' |
| 896 | 13951 | 26909 | 0.9 | 3.5E-02 | U09506.1 | NT | Drosophila melanogaster tigrin mRNA, complete cds |
| 1010 | 14059 | 27011 | 1.38 | 3.5E-02 | AF253417.1 | NT | Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds |
| 1566 | 14599 | 27574 | 1.3 | 3.5E-02 | BF678085.1 | EST_HUMAN | 602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5' |
| 1566 | 14599 | 27575 | 1.3 | 3.5E-02 | BF678085.1 | EST_HUMAN | 602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5' |
| 4241 | 17270 | 30155 | 1.95 | 3.5E-02 | AE001773.1 | NT | Thermotoga maritima section 85 of 136 of the complete genome |
| 4344 | 17371 | 30253 | 3.67 | 3.5E-02 | P53780 | SWISSPROT | CYSTATHIONINE BETA-LYASE PRECURSOR (CBL) (BETA-CYSTATHIONASE) (CYSTEINE LYASE) |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 5265 | 18273 | | 1.04 | 3.5E-02 | P47144 | SWISSPROT | HYPOTHETICAL 80.7 KD PROTEIN IN SOD1-CPA2 INTERGENIC REGION |
| 6347 | 19416 | 32857 | 1.74 | 3.5E-02 | J01238.1 | NT | Malva actin 1 gene (MAc1), complete cds |
| 8310 | 21279 | | 0.78 | 3.5E-02 | H29951.1 | EST_HUMAN | yp44a05.r1 Soares retina N2b5HR Homo sapiens cDNA clone IMAGE:190256 5' similar to contains Alu repetitive element. |
| 8970 | 21836 | 35362 | 2.87 | 3.5E-02 | BE968970.1 | EST_HUMAN | 601644701R2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3928737 3' |
| 10378 | 23301 | 39777 | 1.99 | 3.5E-02 | X76642.1 | NT | L lactis MG1363 gfpE and dhak genes |
| 10425 | 23347 | 36832 | 0.47 | 3.5E-02 | BE561042.1 | EST_HUMAN | 601344661F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677654 5' |
| 11823 | 24706 | 38288 | 1.81 | 3.5E-02 | AW881841.1 | EST_HUMAN | PM1-CT0326-291299-002-h03 CT0326 Homo sapiens cDNA |
| 11823 | 24706 | 38289 | 1.81 | 3.5E-02 | AW881841.1 | EST_HUMAN | PM1-CT0326-291299-002-h03 CT0326 Homo sapiens cDNA |
| 12877 | 25806 | | 5.77 | 3.5E-02 | BE276948.1 | EST_HUMAN | 601178765F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3543833 5' |
| 580 | 13649 | 28562 | 0.91 | 3.4E-02 | AK024424.1 | NT | Homo sapiens mRNA for FLJ00013 protein, partial cds |
| 580 | 13649 | 28563 | 0.91 | 3.4E-02 | AK024424.1 | NT | Homo sapiens mRNA for FLJ00013 protein, partial cds |
| 591 | 13649 | 28562 | 3.42 | 3.4E-02 | AK024424.1 | NT | Homo sapiens mRNA for FLJ00013 protein, partial cds |
| 591 | 13649 | 28563 | 3.42 | 3.4E-02 | AK024424.1 | NT | Homo sapiens mRNA for FLJ00013 protein, partial cds |
| 1053 | 14099 | 27049 | 2.4 | 3.4E-02 | AW274020.1 | EST_HUMAN | x26d07.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814253 3' similar to SW:C211_HUMAN P53801 PUTATIVE SURFACE GLYCOPROTEIN C21ORF1 PRECURSOR ; |
| 1211 | 14249 | | 0.51 | 3.4E-02 | 11345459 | NT | Homo sapiens hypothetical protein FLJ13220 (FLJ13220), mRNA |
| 2401 | 15408 | 28432 | 2.51 | 3.4E-02 | T57160.1 | EST_HUMAN | yc20e05.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:81250 5' similar to contains MER29 repetitive element |
| 3444 | 16491 | 29410 | 1.19 | 3.4E-02 | AL163208.2 | NT | Homo sapiens chromosome 21 segment HS21C008 |
| 3942 | 16982 | 29897 | 3.71 | 3.4E-02 | AW794952.1 | EST_HUMAN | RC8-UM0015-210200-021-A10 UM0015 Homo sapiens cDNA |
| 4828 | 17849 | 30537 | 3.05 | 3.4E-02 | X59789.1 | NT | M.musculus S-antigen gene promoter region |
| 5100 | 18110 | | 2.48 | 3.4E-02 | Q26457 | SWISSPROT | LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG) |
| 5114 | 18124 | 30999 | 1.93 | 3.4E-02 | AJ012489.1 | NT | Caenorhabditis elegans mRNA for DYS-1 protein, partial |
| 6330 | 19400 | | 0.63 | 3.4E-02 | BF131828.1 | EST_HUMAN | 601820445F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052434 5' |
| 7032 | 18364 | 31251 | 3.87 | 3.4E-02 | U24393.1 | NT | Human lysyl oxidase-like protein gene, exon 3 |
| 8604 | 21572 | | 3.14 | 3.4E-02 | A1869629.1 | EST_HUMAN | wf99d04.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2433031 3' |
| 9100 | 22068 | 35492 | 1.58 | 3.4E-02 | AA664886.1 | EST_HUMAN | nu70f08.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1216071 similar to contains Alu repetitive element; contains element MER25 MER25 repetitive element ; |
| | | | | | | | zq04f11.s1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:628749 3' similar to TR:G1017425 G1017425 |
| 9268 | 22234 | | 6.2 | 3.4E-02 | AA194306.1 | EST_HUMAN | IPISGKPLPKVTLSDRGVPLKATMRNTEITAEINTLNKESVTADAGRYEITAANSSGGTTKAFINIVLDRPG |
| 10136 | 23062 | | 0.64 | 3.4E-02 | A1092719.1 | EST_HUMAN | PPT.GPWISDITEESVTLKWEPPKVGSGVNTYLLKRETSTAVWTEVSATVARTMMKMKL ... ; |
| | | | | | | | oz59h08.x1 Soares parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1683519 3' |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 372 | 13458 | | 9.24 | 3.3E-02 | AA398735.1 | EST_HUMAN | z75e08.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728198 3' |
| 1171 | 14212 | 27166 | 14.49 | 3.3E-02 | AB035867.1 | NT | Cricetulus griseus CYP2A17 mRNA for cytochrome P450 2A17, complete cds |
| 1845 | 14677 | 27650 | 1.73 | 3.3E-02 | AF110763.1 | NT | Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds |
| 1753 | 14782 | | 1.29 | 3.3E-02 | AE000700.1 | NT | Aquifex aeolicus section 32 of 109 of the complete genome |
| 2096 | 15113 | | 1.76 | 3.3E-02 | R09112.1 | EST_HUMAN | yf25c09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127888 5' |
| 2458 | 15462 | 28485 | 1.31 | 3.3E-02 | 6755962 | NT | Mus musculus tumor rejection antigen gp96 (Trat), mRNA |
| 3372 | 16422 | 28347 | 8.85 | 3.3E-02 | H02389.1 | EST_HUMAN | yf35h02.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:150771 5' |
| 4206 | 14677 | 27650 | 2.36 | 3.3E-02 | AF110763.1 | NT | Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds |
| 4494 | 17519 | 30407 | 1.81 | 3.3E-02 | 6755962 | NT | Mus musculus tumor rejection antigen gp96 (Trat), mRNA |
| 4848 | 17865 | 30759 | 0.66 | 3.3E-02 | AW276696.1 | EST_HUMAN | xp40b04.x1 NCI CGAP_HN11 Homo sapiens cDNA clone IMAGE:2742799 3' |
| 6570 | 19630 | 32896 | 20.14 | 3.3E-02 | BF245995.1 | EST_HUMAN | 601853910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5' |
| 6570 | 19630 | 32897 | 20.14 | 3.3E-02 | BF245995.1 | EST_HUMAN | 601853910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5' |
| 9677 | 22630 | 36084 | 0.71 | 3.3E-02 | BF115621.1 | EST_HUMAN | 7m82d04.x1 NCI CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3562423 3' |
| 9677 | 22630 | 36085 | 0.71 | 3.3E-02 | BF115621.1 | EST_HUMAN | 7m82d04.x1 NCI CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3562423 3' |
| 9779 | 22720 | 36174 | 0.72 | 3.3E-02 | AA488202.1 | EST_HUMAN | ad08f09.s1 Soares NbHFB Homo sapiens cDNA clone IMAGE:877673 3' similar to gb:X70944_cds1 MYOBLAST CELL SURFACE ANTIGEN 24.1D5 (HUMAN); |
| 9779 | 22720 | 36175 | 0.72 | 3.3E-02 | AA488202.1 | EST_HUMAN | ad08f09.s1 Soares NbHFB Homo sapiens cDNA clone IMAGE:877673 3' similar to gb:X70944_cds1 MYOBLAST CELL SURFACE ANTIGEN 24.1D5 (HUMAN); |
| 10964 | 23894 | | 0.46 | 3.3E-02 | H38109.1 | EST_HUMAN | yp51f11.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:190989 3' |
| 11455 | 24368 | 37945 | 2.47 | 3.3E-02 | BF681107.1 | EST_HUMAN | 602247171F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:4332497 5' |
| 12425 | 25163 | | 3.71 | 3.3E-02 | T96545.1 | EST_HUMAN | ye49f11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121101 5' |
| 12547 | 25270 | | 1.69 | 3.3E-02 | AF289965.1 | NT | Mus musculus EIF4H gene, partial cds; LIMK1 gene, complete cds; and ELN gene, partial cds |
| 12577 | 25286 | | 3.04 | 3.3E-02 | M81890.1 | NT | Human interleukin 11 (IL11) gene, complete mRNA |
| 132 | 13237 | 26168 | 1.27 | 3.2E-02 | AJ002005.1 | NT | Oryzibolagus culiculus gene encoding ileal sodium-dependent bile acid transporter |
| 1128 | 14171 | 27122 | 10.01 | 3.2E-02 | AF098275.1 | NT | Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68a allele, complete cds |
| 1128 | 14171 | 27123 | 10.01 | 3.2E-02 | AF098275.1 | NT | Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68b allele, complete cds |
| 2127 | 15144 | | 3.6 | 3.2E-02 | P28955 | SWISSPROT | LARGE TEGUMENT PROTEIN |
| 3151 | 16208 | 29122 | 9.61 | 3.2E-02 | BE867353.1 | EST_HUMAN | 601442431F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846727 5' |
| 4246 | 17275 | | 16.99 | 3.2E-02 | X94768.1 | NT | H.sapiens RP3 gene (XLRP gene3) |
| 4801 | 17818 | 30712 | 3.75 | 3.2E-02 | AF114182.1 | NT | Saxifraga nidifica maturase (matK) gene, chloroplast gene encoding chloroplast protein, partial cds |
| 5303 | 18306 | | 1.34 | 3.2E-02 | Y08924.1 | NT | P.falciparum mRNA for AARP2 protein |
| 5613 | 18709 | 31866 | 1.56 | 3.2E-02 | X68709.1 | NT | S.griseocarinum whiG-Siv gene |
| 5613 | 18709 | 31867 | 1.56 | 3.2E-02 | X68709.1 | NT | S.griseocarinum whiG-Siv gene |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Description |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 6673 | 19730 | 33006 | 2.23 | 3.2E-02 | M32437.1 | NT | Rat/polyomavirus left junction in cell line W98.14 |
| 6676 | 19733 | | | | | | Yd33h12.e1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:110087 3' similar to contains |
| 6763 | 19817 | 33097 | 30.53 | 3.2E-02 | T89367.1 | EST_HUMAN | Alu repetitive element; contains LTR1 repetitive element; |
| 8039 | 20978 | 34372 | 4.01 | 3.2E-02 | AF173845.1 | NT | Saguius oedipus tissue kallikrein gene, complete cds |
| 8643 | 21611 | 35033 | 0.82 | 3.2E-02 | 11424049 | NT | Homo sapiens cytochrome P450, subfamily 1B (phenobarbital-inducible) (CYP2B), mRNA |
| 9293 | 22259 | | 2.84 | 3.2E-02 | 6880565 | NT | Mus musculus kinesin family member 3c (Kif3c), mRNA |
| 9580 | 22542 | 35992 | 0.7 | 3.2E-02 | AF109718.1 | NT | Homo sapiens chromosome 3 subtelomeric region |
| 9580 | 22542 | 35993 | 1.02 | 3.2E-02 | A1278971.1 | EST_HUMAN | qm17b04.x1 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1882063 3' |
| 10417 | 23339 | | 1.02 | 3.2E-02 | A1278971.1 | EST_HUMAN | qm17b04.x1 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1882063 3' |
| 10723 | 23645 | 37138 | 4.18 | 3.2E-02 | AA719795.1 | EST_HUMAN | zg54b12.e1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:397151 3' similar to |
| 12812 | 25978 | | 0.98 | 3.2E-02 | U96762.1 | NT | gbL08441 CYTOCHROME C OXIDASE POLYPEPTIDE III (HUMAN); |
| 1285 | 14300 | | | | | | Macaca mulatta chemokine receptor CCR5 mRNA, complete cds |
| 1308 | 14344 | 27309 | 1.43 | 3.2E-02 | V00574.1 | NT | Human germ line gene homologous to bladder carcinoma oncogene T24 (Gene code c-Ha-ras-1) with four exons |
| 1909 | 14933 | 27929 | 2.28 | 3.1E-02 | 4503418 | NT | Homo sapiens dual specificity phosphatase 4 (DUSP4) mRNA |
| 1991 | 18012 | | 1.87 | 3.1E-02 | P18845 | SWISSPROT | NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR (GF-ALPHA-3) |
| 5336 | 18441 | 31194 | 1 | 3.1E-02 | 6671594 | NT | Mus musculus adaptor-related protein complex AP-3, delta subunit (Ap3d), mRNA |
| 5434 | 18536 | | 1.18 | 3.1E-02 | Z50097.1 | NT | Drosophila melanogaster mRNA for headcase protein |
| 5731 | 18825 | 32005 | 1.28 | 3.1E-02 | U78104.1 | NT | Human leukemia inhibitory factor receptor (LIFR) gene, promoter and partial exon 1 |
| 5803 | 25645 | 32078 | 2.26 | 3.1E-02 | AA278478.1 | EST_HUMAN | zs81a08.r1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703858 5' |
| 10391 | 23313 | 36793 | 0.81 | 3.1E-02 | BF687742.1 | EST_HUMAN | 602068783F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4066789 5' |
| 1627 | 14680 | | | | | | Neisseria meningitidis DNA for region 2 (flaB- and flaC-homologs, unknown genes) and flanking genes, |
| 2590 | 15591 | 28608 | 0.52 | 3.1E-02 | AJ391284.1 | NT | strain FAM18 |
| 3579 | 18624 | 29545 | 2.55 | 3.1E-02 | AF034778.1 | NT | Enterococcus faecalis surface protein precursor, gene, complete cds |
| 3666 | 18709 | 29624 | | | | | |
| 3758 | 18789 | | | | | | |
| 3969 | 17009 | | 2.21 | 3.0E-02 | AF187125.1 | NT | Ptychoteles minutus cytochrome oxidase I gene, partial cds; mitochondrial gene for mitochondrial product |
| 5092 | 18102 | 30877 | 0.97 | 3.0E-02 | AA402242.1 | EST_HUMAN | z65h03.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727263 5' |
| 5465 | 18587 | | 0.91 | 3.0E-02 | M94176.1 | NT | Saccharomyces cerevisiae stem-loop mutation suppressor SSL2 gene, complete cds |
| | | | 2.77 | 3.0E-02 | AF247644.1 | NT | Pseudomonas fluorescens family II aminotransferase gene, complete cds |
| | | | 0.98 | 3.0E-02 | AW620223.1 | EST_HUMAN | QV2-ST0298-150200-040-a09 ST0298 Homo sapiens cDNA |
| | | | 1.45 | 3.0E-02 | A384003.1 | EST_HUMAN | EST74530 Pineal gland II Homo sapiens cDNA 5' end |
| | | | 7.41 | 3.0E-02 | AF281074.1 | NT | Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced |
| | | | 7.41 | 3.0E-02 | AF281074.1 | NT | Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced |
| | | | 2.99 | 3.0E-02 | AB046763.1 | NT | Homo sapiens mRNA for KIAA1573 protein, partial cds |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 6383 | 19451 | 32663 | 0.58 | 3.0E-02 | N99615.1 | EST_HUMAN | za39a10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294906 5' similar to contains element TAR1 repetitive element ; |
| 6383 | 19451 | 32694 | 0.58 | 3.0E-02 | N99615.1 | EST_HUMAN | za39a10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294906 5' similar to contains element TAR1 repetitive element ; |
| 6957 | 20182 | 33505 | 3.17 | 3.0E-02 | AJ242806.1 | NT | Cyrtinus carpio mRNA for inducible nitric oxide synthase (iNOS gene) |
| 7091 | 20025 | 33327 | 2.8 | 3.0E-02 | BE889948.1 | EST_HUMAN | 601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5' |
| 7091 | 20025 | 33328 | 2.8 | 3.0E-02 | BE889948.1 | EST_HUMAN | 601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5' |
| 7274 | 20009 | 33310 | 2.29 | 3.0E-02 | AF213884.1 | NT | Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds |
| 7274 | 20009 | 33311 | 2.29 | 3.0E-02 | AF213884.1 | NT | Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds |
| 7442 | 20408 | 33760 | 1.29 | 3.0E-02 | M86524.1 | NT | Human dystrophin gene |
| 7836 | 20783 | | 0.75 | 3.0E-02 | BF248361.1 | EST_HUMAN | 601854981F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4074548 5' |
| 8463 | 21432 | | 0.48 | 3.0E-02 | BF679706.1 | EST_HUMAN | 602154364F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4285654 5' |
| 8888 | 21954 | 35378 | 0.74 | 3.0E-02 | BF353889.1 | EST_HUMAN | IL5-HT0704-280600-108-c04 HT0704 Homo sapiens cDNA |
| 9145 | 22111 | | 1.82 | 3.0E-02 | AF275654.1 | NT | Omithorhynchus anathus coagulation factor X mRNA, complete cds |
| 10826 | 23747 | 37248 | 1.66 | 3.0E-02 | AE001797.1 | NT | Thermotoga maritima section 109 of 138 of the complete genome |
| 11566 | 24506 | 38063 | 2.36 | 3.0E-02 | M81357.1 | NT | Human coagulation factor VII (F7) gene exon 1 and factor X (F10) gene, exon 1 |
| 11997 | 24874 | 38470 | 7.84 | 3.0E-02 | AA463216.1 | EST_HUMAN | ne87f04.s1 NCI CGAP Kid1 Homo sapiens cDNA clone IMAGE:911263 |
| 12529 | 25960 | 31316 | 2.02 | 3.0E-02 | R32019.1 | EST_HUMAN | yh83d04.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:134407 3' |
| 12868 | 25470 | | 2.06 | 3.0E-02 | AW895565.1 | EST_HUMAN | QV4-NN0038-270400-167-005 NN0038 Homo sapiens cDNA |
| 12908 | 25954 | | 1.96 | 3.0E-02 | AF046887.1 | NT | Rattus norvegicus UDP-Gal:glucosylceramide beta-1,4-galactosyltransferase mRNA, complete cds |
| 2442 | 15993 | 28487 | 1 | 2.9E-02 | AF228703.1 | NT | Homo sapiens mitochondrial glutathione reductase and cytosolic glutathione reductase (GRD1) gene, complete cds, alternatively spliced |
| 3005 | 16063 | 28982 | 1.14 | 2.9E-02 | BE865644.1 | EST_HUMAN | 601338428F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680695 5' |
| 3005 | 16063 | 28983 | 1.14 | 2.9E-02 | BE865644.1 | EST_HUMAN | 601338428F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680695 5' |
| 3573 | 16618 | 28540 | 0.8 | 2.9E-02 | X55294.1 | NT | Sheep gene for ultra high-sulphur keratin protein |
| 3950 | 16990 | 28906 | 0.72 | 2.9E-02 | H72805.1 | EST_HUMAN | yu07e10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:233130 5' |
| 6181 | 19256 | 32489 | 1.13 | 2.9E-02 | AF060221.1 | NT | Sus scrofa deoxyribonuclease II mRNA, complete cds |
| 6424 | 19491 | 32743 | 7.33 | 2.9E-02 | BF032233.1 | EST_HUMAN | 601452681F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3856598 5' |
| 7142 | 20118 | 33431 | 0.52 | 2.9E-02 | AJ391284.1 | NT | Neisseria meningitidis DNA for region 2 (flaB- and flacC-homologs, unknown genes) and flanking genes, strain FAM18 |
| 7460 | 20426 | 33782 | 10.95 | 2.9E-02 | BE271437.1 | EST_HUMAN | 601140729F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049830 5' |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 7657 | 20617 | 33982 | 0.67 | 2.9E-02 | D29214.1 | EST_HUMAN | HUMNK262 Human epidermal keratinocyte Homo sapiens cDNA clone 262 |
| 8169 | 21107 | 34506 | 0.53 | 2.9E-02 | AE003932.1 | NT | Xyella fastidiosa, section 78 of 229 of the complete genome |
| 8331 | 21300 | 34716 | 0.83 | 2.9E-02 | AF129279.1 | NT | Buchnera aphidicola natural-host Schlechtendalia chinensis gluconate-6-phosphate dehydrogenase (gnd) gene, partial cds |
| 8331 | 21300 | 34717 | 0.83 | 2.9E-02 | AF129279.1 | NT | Buchnera aphidicola natural-host Schlechtendalia chinensis gluconate-6-phosphate dehydrogenase (gnd) gene, partial cds |
| 10016 | 22943 | 36409 | 2.26 | 2.9E-02 | AW875979.1 | EST_HUMAN | CM3-PT0014-071299-051-c04 PT0014 Homo sapiens cDNA |
| 10016 | 22943 | 36410 | 2.28 | 2.9E-02 | AW875979.1 | EST_HUMAN | CM3-PT0014-071299-051-c04 PT0014 Homo sapiens cDNA |
| 10233 | 23158 | | 0.67 | 2.9E-02 | AW976597.1 | EST_HUMAN | EST388706 MAGE resequences, MAGN Homo sapiens cDNA |
| 10710 | 23632 | 37127 | 1.07 | 2.9E-02 | AP000064.1 | NT | Aeropyrum pernix genomic DNA, section 777 |
| 11388 | 16818 | 29540 | 1.6 | 2.9E-02 | X55294.1 | NT | Sheep gene for ultra high-sulphur keratin protein |
| 12531 | 25870 | | 1.46 | 2.9E-02 | AU135817.1 | EST_HUMAN | AU135817 PLACE1 Homo sapiens cDNA clone PLACE1002962 5' |
| 567 | 13637 | | 1.93 | 2.9E-02 | AW970153.1 | EST_HUMAN | EST382234 MAGE resequences, MAGK Homo sapiens cDNA |
| 3380 | 16429 | 29355 | 1.27 | 2.9E-02 | AF066063.1 | NT | Homo sapiens retinal fascic (FSCN2) gene, exon 2 |
| 3380 | 16429 | 29356 | 1.27 | 2.9E-02 | AF066063.1 | NT | Homo sapiens retinal fascic (FSCN2) gene, exon 2 |
| 4341 | 17368 | | 0.67 | 2.9E-02 | 8393751 | NT | Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA |
| 5206 | 18215 | 31090 | 3.2 | 2.8E-02 | N87073.1 | EST_HUMAN | L2083F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone L2083 5' similar to TRNA-GUANINE TRANSGLYCOSYLASE |
| 5294 | 18299 | | 0.93 | 2.8E-02 | M58493.1 | NT | Dengue virus type 2 non-structural protein 1 (NS1) gene, partial cds |
| 5565 | 18662 | 31622 | 10.89 | 2.8E-02 | BE741083.1 | EST_HUMAN | 601594078F1 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:3948067 5' |
| 6991 | 20204 | 33533 | 1.13 | 2.8E-02 | T78960.1 | EST_HUMAN | y421b08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108855 5' |
| 8671 | 21639 | 35063 | 2.24 | 2.8E-02 | AJ005820.1 | NT | Craterosigma plantagineum mRNA for homeodomain leucine zipper protein (hb-1) |
| 9371 | 22336 | 35786 | 0.82 | 2.8E-02 | AA280762.1 | EST_HUMAN | zs96c06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:711468 5' |
| 9563 | 22825 | 35974 | 1.03 | 2.8E-02 | AF187872.1 | NT | Cavia porcellus inwardly-rectifying potassium channel Kir2.1 (KCNJ2) gene, complete cds |
| 9667 | 22620 | 36071 | 0.71 | 2.8E-02 | AE001092.1 | NT | Archaeoglobus fulgidus section 15 of 172 of the complete genome |
| 10980 | 23900 | 37413 | 0.42 | 2.8E-02 | BF527244.1 | EST_HUMAN | 602039477F2 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4177267 5' |
| 12809 | 25801 | | 1.6 | 2.8E-02 | R08966.1 | EST_HUMAN | yf12h02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:126675 5' |
| 12815 | 25438 | | 1.57 | 2.8E-02 | X06322.1 | NT | Yeast CN31C chromosome III RAHS DNA (right arm transcription hot-spot) |
| | | | | | | | Human gamma T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S> |
| 1485 | 14518 | 27491 | 1.07 | 2.7E-02 | U66059.1 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6 |
| 3445 | 16492 | 29411 | 1.88 | 2.7E-02 | AL161494.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6 |
| 4230 | 17259 | 30143 | 2.01 | 2.7E-02 | N47258.1 | EST_HUMAN | y98h12.r1 Soares multiple_sclerosis_2NbrMSP Homo sapiens cDNA clone IMAGE:280487 5' |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 4230 | 17269 | 30144 | 2.01 | 2.7E-02 | N47268.1 | EST_HUMAN | y66h12.r1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:280487 5' |
| 5319 | 18425 | 31176 | 0.52 | 2.7E-02 | BF245672.1 | EST_HUMAN | 60186481F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4083075 5' |
| 5516 | 18616 | 31549 | 1.09 | 2.7E-02 | R12245.1 | EST_HUMAN | y63d09.r1 Soares fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:128637 5' similar to SP-JC2264 JC2264 TISSUE FACTOR PATHWAY INHIBITOR - RHESUS ; |
| 6005 | 19088 | 32288 | 0.68 | 2.7E-02 | XG1670.1 | NT | T.aestivum pTTH20 mRNA for wheat type V thionin |
| 6087 | 19167 | 32379 | 0.51 | 2.7E-02 | AB004799.1 | NT | Oryza sativa mRNA for ascorbate oxidase, partial cds |
| 6754 | 19808 | | 1.03 | 2.7E-02 | X97580.1 | NT | A.bisporus pgkA gene |
| 7289 | 20004 | 33304 | 1.93 | 2.7E-02 | AA983571.1 | EST_HUMAN | at9dh03.s1 Soares total_fetus Nb2HF8 9w Homo sapiens cDNA clone IMAGE:1624661 3' |
| 8140 | 21077 | | 0.53 | 2.7E-02 | AK024456.1 | NT | Homo sapiens mRNA for FLJ00048 protein, partial cds |
| 8160 | 21088 | 34497 | 0.59 | 2.7E-02 | 9256542 | NT | Mus musculus G21 protein (G21), mRNA |
| 8697 | 21665 | | 1.23 | 2.7E-02 | AI377036.1 | EST_HUMAN | tc28g08.x1 Soares total_fetus Nb2HF8 9w Homo sapiens cDNA clone IMAGE:2065982 3' similar to contains Alu repetitive element; |
| 573 | 13642 | 28556 | 1.25 | 2.6E-02 | AL163282.2 | NT | Homo sapiens chromosome 21 segment HS21C082 |
| 2374 | 15382 | 28404 | 2.54 | 2.6E-02 | AA490021.1 | EST_HUMAN | ab02b02.s1 Stratagene fetal retina 537202 Homo sapiens cDNA clone IMAGE:839595 3' |
| 2376 | 15384 | 28406 | 3.05 | 2.6E-02 | 6754241 | NT | Mus musculus histidine rich calcium binding protein (Hrc), mRNA |
| 2376 | 15384 | 28407 | 3.05 | 2.6E-02 | 6754241 | NT | Mus musculus histidine rich calcium binding protein (Hrc), mRNA |
| 2926 | 15984 | | 1.52 | 2.6E-02 | AF109906.1 | NT | Mus musculus MHC class III region RD gene, partial cds; Bf, C2, G8A, NG22, G9, HSP70, HSP70, HSC70L, and smRNP genes, complete cds; G7A gene, partial cds; and unknown genes |
| 3988 | 17028 | | 0.91 | 2.6E-02 | AW181945.1 | EST_HUMAN | xj68f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2662409 3' |
| 4942 | 17958 | 30848 | 3.25 | 2.6E-02 | L12032.1 | NT | Chicken dorsalin-1 mRNA, complete cds |
| 5104 | 18114 | 30987 | 1.8 | 2.6E-02 | AE002014.1 | NT | Deinococcus radiodurans R1 section 151 of 229 of the complete chromosome 1 |
| 5128 | 18137 | 31014 | 3.05 | 2.6E-02 | AW241154.1 | EST_HUMAN | xa52b04.x1 NCL_CGAP_Sar4 Homo sapiens cDNA clone IMAGE:2570383 3' similar to SW:Y069_HUMAN Q15041 HYPOTHETICAL PROTEIN KIAA0069 ; |
| 5944 | 19030 | | 0.6 | 2.6E-02 | AL161563.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63 |
| 5992 | 19076 | | 0.55 | 2.6E-02 | AL161563.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63 |
| 6345 | 19414 | | 6.38 | 2.6E-02 | AI206030.1 | EST_HUMAN | qq27f11.x1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1762317 3' |
| 6565 | 19625 | 32890 | 1.88 | 2.6E-02 | BE621748.1 | EST_HUMAN | 601493473T1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895578 3' |
| 7001 | 20127 | 33441 | 0.82 | 2.6E-02 | Z99064.1 | NT | Vaccinia virus ORF1L, strain Wyeth |
| 7001 | 20127 | 33442 | 0.82 | 2.6E-02 | Z99064.1 | NT | Vaccinia virus ORF1L, strain Wyeth |
| 7095 | 20029 | 33333 | 6.03 | 2.6E-02 | 6981271 | NT | Rattus norvegicus Nerve growth factor receptor, fast (Ngfr), mRNA |
| 7516 | 20481 | 33842 | 0.55 | 2.6E-02 | P21894 | SWISSPROT | ALANYL-TRNA SYNTHETASE (ALANINE-TRNA LIGASE) (ALARS) |
| 8850 | 21817 | 35237 | 0.71 | 2.6E-02 | AA860946.1 | EST_HUMAN | ak22f04.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1406719 3' |
| 9715 | 22743 | 36194 | 1.27 | 2.6E-02 | 11432020 | NT | Homo sapiens KIAA1070 protein (KIAA1070), mRNA |

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Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 10072 | 22999 | 36468 | 0.7 | 2.8E-02 | AF114952.1 | NT | Saccharomyces dairenensis NRRL Y-12639(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene encoding mitochondrial protein, complete cds |
| 10072 | 22999 | 36469 | 0.7 | 2.8E-02 | AF114952.1 | NT | Saccharomyces dairenensis NRRL Y-12639(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene encoding mitochondrial protein, complete cds |
| 10768 | 23689 | 37188 | 4.31 | 2.8E-02 | AL163303.2 | NT | Homo sapiens chromosome 21 segment HS21C103 |
| 11717 | 24690 | | 2.02 | 2.8E-02 | AA279351.1 | EST_HUMAN | z884c02.f1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704162 5' |
| 11869 | 24770 | 38359 | 1.61 | 2.8E-02 | AW500547.1 | EST_HUMAN | U14F-BND-alc-e-10-0-UJ.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077466 5' |
| 12457 | 25944 | 31313 | 1.96 | 2.8E-02 | BF343827.1 | EST_HUMAN | 602015601F1 NCI_CGAP_Bn64 Homo sapiens cDNA clone IMAGE:4150944 5' |
| 533 | 13604 | 26522 | 1.85 | 2.8E-02 | AI793130.1 | EST_HUMAN | on26f06.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5' |
| 533 | 13604 | 26523 | 1.85 | 2.8E-02 | AI793130.1 | EST_HUMAN | on26f06.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5' |
| 810 | 13668 | 26817 | 9.19 | 2.8E-02 | BE974314.1 | EST_HUMAN | 601680305F2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950685 3' |
| 870 | 13926 | 26894 | 6.9 | 2.8E-02 | BE974314.1 | EST_HUMAN | 601680305F2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950685 3' |
| 2773 | 15765 | | 2.26 | 2.8E-02 | U12571.1 | NT | Rattus norvegicus rabphilin-3A mRNA, complete cds |
| 2968 | 16026 | 28949 | 3.43 | 2.8E-02 | X99697.1 | NT | H. carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1 |
| 2968 | 16026 | 28950 | 3.43 | 2.8E-02 | X99697.1 | NT | H. carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1 |
| 4075 | 18316 | 30005 | 1.02 | 2.8E-02 | BE701165.1 | EST_HUMAN | PM2-NN0128-080700-001-a12 NN0128 Homo sapiens cDNA |
| 4075 | 18316 | 30006 | 1.02 | 2.8E-02 | BE701165.1 | EST_HUMAN | PM2-NN0128-080700-001-a12 NN0128 Homo sapiens cDNA |
| 4233 | 17262 | 30146 | 6.52 | 2.8E-02 | AW592114.1 | EST_HUMAN | nf36h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2834015 3' |
| 5799 | 18891 | 32073 | 0.65 | 2.8E-02 | AI732776.1 | EST_HUMAN | zx83c10.x5 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:810364 3' |
| 6317 | 19388 | | 4.71 | 2.8E-02 | BE870128.1 | EST_HUMAN | 7e30e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284008 3' similar to contains L1.t1 L1 repetitive element ; |
| 6334 | 19403 | | 4.42 | 2.8E-02 | BE746888.1 | EST_HUMAN | 601579393F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928054 5' |
| 6470 | 19535 | 32783 | 0.97 | 2.8E-02 | L29029.1 | NT | Chlamydomonas reinhardtii VSP-3 mRNA, complete cds |
| 7927 | 20870 | 34258 | 1.48 | 2.8E-02 | BF526722.1 | EST_HUMAN | 602070562F1 NCI_CGAP_Bn64 Homo sapiens cDNA clone IMAGE:4213406 5' |
| 7927 | 20870 | 34259 | 1.48 | 2.8E-02 | BF526722.1 | EST_HUMAN | 602070562F1 NCI_CGAP_Bn64 Homo sapiens cDNA clone IMAGE:4213406 5' |
| 8137 | 21074 | 34474 | 0.54 | 2.8E-02 | AF129458.1 | NT | Chlamydomonas reinhardtii class II DNA photolyase (PHR2) gene, complete cds |
| 9177 | 22143 | 35570 | 0.82 | 2.8E-02 | Q91713 | SWISSPROT | CHORDIN PRECURSOR (ORGANIZER-SPECIFIC SECRETED DORSALIZING FACTOR) |
| 9315 | 22280 | 35710 | 0.46 | 2.8E-02 | AW026821.1 | EST_HUMAN | wu08c10.x1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:2516370 3' |
| 10428 | 23348 | | 0.55 | 2.8E-02 | X71303.1 | NT | D radicum 28S ribosomal RNA, D2 domain |
| 10947 | 23867 | 37381 | 0.67 | 2.8E-02 | AI147615.1 | EST_HUMAN | qb22ad08.x1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone IMAGE:1696982 3' |
| 11161 | 24119 | 37646 | 2.15 | 2.8E-02 | Q10335 | SWISSPROT | HYPOTHETICAL 48.7 KD PROTEIN C19G10.05 IN CHROMOSOME I |
| 11161 | 24119 | 37647 | 2.15 | 2.8E-02 | Q10335 | SWISSPROT | HYPOTHETICAL 48.7 KD PROTEIN C19G10.05 IN CHROMOSOME I |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 11227 | 24180 | | 3.01 | 2.5E-02 | AF050157.1 | NT | Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (IiAlpha) and major histocompatibility protein class II beta chain (IiBeta) genes, complete cds; |
| 12059 | 24932 | | 1.47 | 2.5E-02 | AB007546.1 | NT | butyrophilin-like (NG9), butyrophilin-IP |
| 12418 | 25885 | | 3.35 | 2.5E-02 | 11420078 | NT | Homo sapiens gene for LECT2, complete cds |
| 12598 | 25751 | | 1.47 | 2.5E-02 | 11433220 | NT | Homo sapiens similar to ALEX3 protein (H. sapiens) (LOC63634), mRNA |
| 12686 | 25353 | | 2.24 | 2.5E-02 | U60169.1 | NT | Homo sapiens mitogen-activated protein kinase kinase kinase 13 (MAP3K13), mRNA |
| 12709 | 25365 | 31770 | 3.42 | 2.5E-02 | BE973327.1 | EST_HUMAN | Dicotyledonous dicotyledon putative protein kinase MkcA (mkcA) gene, complete cds |
| 175 | 13276 | 26203 | 0.99 | 2.4E-02 | A1376582.1 | EST_HUMAN | 601662365R2 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:2070156 3' |
| 1802 | 14634 | 27610 | 2.24 | 2.4E-02 | H65884.1 | EST_HUMAN | tc75c07.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:2070156 3' |
| 2060 | 15884 | 28098 | 1.73 | 2.4E-02 | P01901 | SWISSPROT | yt75f11.1 Soares_fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211149 5' |
| 2060 | 15884 | 28099 | 1.73 | 2.4E-02 | P01901 | SWISSPROT | H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B)) |
| 4396 | 17424 | 30308 | 1.43 | 2.4E-02 | J05110.1 | NT | H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B)) |
| 4549 | 17572 | 30461 | 1.43 | 2.4E-02 | P01901 | SWISSPROT | T.thermophila calcium-binding 25 kDa (TCBP 25) protein mRNA, complete cds |
| 4549 | 17572 | 30462 | 1.43 | 2.4E-02 | P01901 | SWISSPROT | H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B)) |
| 5227 | 18235 | | 0.9 | 2.4E-02 | AL161595.2 | NT | H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B)) |
| 6340 | 19409 | 32650 | 0.97 | 2.4E-02 | W86680.1 | EST_HUMAN | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91 |
| 6496 | 19560 | 32611 | 0.85 | 2.4E-02 | M31650.1 | NT | zh63h04.s1 Soares_fetal liver spleen 1NFLS_S1 Homo sapiens cDNA clone IMAGE:416791 3' |
| 6496 | 19560 | 32612 | 0.85 | 2.4E-02 | M31650.1 | NT | Chicken myristoylated alanine-rich C kinase substrate (MARCKS) mRNA, complete cds |
| 7431 | 20398 | 33750 | 1.38 | 2.4E-02 | Z20573.1 | EST_HUMAN | Chicken myristoylated alanine-rich C kinase substrate (MARCKS) mRNA, complete cds |
| 7448 | 20414 | 33767 | 1.05 | 2.4E-02 | X12925.1 | NT | HSAACCKVX T; Human adult Rhabdomyosarcoma cell-line Homo sapiens cDNA |
| 7448 | 20414 | 33768 | 1.05 | 2.4E-02 | X12925.1 | NT | Rat gene for uncoupling protein (UCP) |
| 8159 | 21097 | 34495 | 0.52 | 2.4E-02 | P98092 | SWISSPROT | Rat gene for uncoupling protein (UCP) |
| 8159 | 21097 | 34496 | 0.52 | 2.4E-02 | P98092 | SWISSPROT | HEMOCYTIN PRECURSOR (HUMORAL LECTIN) |
| 8222 | 21191 | | 0.57 | 2.4E-02 | AW813007.1 | EST_HUMAN | HEMOCYTIN PRECURSOR (HUMORAL LECTIN) |
| 8275 | 21244 | | 0.58 | 2.4E-02 | M16780.1 | NT | RC3-ST0186-230300-019-h08 ST0186 Homo sapiens cDNA |
| 8784 | 21751 | | 0.53 | 2.4E-02 | H78376.1 | EST_HUMAN | Human retrotransposon 3' long terminal repeat |
| 8876 | 21843 | 35285 | 11.43 | 2.4E-02 | N69442.1 | EST_HUMAN | yu12c05.s1 Soares_fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:233576 3' similar to contains |
| 9338 | 22303 | 35731 | 0.49 | 2.4E-02 | AE001125.1 | NT | Alu repetitive element; contains A3R repetitive element ; |
| | | | | | | | za35g11.s1 Soares_fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294598 3' similar to |
| | | | | | | | gb K02909 RATSRK Rat (RNA); contains A3R.b1 A3R repetitive element ; |
| | | | | | | | Borrelia burgdorferi (section 11 of 70) of the complete genome |
| | | | | | | | zu97c06.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745354 3' similar to gb:J04422 [SLET |
| 9363 | 22328 | 35757 | 0.81 | 2.4E-02 | AA625680.1 | EST_HUMAN | AMYLOID POLYPEPTIDE PRECURSOR (HUMAN); contains Alu repetitive element; contains element XTR |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 10050 | 22877 | 36443 | 0.46 | 2.4E-02 | AF124160.1 | NT | Arabidopsis thaliana molybdopter in synthase sulphurylase (cnx5) gene, complete cds |
| 10050 | 22877 | 36444 | 0.46 | 2.4E-02 | AF124160.1 | NT | Arabidopsis thaliana molybdopter in synthase sulphurylase (cnx5) gene, complete cds |
| 10165 | 23090 | 36568 | 2.57 | 2.4E-02 | AV692954.1 | EST_HUMAN | AV692954 GKC Homo sapiens cDNA clone GKDCSC03 5' |
| 10340 | 23284 | 38743 | 2.76 | 2.4E-02 | AA493894.1 | EST_HUMAN | nh07b12.s1 NCI_CGAP_Thyl1 Homo sapiens cDNA clone IMAGE:943583 similar to contains Alu repetitive element; contains element PTR5 repetitive element; |
| 10976 | 23896 | | 1.35 | 2.4E-02 | BE387111.1 | EST_HUMAN | 601274962F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615902 5' |
| 11900 | 24781 | 38368 | 1.81 | 2.4E-02 | AF109905.1 | NT | Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes |
| 11900 | 24781 | 38369 | 1.81 | 2.4E-02 | AF109905.1 | NT | Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes |
| 12208 | 25050 | | 2.39 | 2.4E-02 | 9627909 | NT | Bacteriophage bil67, complete genome |
| 12363 | 25152 | 31855 | 1.7 | 2.4E-02 | 6753836 | NT | Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA |
| 12418 | 25188 | 31823 | 3.48 | 2.4E-02 | BE928689.1 | EST_HUMAN | MRO-F10175-310800-202-406 F10175 Homo sapiens cDNA |
| 12474 | 25222 | 31791 | 1.59 | 2.4E-02 | U78167.1 | NT | Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEFI) mRNA, complete cds |
| 12474 | 25222 | 31833 | 1.59 | 2.4E-02 | U78167.1 | NT | Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEFI) mRNA, complete cds |
| 12843 | 26327 | | 7.88 | 2.4E-02 | AB008569.1 | NT | Caenorhabditis elegans mRNA for iron-sulfur subunit of mitochondrial succinate dehydrogenase, complete cds |
| 1888 | 14913 | | 5.26 | 2.3E-02 | W05340.1 | EST_HUMAN | z884g08.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:288294 5' |
| 1904 | 14928 | | 8.44 | 2.3E-02 | U94165.1 | NT | 4 Homo sapiens mammary tumor-associated protein INT6 (INT6) gene, exon 4 |
| 2358 | 15366 | 28388 | 3.16 | 2.3E-02 | Z74293.1 | NT | S. cerevisiae chromosome IV reading frame ORF YDL245c |
| 3694 | 16737 | 29650 | 4.2 | 2.3E-02 | Z20377.1 | EST_HUMAN | HSAACADH P, Human foetal Brain Whole tissue Homo sapiens cDNA |
| 4176 | 17207 | 30093 | 0.8 | 2.3E-02 | L24799.1 | NT | Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds |
| 4176 | 17207 | 30094 | 0.8 | 2.3E-02 | L24799.1 | NT | Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds |
| 4450 | 17476 | 30364 | 1.52 | 2.3E-02 | AW899107.1 | EST_HUMAN | CM4-NN0080-280400-160-504 NN0080 Homo sapiens cDNA |
| 4477 | 17503 | 30388 | 0.78 | 2.3E-02 | BE935225.1 | EST_HUMAN | CM3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA |
| 4477 | 17503 | 30389 | 0.78 | 2.3E-02 | BE935225.1 | EST_HUMAN | CM3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA |
| 4478 | 18317 | 30390 | 1.23 | 2.3E-02 | AW593693.1 | EST_HUMAN | xs25d08.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2770671 3' |
| 4478 | 18317 | 30391 | 1.23 | 2.3E-02 | AW593693.1 | EST_HUMAN | xs25d08.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2770671 3' |
| 4625 | 17846 | 30534 | 2.89 | 2.3E-02 | BF028487.1 | EST_HUMAN | 601672279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955388 5' |
| 4625 | 17846 | 30535 | 2.89 | 2.3E-02 | BF028487.1 | EST_HUMAN | 601672279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955388 5' |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 5203 | 18212 | 31086 | 1.19 | 2.3E-02 | AF257110.1 | NT | Rattus norvegicus guanine nucleotide binding protein gamma subunit 11 mRNA, complete cds |
| 5203 | 18212 | 31087 | 1.19 | 2.3E-02 | AF257110.1 | NT | Rattus norvegicus guanine nucleotide binding protein gamma subunit 11 mRNA, complete cds |
| 5449 | 18551 | 31463 | 3.35 | 2.3E-02 | U86303.1 | NT | Caulobacter crescentus topoisomerase IV ParE subunit (parE) gene, complete cds, and propionyl-CoA carboxylase beta chain (pccB) homolog gene, partial cds |
| 6363 | 19432 | 32675 | 0.55 | 2.3E-02 | BF106464.1 | EST_HUMAN | 601822921R1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4042829 3' |
| 6774 | 19829 | 33112 | 4.22 | 2.3E-02 | AL161505.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 17 |
| 7172 | 18403 | 31201 | 0.84 | 2.3E-02 | BE141475.1 | EST_HUMAN | MRO-HT0080-011099-002-c09 HT0080 Homo sapiens cDNA |
| 7695 | 20653 | 34018 | 0.52 | 2.3E-02 | AL163303.2 | NT | Homo sapiens chromosome 21 segment HS21C103 |
| 8208 | 21178 | 34688 | 5.55 | 2.3E-02 | U63610.1 | NT | Human plectin (PLEC1) gene, exons 3-32, and complete cds |
| 8815 | 21782 | 35207 | 0.87 | 2.3E-02 | AJ298105.1 | NT | Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11 |
| 8815 | 21782 | 35208 | 0.87 | 2.3E-02 | AJ298105.1 | NT | Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11 |
| 9044 | 22010 | 35431 | 0.74 | 2.3E-02 | AI685390.1 | EST_HUMAN | wa76h10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302147 3' |
| 9044 | 22010 | 35432 | 0.74 | 2.3E-02 | AI685390.1 | EST_HUMAN | wa76h10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302147 3' |
| 9493 | 22457 | 35897 | 0.89 | 2.3E-02 | P41996 | SWISSPROT | HYPOTHETICAL 55.6 KD PROTEIN B0280.5 IN CHROMOSOME III PRECURSOR |
| 10218 | 23143 | 36632 | 0.77 | 2.3E-02 | P50532 | SWISSPROT | CHROMOSOME ASSEMBLY PROTEIN XCAP-C |
| 10390 | 23312 | 36791 | 1.47 | 2.3E-02 | AE000199.1 | NT | Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome |
| 10390 | 23312 | 36792 | 1.47 | 2.3E-02 | AE000199.1 | NT | Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome |
| 11135 | 24095 | 37624 | 1.71 | 2.3E-02 | P08640 | SWISSPROT | GLUCOAMYLASE S/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE) |
| 12336 | 25738 | 37624 | 7.99 | 2.3E-02 | BE278331.1 | EST_HUMAN | 601179958F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3546667 5' |
| 12742 | 25392 | 31755 | 1.5 | 2.3E-02 | BF528462.1 | EST_HUMAN | 602043629F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4181454 5' |
| 12742 | 25392 | 31756 | 1.5 | 2.3E-02 | BF528462.1 | EST_HUMAN | 602043629F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4181454 5' |
| 12843 | 25453 | 31724 | 3.2 | 2.3E-02 | U39394.1 | NT | Streptomyces sp. alpha-1,3/4-fucosidase precursor gene, complete cds |
| 12897 | 25983 | | 2.48 | 2.3E-02 | U11077.1 | NT | Dictyostellium discoideum extracellular signal-regulated protein kinase (ERK1) mRNA, complete cds |
| 13100 | 25833 | | 1.82 | 2.3E-02 | 11426388 | NT | Homo sapiens deaf ringer (Drosophila)-like 1 (DRLL1), mRNA |
| 739 | 13800 | 26739 | 4.3 | 2.2E-02 | AF018267.1 | NT | Columbia lilia nucleoside diphosphate kinase (NDPK) gene, nuclear gene encoding mitochondrial protein, complete cds |
| 1762 | 14781 | | 1.59 | 2.2E-02 | 4657448 | NT | Homo sapiens chromodomain helicase DNA binding protein 2 (CHD2) mRNA |
| 2031 | 15050 | 28085 | 1.68 | 2.2E-02 | Z82001.1 | NT | S.pneumoniae pcpA gene and open reading frames |
| 3448 | 16495 | | 2.15 | 2.2E-02 | AA577785.1 | EST_HUMAN | hn24ap04.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084782 3' |
| 3650 | 16703 | | 3.48 | 2.2E-02 | AF083094.1 | NT | Infectious bursal disease virus segment B strain IL4 VP1 gene, complete cds |
| 3867 | 16906 | 29814 | 1.26 | 2.2E-02 | AW601317.1 | EST_HUMAN | PMO-BT0340-170100-004-b03 BT0340 Homo sapiens cDNA |
| 3941 | 16981 | 29896 | 0.74 | 2.2E-02 | Z74293.1 | NT | S.cerevisiae chromosome IV reading frame ORF YDL245c |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 5105 | 18115 | 30988 | 1.17 | 2.2E-02 | Z73597.1 | NT | S. cerevisiae chromosome XVI reading frame ORF YPL241c |
| 7458 | 20424 | 33760 | 3.37 | 2.2E-02 | AV699721.1 | EST_HUMAN | AV699721 GKB Homo sapiens cDNA clone GKBAND03 3' |
| 8714 | 21682 | 35109 | 2.28 | 2.2E-02 | AL161615.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27 |
| 8714 | 21682 | 35110 | 2.28 | 2.2E-02 | AL161615.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27 |
| 9161 | 22127 | 35555 | 0.77 | 2.2E-02 | X79468.1 | NT | P. vulgata alpha tub 2 mRNA |
| 10045 | 22972 | 38438 | 2.26 | 2.2E-02 | AB026898.1 | NT | Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds) |
| 10045 | 22972 | 38439 | 2.26 | 2.2E-02 | AB026898.1 | NT | Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds) |
| 10565 | 23487 | | 0.91 | 2.2E-02 | 6678140 | NT | Mus musculus Sjogren syndrome antigen A1 (Ssa1), mRNA |
| 11540 | 24481 | 38033 | 1.8 | 2.2E-02 | BE797601.1 | EST_HUMAN | 601584309F1 NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3938571 5' |
| 12602 | 25304 | | 5.72 | 2.2E-02 | AA503563.1 | EST_HUMAN | ne47h07.at NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:900541 3' similar to contains Alu repetitive element |
| 419 | 13492 | | 5.37 | 2.1E-02 | AV781502.1 | EST_HUMAN | AV781502 MDS Homo sapiens cDNA clone MDSADG01 5' |
| 449 | 13522 | | 8.77 | 2.1E-02 | AF029726.1 | NT | Dichytellum discoidium histidine kinase C (dhkC) mRNA, complete cds |
| 1268 | 14303 | 27264 | 8.3 | 2.1E-02 | U72073.1 | NT | Bacillus subtilis coKLM cluster, CoK (cotK), and spore coat protein CotM (cotM) genes, complete cds |
| 1387 | 14420 | 27389 | 0.99 | 2.1E-02 | AF204395.1 | NT | Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds |
| 1387 | 14420 | 27390 | 0.99 | 2.1E-02 | AF204395.1 | NT | Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds |
| 1787 | 14826 | 27811 | 1.26 | 2.1E-02 | P02438 | SWISSPROT | KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A |
| 1787 | 14826 | 27812 | 1.26 | 2.1E-02 | P02438 | SWISSPROT | KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A |
| 1787 | 14826 | 27813 | 1.26 | 2.1E-02 | P02438 | SWISSPROT | KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A |
| 1980 | 15001 | 28004 | 1.01 | 2.1E-02 | AF190899.1 | NT | Tegula aureodincta major acrosomal protein precursor (TMAP) mRNA, complete cds |
| 2050 | 15069 | 28089 | 0.9 | 2.1E-02 | BE072546.1 | EST_HUMAN | PM2-BT0546-120100-001-f11 BT0546 Homo sapiens cDNA |
| 2050 | 15069 | 28090 | 0.9 | 2.1E-02 | BE072546.1 | EST_HUMAN | PM2-BT0546-120100-001-f11 BT0546 Homo sapiens cDNA |
| 2591 | 15592 | 28609 | 1.04 | 2.1E-02 | AA225095.1 | EST_HUMAN | nc27g03.r1 NCI_CGAP_P71 Homo sapiens cDNA clone IMAGE:1008820 |
| 2827 | 13839 | 26784 | 4.45 | 2.1E-02 | N29266.1 | EST_HUMAN | yx43h07.r1 Soares melanocyte 2NbrHM Homo sapiens cDNA clone IMAGE:284541 5' |
| 3164 | 15069 | 28089 | 1.02 | 2.1E-02 | BE072546.1 | EST_HUMAN | PM2-BT0546-120100-001-f11 BT0546 Homo sapiens cDNA |
| 3164 | 15069 | 28090 | 1.02 | 2.1E-02 | BE072546.1 | EST_HUMAN | PM2-BT0546-120100-001-f11 BT0546 Homo sapiens cDNA |
| 3597 | 16642 | 29561 | 0.98 | 2.1E-02 | AA461271.1 | EST_HUMAN | z663b09.r1 Soares fetal, fetus, Nb2Hf8_9w Homo sapiens cDNA clone IMAGE:798121 5' |
| 4028 | 17068 | 29987 | 0.97 | 2.1E-02 | BF203457.1 | EST_HUMAN | 601885890F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4098407 5' |
| 4157 | 17183 | 30076 | 0.64 | 2.1E-02 | Z74293.1 | NT | S. cerevisiae chromosome IV reading frame ORF YDL245c |
| 4339 | 17366 | 30249 | 1.4 | 2.1E-02 | BF343655.1 | EST_HUMAN | 602015306F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4751161 5' |
| 4473 | 17499 | 30384 | 2.15 | 2.1E-02 | U44914.1 | NT | Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds; and unknown genes |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 4483 | 17508 | 30397 | 1.13 | 2.1E-02 | AI768127.1 | EST_HUMAN | wg81d11.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371509 3' |
| 4739 | 17759 | 30654 | 5.69 | 2.1E-02 | Y08501.1 | NT | A.thaliana mitochondrial genome, part A |
| 4761 | 17781 | 30677 | 1.5 | 2.1E-02 | AA665737.1 | EST_HUMAN | ag55g12.s1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1126918 3' |
| 5256 | 18284 | 31133 | 1.07 | 2.1E-02 | BF028405.1 | EST_HUMAN | 601671411F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954410 5' |
| 5723 | 18817 | 31986 | 0.75 | 2.1E-02 | AW379529.1 | EST_HUMAN | CM4-H10244-111199-040-H05 HT0244 Homo sapiens cDNA |
| 7268 | 20003 | 33303 | 0.65 | 2.1E-02 | BF086199.1 | EST_HUMAN | QV3-GN0058-120900-329-a12 GN0058 Homo sapiens cDNA |
| 8664 | 21831 | 35254 | 0.66 | 2.1E-02 | 9790238 | NT | Mus musculus sorting nexin 1 (Snx1), mRNA |
| 9861 | 22797 | 36250 | 0.51 | 2.1E-02 | AA984288.1 | EST_HUMAN | am83e07.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629732 3' similar to contains Alu repetitive element; contains element MER11 repetitive element; |
| 9889 | 22916 | 36381 | 2.63 | 2.1E-02 | AJ243213.1 | NT | Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5 |
| 9989 | 22916 | 36382 | 2.63 | 2.1E-02 | AJ243213.1 | NT | Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5 |
| 10343 | 23267 | 36746 | 1.13 | 2.1E-02 | L26324.1 | NT | Streptococcus pneumoniae integrase, excisionase, repressor protein, relaxase, UmuC MucB homolog, and UmuD MucA homolog genes, complete cds; and unknown genes |
| 10421 | 23343 | 36829 | 0.68 | 2.1E-02 | AA984288.1 | EST_HUMAN | am83e07.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629732 3' similar to contains Alu repetitive element; contains element MER11 repetitive element; |
| 12584 | 18345 | | 8.95 | 2.1E-02 | Y19213.1 | NT | Homo sapiens putative psfHbA pseudogene for hair keratin, exons 2 to 7 |
| 12624 | 25735 | 31617 | 1.4 | 2.1E-02 | L34170.1 | NT | Human germline UBE1L gene similar to the gene for ubiquitin-activating enzyme, exons 1-22 |
| 13003 | 25557 | 31693 | 3.5 | 2.1E-02 | AF183913.1 | NT | Azospirillum brasilense major outer membrane protein OmaA precursor (omaA) gene, complete cds |
| 19 | 13139 | 26037 | 1.39 | 2.0E-02 | BF002832.1 | EST_HUMAN | 7g51c08.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3309998 3' similar to contains MER1.13 |
| 20 | 13140 | 26038 | 10.76 | 2.0E-02 | AW895565.1 | EST_HUMAN | QV4-NN0038-270400-187-H05 NN0038 Homo sapiens cDNA |
| 259 | 13356 | 26280 | 3.29 | 2.0E-02 | 6753635 | NT | Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA |
| 295 | 13389 | 26317 | 2.85 | 2.0E-02 | AA456538.1 | EST_HUMAN | aar15b10.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5' |
| 799 | 13858 | 26805 | 1.27 | 2.0E-02 | 6753635 | NT | Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA |
| 1089 | 14133 | 27085 | 1.03 | 2.0E-02 | AL096805.1 | NT | Homo sapiens genomic region containing hypervariable minisatellites chromosome 1[1p36.33] of Homo sapiens |
| 1204 | 14243 | 27201 | 0.79 | 2.0E-02 | 8922391 | NT | Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA |
| 1204 | 14243 | 27202 | 0.79 | 2.0E-02 | 8922391 | NT | Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA |
| 1890 | 14915 | 27909 | 2.08 | 2.0E-02 | 8922453 | NT | Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA |
| 1890 | 14915 | 27910 | 2.08 | 2.0E-02 | 8922453 | NT | Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA |
| 2810 | 15802 | | 4.57 | 2.0E-02 | AL161532.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32 |
| 3095 | 13139 | 26037 | 1.61 | 2.0E-02 | BF002832.1 | EST_HUMAN | 7g51c08.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3309998 3' similar to contains MER1.13 |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 3159 | 16215 | | 1.83 | 2.0E-02 | 7305474 | NT | Mus musculus sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B (Sema6b), mRNA |
| 3241 | 16296 | | 1.8 | 2.0E-02 | AF095888.1 | NT | Arabidopsis thaliana C2H2 zinc finger protein FZF mRNA, complete cds |
| 4032 | 17070 | 29971 | 1.4 | 2.0E-02 | M18095.1 | NT | P. vulgaris hydroxyproline-rich glycoprotein (HRGP) mRNA, 3' end |
| 5153 | 18163 | | 0.7 | 2.0E-02 | AI271995.1 | EST_HUMAN | qB3603.x1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1868076 3' |
| 5175 | 18184 | 31061 | 0.94 | 2.0E-02 | AL163278.2 | NT | Homo sapiens chromosome 21 segment HS21C078 |
| 5718 | 18812 | 31991 | 0.59 | 2.0E-02 | U34778.1 | NT | Caenorhabditis elegans sma-2 mRNA, complete cds |
| 6000 | 19083 | 32282 | 0.73 | 2.0E-02 | L35321.2 | NT | Dictyostellium discoideum class VII unconventional myosin (myoI) gene, complete cds |
| 7799 | 20751 | 34126 | 1.09 | 2.0E-02 | AP000004.1 | NT | Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt, position (4/7) |
| 7799 | 20751 | 34127 | 1.09 | 2.0E-02 | AP000004.1 | NT | Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt, position (4/7) |
| 10236 | 23161 | | 1.99 | 2.0E-02 | U70408.1 | NT | Japanese encephalitis virus envelope protein mRNA, partial cds |
| 10726 | 23849 | 37141 | 1.54 | 2.0E-02 | AI840342.1 | EST_HUMAN | wat7502.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2288316 3' |
| 11005 | 23971 | 37495 | 1.84 | 2.0E-02 | Z73956.1 | NT | Mycobacterium tuberculosis H37Rv complete genome, segment 93/162 |
| 11699 | 24664 | 38241 | 2.26 | 2.0E-02 | D88184.1 | NT | Equus caballus DNA for 17alpha-hydroxylase/17,20-lyase, complete cds |
| 12148 | 18351 | 31296 | 3.03 | 2.0E-02 | AA456338.1 | EST_HUMAN | ea15b10.r1 Soares_NihMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5' |
| 12621 | 15802 | | 1.99 | 2.0E-02 | AL161532.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32 |
| 13076 | 25608 | | 3.4 | 2.0E-02 | T80037.1 | EST_HUMAN | y04c09.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:24875 5' |
| 694 | 13756 | 26688 | 2.55 | 1.9E-02 | AA572764.1 | EST_HUMAN | nf19a07.s1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:914186 similar to contains L1.11 L1 repetitive element |
| 1619 | 14652 | 27628 | 1.03 | 1.9E-02 | P18488 | SWISSPROT | EMPTY SPIRACLES HOMEOTIC PROTEIN |
| 2055 | 15074 | 28093 | 3.04 | 1.9E-02 | AL163303.2 | NT | Homo sapiens chromosome 21 segment HS21C103 |
| 2055 | 15074 | 28094 | 3.04 | 1.9E-02 | AL163303.2 | NT | Homo sapiens chromosome 21 segment HS21C103 |
| 2514 | 15517 | 28540 | 1.07 | 1.9E-02 | AL161550.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50 |
| 2916 | 15974 | 28897 | 8.5 | 1.9E-02 | AA713856.1 | EST_HUMAN | hw04f05.s1 NCL_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1239337 3' |
| 2964 | 15022 | 28947 | 1.46 | 1.9E-02 | AV648669.1 | EST_HUMAN | AV648669 GLC Homo sapiens cDNA clone GLCBLH07 3' |
| 3273 | 19327 | | 0.72 | 1.9E-02 | AB033611.1 | NT | Utricularia talpoides mitochondrial gene for cytochrome b, complete cds |
| 3625 | 18686 | | 1.36 | 1.9E-02 | N52250.1 | EST_HUMAN | y28b02.s1 Soares_multiple_celerosis_2NbhMSP Homo sapiens cDNA clone IMAGE:284331 3' |
| 3718 | 16761 | | 8.23 | 1.9E-02 | BE738088.1 | EST_HUMAN | 601572682F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839564 5' |
| 3727 | 16769 | 29681 | 0.69 | 1.9E-02 | AI301183.1 | EST_HUMAN | qn04c07.x1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1897260 3' similar to contains Alu repetitive element |
| 4077 | 17112 | 30008 | 1.59 | 1.9E-02 | AF141940.1 | NT | Mycoplasma imitans VihA1 precursor (vihA1) and VihA2 precursor (vihA2) genes, partial cds |
| 4222 | 17251 | 30137 | 1.62 | 1.9E-02 | P09081 | SWISSPROT | HOMEOTIC BICOID PROTEIN (PRD-4) |
| 4222 | 17251 | 30138 | 1.62 | 1.9E-02 | P09081 | SWISSPROT | HOMEOTIC BICOID PROTEIN (PRD-4) |

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|-------------------------------|--|
| 4572 | 17594 | 30488 | 3.65 | 1.9E-02 | EST_HUMAN | U46D04.x1 Soares_NSF_F8_9W_OT_PA_S1 Homo sapiens cDNA clone IMAGE:2144551 3' similar to contains Alu repetitive element; |
| 5048 | 15517 | 28540 | 2.68 | 1.9E-02 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50 |
| 5389 | 18492 | 31369 | 0.91 | 1.9E-02 | NT | Mus musculus T cell receptor gamma locus, TCR gamma 1 and gamma 3 gene clusters |
| 5544 | 18641 | 31581 | 1.25 | 1.9E-02 | NT | Meleagris gallopavo paraoxonase-2 (PON2) mRNA, complete cds |
| 5885 | 18974 | | 1.24 | 1.9E-02 | NT | Drosophila kanekel gene for glycerol-3-phosphate dehydrogenase, complete cds |
| 7308 | 20279 | 33617 | 1.34 | 1.9E-02 | NT | Homo sapiens interferon-gamma receptor alpha chain gene, exon 1 |
| 7308 | 20279 | 33618 | 1.34 | 1.9E-02 | NT | Homo sapiens interferon-gamma receptor alpha chain gene, exon 1 |
| 8917 | 21883 | | 1.2 | 1.8E-02 | NT | Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 3/7 |
| 9686 | 22639 | 36096 | 0.78 | 1.9E-02 | EST_HUMAN | 601896130F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125482 5' |
| 10071 | 22988 | 36467 | 0.43 | 1.9E-02 | NT | Nicotiana tabacum type II phytochrome (phyB) gene, complete cds |
| 10405 | 23327 | 36811 | 1.09 | 1.9E-02 | EST_HUMAN | 601852385F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076253 5' |
| 10510 | 23432 | 36929 | 0.45 | 1.9E-02 | EST_HUMAN | y46f08.s1 Soares_multiple sclerosis_2NBHMSF Homo sapiens cDNA clone IMAGE:276839 3' |
| 10614 | 23536 | 37034 | 0.5 | 1.9E-02 | NT | Synechococcus sp. PCC6803 complete genome, 20/27, 2539000-2644794 |
| 12372 | 25742 | 31620 | 3.14 | 1.9E-02 | NT | Hirudo medicinalis intermediate filament gilafrin mRNA, complete cds |
| 13028 | 25574 | 31696 | 1.4 | 1.9E-02 | NT | H.sapiens MUC18 gene exon 16 |
| 346 | 13435 | 26357 | 1.35 | 1.8E-02 | EST_HUMAN | hm52c06.x1 NCI_CGAP_Co17 Homo sapiens cDNA clone IMAGE:3027274 3' similar to contains element MER29 repetitive element; |
| 686 | 13749 | 26675 | 1.39 | 1.8E-02 | EST_HUMAN | 601894329F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139983 5' |
| 1164 | 14203 | 27159 | 1.87 | 1.8E-02 | NT | H.francisci mRNA for myelin basic protein (MBP) |
| 2687 | 15683 | 28701 | 1.78 | 1.8E-02 | NT | Pseudomonas aeruginosa PAO1, section 105 of 529 of the complete genome |
| 3224 | 16279 | | 1.06 | 1.8E-02 | EST_HUMAN | tes2a08.x1 Soares_NFL_T_G8C_S1 Homo sapiens cDNA clone IMAGE:2090296 3' |
| 3902 | 16942 | 29853 | 1.01 | 1.8E-02 | EST_HUMAN | MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA |
| 3902 | 16942 | 29854 | 1.01 | 1.8E-02 | EST_HUMAN | MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA |
| 4113 | 17147 | | 1.04 | 1.8E-02 | EST_HUMAN | ak24h04.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1406935 3' |
| 4481 | 17487 | 30374 | 1.49 | 1.8E-02 | EST_HUMAN | QV4-DT0021-301299-071-b11 DT0021 Homo sapiens cDNA |
| 4982 | 18007 | 30895 | 0.98 | 1.8E-02 | SWISSPROT | HYPOTHETICAL PROTEIN DJ845024.2 |
| 5287 | 18283 | 31154 | 0.68 | 1.8E-02 | NT | Oryza sativa putative histone deacetylase HD2 mRNA, complete cds |
| 6524 | 19587 | 32845 | 0.59 | 1.8E-02 | NT | Neisseria meningitidis serogroup B strain MC58 section 160 of 206 of the complete genome |
| 6524 | 19587 | 32846 | 0.59 | 1.8E-02 | NT | Neisseria meningitidis serogroup B strain MC58 section 160 of 206 of the complete genome |
| 6882 | 20205 | 33534 | 4.59 | 1.8E-02 | SWISSPROT | HYPOTHETICAL 7.9 KD PROTEIN IN FIXW 5'REGION |
| 7699 | 20657 | 34021 | 0.65 | 1.8E-02 | EST_HUMAN | 601763268F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026280 5' |
| 7722 | 20657 | 34021 | 0.58 | 1.8E-02 | EST_HUMAN | 601763268F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026280 5' |
| 8467 | 21436 | 34854 | 0.77 | 1.8E-02 | NT | Mus musculus carbonic anhydrase IV gene, complete cds |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 8811 | 21778 | 35203 | 0.79 | 1.8E-02 | AW905327.1 | EST_HUMAN | QV2-NN1073-220400-159-h09 NN1073 Homo sapiens cDNA |
| 8857 | 21824 | 35247 | 0.75 | 1.8E-02 | 6678943 | NT | Mus musculus microtubule-associated protein 2 (Mtap2), mRNA |
| 8849 | 22785 | 36238 | 0.5 | 1.8E-02 | BF241924.1 | EST_HUMAN | 601877028F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105303 5' |
| 9849 | 22785 | 36239 | 0.5 | 1.8E-02 | BF241924.1 | EST_HUMAN | 601877028F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105303 5' |
| 10000 | 22927 | | 2.03 | 1.8E-02 | AA897543.1 | EST_HUMAN | q6209.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1394921 3' similar to gbL11672 ZINC FINGER PROTEIN 91 (HUMAN); |
| 10423 | 23345 | 36830 | 1.55 | 1.8E-02 | BE778274.1 | EST_HUMAN | 601463545F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3868983 5' |
| 10585 | 23508 | 37000 | 1.2 | 1.8E-02 | X96933.1 | NT | L.sialinellus mRNA for myomodulin neuropeptide precursor |
| 11765 | 23920 | 37438 | 1.7 | 1.8E-02 | AB002337.2 | NT | Homo sapiens mRNA for KIAA0339 protein, partial cds |
| 11765 | 23920 | 37439 | 1.7 | 1.8E-02 | AB002337.2 | NT | Homo sapiens mRNA for KIAA0339 protein, partial cds |
| 11935 | 24816 | 38413 | 2.73 | 1.8E-02 | AP000006.1 | NT | Pyrococcus horikoshii OT3 genomic DNA, 1186001-1485000 nt. position (6/7) |
| 11948 | 24827 | 38422 | 3.16 | 1.8E-02 | U62749.1 | NT | Zea mays acidic ribosomal protein P2a-3 (pp2a-3) mRNA, partial cds |
| 13105 | 25626 | 31680 | 1.35 | 1.8E-02 | R40255.1 | EST_HUMAN | y80d01.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:26985 3' similar to gb:M62783 ALPHA-N-ACETYL GALACTOSAMINIDASE PRECURSOR (HUMAN); |
| 13105 | 25626 | 31681 | 1.36 | 1.8E-02 | R40255.1 | EST_HUMAN | y80d01.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:26985 3' similar to gb:M62783 ALPHA-N-ACETYL GALACTOSAMINIDASE PRECURSOR (HUMAN); |
| 907 | 13962 | 26918 | 0.8 | 1.7E-02 | BE394869.1 | EST_HUMAN | 601310626F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632190 5' |
| 1806 | 14834 | 27823 | 2.15 | 1.7E-02 | AW573183.1 | EST_HUMAN | h334a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L1.11 L1 repetitive element; |
| 1806 | 14834 | 27824 | 2.15 | 1.7E-02 | AW573183.1 | EST_HUMAN | h334a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L1.11 L1 repetitive element; |
| 1887 | 14912 | | 4.23 | 1.7E-02 | AL163204.2 | NT | Homo sapiens chromosome 21 segment HS21C004 |
| 2121 | 15138 | | 11.19 | 1.7E-02 | AB004816.1 | NT | Oryctolagus cuniculus mRNA for mitsugumin28, complete cds |
| 2301 | 15313 | 28333 | 1.03 | 1.7E-02 | S74186.1 | NT | [microsatellite INRA41] [Ovis aries=sheep, Genomic, 361 nt, segment 1 of 2] |
| 2648 | 15845 | | 1.18 | 1.7E-02 | 7657495 | NT | Homo sapiens putative Rab5 GDP/GTP exchange factor homologue (RABEX5), mRNA |
| 3011 | 16069 | 28990 | 0.96 | 1.7E-02 | AI147615.1 | EST_HUMAN | qb22a08.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1696982 3' |
| 3523 | 16569 | | 5.52 | 1.7E-02 | AW827368.1 | EST_HUMAN | hm45a04.x1 NCI_CGAP_RDF1 Homo sapiens cDNA clone IMAGE:3015534 3' similar to contains MER19.b1 MER19 repetitive element; |
| 4198 | 17229 | | 0.96 | 1.7E-02 | AA669818.1 | EST_HUMAN | ac18704.s1 Stratigene ovary (#937217) Homo sapiens cDNA clone IMAGE:856927 3' similar to contains Alu repetitive element; contains element MER24 repetitive element; |
| 4228 | 17257 | | 2.04 | 1.7E-02 | R02506.1 | EST_HUMAN | ye86f08.r1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:124647 5' |
| 4482 | 17507 | 30396 | 0.7 | 1.7E-02 | AI305279.1 | EST_HUMAN | qm08g07.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881276 3' similar to gb:X62359 ZINC FINGER PROTEIN 30 (HUMAN); |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 4557 | 17580 | 30471 | 1.52 | 1.7E-02 | AW573183.1 | EST_HUMAN | h34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L1.t1 L1 repetitive element; |
| 4744 | 17764 | 30658 | 1.54 | 1.7E-02 | V00641.1 | NT | Messenger RNA for anglerfish (<i>Lophius americanus</i>) somatostatin II |
| 4851 | 17858 | | 7.05 | 1.7E-02 | AI015076.1 | EST_HUMAN | ov61e02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640858 3' |
| 5106 | 18116 | 30889 | 0.74 | 1.7E-02 | 6981289 | NT | Rattus norvegicus N-arginine diisic convertase 1 (Nrd1), mRNA |
| 5229 | 18237 | | 0.91 | 1.7E-02 | AJ229041.1 | NT | Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3 |
| 6248 | 19321 | 32551 | 1.63 | 1.7E-02 | AI769247.1 | EST_HUMAN | wg35f09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2387113 3' similar to contains Alu repetitive element; |
| 6618 | 19676 | | 0.64 | 1.7E-02 | Z28383.1 | NT | T.niveum (ATCC34921) simA gene for cyclosporine synthetase |
| 6731 | 19787 | 33065 | 1.37 | 1.7E-02 | AI039280.1 | EST_HUMAN | ov65h03.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1672661 3' |
| 7251 | 19986 | 33284 | 1.31 | 1.7E-02 | AF190930.1 | NT | Macaca fascicularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds |
| 7411 | 20378 | 33729 | 1.95 | 1.7E-02 | 8400716 | NT | Homo sapiens nebulin (NEB), mRNA |
| 7581 | 20543 | 33902 | 0.85 | 1.7E-02 | L07899.1 | NT | Human apolipoprotein (a) gene, exon 1 |
| 7651 | 20643 | 33903 | 0.85 | 1.7E-02 | L07899.1 | NT | Human apolipoprotein (a) gene, exon 1 |
| 8016 | 20954 | | 1.98 | 1.7E-02 | AJ010770.1 | NT | Homo sapiens hyperion gene, exons 1-50 |
| 9791 | 21114 | 34514 | 0.91 | 1.7E-02 | U21854.1 | NT | Caenorhabditis elegans cCAF1 protein gene, complete cds |
| 10057 | 22884 | 36453 | 1.31 | 1.7E-02 | AL040354.1 | EST_HUMAN | DKFZp434i0314_r1 434 (synonym: hlec3) Homo sapiens cDNA clone DKFZp434i0314 5' |
| 12084 | 24956 | 38551 | 1.59 | 1.7E-02 | 5902007 | NT | Homo sapiens serum constituent protein (MSE55), mRNA |
| 12910 | 25910 | 31424 | 3.15 | 1.7E-02 | AW903482.1 | EST_HUMAN | CM4-NN1030-040400-130-f06 NN1030 Homo sapiens cDNA |
| 13059 | 25595 | 31687 | 1.31 | 1.7E-02 | AA846926.1 | EST_HUMAN | ce08d04.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1385287 similar to contains element MSR1 repetitive element; |
| 512 | 13583 | | 2.22 | 1.6E-02 | AL021929.1 | NT | Mycobacterium tuberculosis H37Rv complete genome; segment 13/162 |
| 1665 | 14687 | 27673 | 0.91 | 1.6E-02 | Y18889.1 | NT | Treponema maltophilum flaB2, flaB3 and flID genes for flagellin subunit proteins and CAP protein homologue |
| 2572 | 15573 | 28593 | 0.95 | 1.6E-02 | AJ006345.1 | NT | Homo sapiens KVLT1 gene |
| 2651 | 15648 | 28671 | 1.45 | 1.6E-02 | AA494872.1 | EST_HUMAN | ne81d06.s1 NCI_CGAP_Ewt1 Homo sapiens cDNA clone IMAGE:910667 |
| 2704 | 15700 | | 1.37 | 1.6E-02 | AB014834.1 | NT | Homo sapiens mRNA for KIAA0634 protein, partial cds |
| 3537 | 16593 | 29506 | 4.46 | 1.6E-02 | AW850652.1 | EST_HUMAN | IL3-CT0219-160200-063-C07 CT0219 Homo sapiens cDNA |
| 4204 | 17235 | | 2.14 | 1.6E-02 | AF110520.1 | NT | Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RelGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial> |
| 4329 | 17367 | 30245 | 0.96 | 1.6E-02 | AW875407.1 | EST_HUMAN | QV2-PT0012-140100-030-107 PT0012 Homo sapiens cDNA |
| 5172 | 18181 | | 0.76 | 1.6E-02 | N80156.1 | EST_HUMAN | z665e07.s1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:287444 3' |
| 5325 | 18431 | 31183 | 0.49 | 1.6E-02 | AI281385.1 | EST_HUMAN | qu42b09.x1 NCI_CGAP_Lym5 Homo sapiens cDNA clone IMAGE:1967417 3' |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 6705 | 18800 | 31977 | 1.33 | 1.6E-02 | 6871715 | NT | Mus musculus CD5 antigen (Cd5), mRNA |
| 6799 | 19853 | 33138 | 2.07 | 1.6E-02 | AB015281.1 | NT | Candida albicans CaGCR3 gene, complete cds |
| 7117 | 20051 | 33354 | 0.93 | 1.6E-02 | AB027571.1 | NT | Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds |
| 7117 | 20051 | 33355 | 0.93 | 1.6E-02 | AB027571.1 | NT | Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds |
| 7878 | 20817 | 34308 | 1.08 | 1.6E-02 | AL161508.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20 |
| 8458 | 21427 | 34844 | 0.72 | 1.6E-02 | AJ277662.1 | NT | Homo sapiens partial TUB gene for tubby (mouse) homolog and LMO1 gene for LIM domain only 1 protein |
| 8519 | 21487 | | 1.5 | 1.6E-02 | X05151.1 | NT | Human apoC-II gene for preproapolipoprotein C-II |
| 10400 | 23322 | | 1.98 | 1.6E-02 | AJ079764.1 | NT | Drosophila melanogaster enhancer of polycomb (E(Pc)) mRNA, complete cds |
| 10785 | 23706 | 37206 | 1.2 | 1.6E-02 | AA572818.1 | EST_HUMAN | nf19g03.s1 NCL CGAP_P1 Homo sapiens cDNA clone IMAGE:914260 similar to SW:TELO_RABIT |
| 10785 | 23706 | 37207 | 1.2 | 1.6E-02 | AA572818.1 | EST_HUMAN | nf19g03.s1 NCL CGAP_P1 Homo sapiens cDNA clone IMAGE:914260 similar to SW:TELO_RABIT |
| 11255 | 25705 | 37730 | 1.83 | 1.6E-02 | Z04828.1 | NT | G gallus microsatellite DNA (LEI0260) (=T1611E11) |
| 11547 | 24488 | 38042 | 1.7 | 1.6E-02 | AL161508.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20 |
| 11547 | 24488 | 38043 | 1.7 | 1.6E-02 | AL161508.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20 |
| 11839 | 24722 | 38307 | 1.66 | 1.6E-02 | AJ373558.1 | EST_HUMAN | qz96e10.x1 Soares pregnant uterus_NbHPU Homo sapiens cDNA clone IMAGE:2042442 3' |
| 12347 | 18334 | 31172 | 1.39 | 1.6E-02 | Q84176 | SWISSPROT | LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22) |
| 12347 | 18334 | 31173 | 1.39 | 1.6E-02 | Q84176 | SWISSPROT | LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22) |
| 752 | 13813 | | 20.75 | 1.5E-02 | 8923734 | NT | Homo sapiens transcription factor (HSA130894), mRNA |
| 2152 | 15168 | 28184 | 4.44 | 1.5E-02 | N39521.1 | EST_HUMAN | y27b07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243925 3' |
| 2185 | 15200 | 28220 | 1.82 | 1.5E-02 | AL161594.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90 |
| 3074 | 16131 | 29043 | 2.54 | 1.5E-02 | AJ008216.1 | NT | Homo sapiens CACNA1F gene, exons 1 to 48 |
| 3074 | 16131 | 29044 | 2.54 | 1.5E-02 | AJ008216.1 | NT | Homo sapiens CACNA1F gene, exons 1 to 48 |
| 3737 | 18779 | 29692 | 1.06 | 1.5E-02 | BF082842.1 | EST_HUMAN | MR4-TN0115-080900-201-b12 TN0115 Homo sapiens cDNA |
| 8428 | 19483 | 32745 | 1.33 | 1.5E-02 | Q08711 | SWISSPROT | HYPOTHETICAL CALCIUM-BINDING PROTEIN C18B11.04 IN CHROMOSOME I |
| 7541 | 20504 | | 1.59 | 1.5E-02 | 11467282 | NT | Cyanophora paradoxa cyanelle, complete genome |
| 7631 | 20591 | 33954 | 1.38 | 1.5E-02 | 11418713 | NT | Homo sapiens KIAA1009 protein (KIAA1009), mRNA |
| 8206 | 21176 | 34585 | 1.5 | 1.5E-02 | AL163303.2 | NT | Homo sapiens chromosome 21 segment HS21C103 |
| 8213 | 21182 | 34593 | 4.62 | 1.5E-02 | 11417739 | NT | Homo sapiens valyl-tRNA synthetase 2 (VAR52), mRNA |
| 9182 | 22148 | 35575 | 0.83 | 1.5E-02 | BF345554.1 | EST_HUMAN | 002019136F1 NCL CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4154504 5' |
| 9823 | 22672 | | 0.58 | 1.5E-02 | AF008774.1 | NT | Homo sapiens kinase-related protein isoform 1 mRNA, complete cds |
| 9929 | 22812 | 36266 | 1.58 | 1.5E-02 | D44606.1 | NT | Saccharomyces cerevisiae chromosome VI plasmid GapC |
| 10170 | 23095 | 36574 | 0.95 | 1.5E-02 | R32867.1 | EST_HUMAN | yh54b10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133531 5' |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|-----------------------------|-------------------------------|--|
| 10170 | 23095 | 36575 | 0.95 | 1.5E-02 | R32667.1 | EST_HUMAN | yh5b10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133531 5' |
| 11503 | 24445 | 37997 | 2.75 | 1.5E-02 | L40609.1 | NT | Plasmodium falciparum (strain FOR3) variant-specific surface protein (var-2, var-3) genes, complete cds's |
| 11537 | 24478 | 38028 | 2.52 | 1.5E-02 | AL111238.1 | NT | Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation |
| 12564 | 25783 | | 2.04 | 1.5E-02 | AW750834.1 | EST_HUMAN | RC4-CN0049-140100-011-011 CN0049 Homo sapiens cDNA |
| 13078 | 25610 | | 1.3 | 1.5E-02 | AI763127.1 | EST_HUMAN | w06h03.x1 NCI_CGAP_CL11 Homo sapiens cDNA clone IMAGE:2389493 3' similar to contains Alu repetitive element; contains element MER28 MSR1 repetitive element; |
| 417 | 13490 | | 1.99 | 1.4E-02 | AE002230.2 | NT | Chlamydia pneumoniae AR39, section 58 of 94 of the complete genome |
| 1120 | 14164 | 27115 | 5.44 | 1.4E-02 | 7705980 | NT | Homo sapiens NESH protein (LOC51225), mRNA |
| 1261 | 14286 | | 1.74 | 1.4E-02 | U32800.1 | NT | Haemophilus influenzae Rd section 115 of 163 of the complete genome |
| 1301 | 14337 | | 3.4 | 1.4E-02 | U67779.1 | NT | Xenopus laevis neurogenin related 1b (X-NGNR-1b) mRNA, complete cds |
| 1520 | 14552 | | 1.03 | 1.4E-02 | AV723785.1 | EST_HUMAN | AV723785 HTB Homo sapiens cDNA clone HTBA1H11 5' |
| 3226 | 16281 | 29204 | 2.04 | 1.4E-02 | AF160989.2 | NT | Blifidobacterium longum Nav/H+ antiporter (nhaB), cytosine deaminase, and alpha-galactosidase (aglL) genes, complete cds; and N-acetylglucosamine/xylose repressor protein (nagC/xylR) gene, partial cds |
| 3409 | 16458 | 29380 | 0.98 | 1.4E-02 | AW074212.1 | EST_HUMAN | x08009.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575793 3' |
| 3496 | 16543 | 29467 | 6.29 | 1.4E-02 | AL161586.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82 |
| 3496 | 16543 | 29468 | 6.29 | 1.4E-02 | AL161586.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82 |
| 3669 | 16712 | 29627 | 6.69 | 1.4E-02 | 6996918 | NT | Mus musculus histocompatibility 2, complement component factor B (H2-Bf), mRNA |
| 4516 | 17541 | 30427 | 6.1 | 1.4E-02 | AW962688.1 | EST_HUMAN | EST374761 IMAGE resequences, MAGG Homo sapiens cDNA |
| 4516 | 17541 | 30428 | 6.1 | 1.4E-02 | AW962688.1 | EST_HUMAN | EST374761 IMAGE resequences, MAGG Homo sapiens cDNA |
| 4911 | 17928 | 30818 | 8.08 | 1.4E-02 | BE733142.1 | EST_HUMAN | 601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5' |
| 4911 | 17928 | 30819 | 8.08 | 1.4E-02 | BE733142.1 | EST_HUMAN | 601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5' |
| 5130 | 18139 | 31017 | 1.01 | 1.4E-02 | AW948453.1 | EST_HUMAN | OM0-FN0041-120500-370-009 FN0041 Homo sapiens cDNA |
| 5888 | 25992 | | 0.95 | 1.4E-02 | X91338.1 | NT | H. sapiens La/SS-B pseudogene 3 |
| 6555 | 19615 | 32880 | 4.8 | 1.4E-02 | AA559030.1 | EST_HUMAN | n111c04.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1029990 3' similar to contains Alu repetitive element; |
| 6555 | 19615 | 32881 | 4.9 | 1.4E-02 | AA559030.1 | EST_HUMAN | n111c04.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1029990 3' similar to contains Alu repetitive element; |
| 8478 | 21447 | | 1.61 | 1.4E-02 | AL022073.1 | NT | Mycobacterium tuberculosis H37Rv complete genome, segment 88/162 |
| 9249 | 22215 | 35645 | 0.77 | 1.4E-02 | M81702.1 | NT | Candida biddinii methanol oxidase (AOD1) gene, complete cds |
| 9510 | 22473 | 35917 | 0.9 | 1.4E-02 | AJ272265.1 | NT | Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8 |
| 9755 | 22696 | 38153 | 2.15 | 1.4E-02 | BE544591.1 | EST_HUMAN | 601078239F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464241 5' |
| 10923 | 23843 | | 0.58 | 1.4E-02 | AL163218.2 | NT | Homo sapiens chromosome 21 segment HS21C018 |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 12564 | 25080 | 38172 | 2.14 | 1.4E-02 | X60459.1 | NT | Human IFNAR gene for interferon alpha/beta receptor |
| 12616 | 25312 | | 1.47 | 1.4E-02 | AF324985.1 | NT | Arabidopsis thaliana F21J9.2 mRNA, complete cds |
| 12882 | 25474 | | 1.96 | 1.4E-02 | 11429988 | NT | Homo sapiens sperm associated antigen 7 (SPAG7), mRNA |
| 1972 | 14993 | 27994 | 2.05 | 1.3E-02 | AL163201.2 | NT | Homo sapiens chromosome 21 segment HS21C001 |
| 3227 | 16282 | 29205 | 2.31 | 1.3E-02 | BF697081.1 | EST_HUMAN | 602129475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286203 5' |
| 3227 | 16282 | 29206 | 2.31 | 1.3E-02 | BF697081.1 | EST_HUMAN | 602129475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286203 5' |
| 3993 | 17033 | | 1.38 | 1.3E-02 | AF169288.1 | NT | Mus musculus beta-sarcoglycan gene, complete cds |
| 4984 | 17979 | 30869 | 1.06 | 1.3E-02 | U60061.1 | NT | Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV5S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2, > |
| 5317 | 18423 | 31225 | 1.79 | 1.3E-02 | AL049866.2 | NT | Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mnxq28orf |
| 5317 | 18423 | 31226 | 1.79 | 1.3E-02 | AL049866.2 | NT | Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mnxq28orf |
| 6288 | 19360 | 32597 | 1.21 | 1.3E-02 | U80017.1 | NT | Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nailp) and survival motor neuron protein (smn) genes, complete cds |
| 6322 | 19393 | 32634 | 0.7 | 1.3E-02 | M62862.1 | NT | C.reinhardtii ribulose 1,5-bisphosphate carboxylase/oxygenase activase mRNA, complete cds |
| 7154 | 18386 | 31228 | 1.25 | 1.3E-02 | AL161546.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46 |
| 7154 | 18386 | 31229 | 1.25 | 1.3E-02 | AL161546.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46 |
| 7829 | 20777 | 34155 | 4.86 | 1.3E-02 | A1031593.1 | EST_HUMAN | ow06g05.x1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1646072 3' similar to contains Alu repetitive element; |
| 8826 | 21793 | 35216 | 1.48 | 1.3E-02 | AF159961.1 | NT | Homo sapiens human endogenous retrovirus W gagC3.37 G gag (gag) gene, complete cds |
| 10567 | 23489 | 36981 | 2.18 | 1.3E-02 | M63707.1 | NT | Mouse kidney androgen-regulated protein (KAP) gene, complete cds |
| 10641 | 23563 | 37059 | 0.63 | 1.3E-02 | AE001304.1 | NT | Chlamydia trachomatis section 31 of 87 of the complete genome |
| 10988 | 23908 | 37421 | 0.44 | 1.3E-02 | AA707741.1 | EST_HUMAN | zh24a07.e1 Soares_pituitary_gland_N3HPG Homo sapiens cDNA clone IMAGE:412980 3' |
| 11336 | 24286 | 37809 | 3.74 | 1.3E-02 | AW268563.1 | EST_HUMAN | xc34e03.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3' |
| 11336 | 24286 | 37810 | 3.74 | 1.3E-02 | AW268563.1 | EST_HUMAN | xc34e03.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3' |
| 12622 | 25923 | | 1.4 | 1.3E-02 | Z99117.1 | NT | Bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870 |
| 12714 | 25368 | | 2.51 | 1.3E-02 | 9633069 | NT | Human herpesvirus 6B, complete genome |
| 12886 | 25718 | | 16.88 | 1.3E-02 | AF152238.1 | NT | Homo sapiens V1b vasopressin receptor (VPR3) gene, complete cds |
| 214 | 13314 | | 0.67 | 1.2E-02 | X87344.1 | NT | H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 355 | 13443 | 26368 | 4.67 | 1.2E-02 | AA059299.1 | EST_HUMAN | zf65g01.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381840 5' similar to contains element L1 repetitive element; |
| 453 | 13526 | 26456 | 1.81 | 1.2E-02 | P38898 | SWISSPROT | HYPOTHETICAL 17.1 KD PROTEIN IN PUR5 3'REGION |
| 740 | 13801 | 26740 | 3.32 | 1.2E-02 | A1163522.1 | EST_HUMAN | qd68e12.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1734670 3' similar to contains L1.L1 L1 repetitive element; |
| 2187 | 15202 | 28222 | 1.82 | 1.2E-02 | AL163213.2 | NT | Homo sapiens chromosome 21 segment HS21C013 |
| 2190 | 15205 | 28225 | 1.44 | 1.2E-02 | AV731704.1 | EST_HUMAN | AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5' |
| 2449 | 15454 | 28476 | 1.65 | 1.2E-02 | AW172350.1 | EST_HUMAN | X37e09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3' |
| 2505 | 15508 | 28534 | 0.99 | 1.2E-02 | BE538310.1 | EST_HUMAN | 601068406F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3454608 5' |
| 2505 | 15508 | 28535 | 0.99 | 1.2E-02 | BE538310.1 | EST_HUMAN | 601068406F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3454608 5' |
| 2643 | 15454 | 28476 | 1.31 | 1.2E-02 | AW172350.1 | EST_HUMAN | X37e09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3' |
| 3118 | 16175 | | 6.56 | 1.2E-02 | AA075418.1 | EST_HUMAN | zn88e03.r1 Siralagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:545020 5' |
| 3301 | 16354 | 29273 | 2.62 | 1.2E-02 | R62805.1 | EST_HUMAN | yf11b08.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138903 3' |
| 4917 | 17934 | 30826 | 8.36 | 1.2E-02 | 6754367 | NT | Mus musculus interferon regulatory factor 5 (Irf5), mRNA |
| 4953 | 17998 | 30858 | 1.66 | 1.2E-02 | U91328.1 | NT | Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds |
| 5090 | 18090 | | 1.54 | 1.2E-02 | AB019786.1 | NT | Cynops pyrrhogaster CpUbiqT mRNA, partial cds |
| 5121 | 18131 | 31008 | 2.09 | 1.2E-02 | AV731704.1 | EST_HUMAN | AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5' |
| 5259 | 18267 | 31135 | 1.01 | 1.2E-02 | AF185576.1 | NT | Mus musculus POZ/zinc finger transcription factor ODA-8 mRNA, complete cds |
| 5769 | 18861 | | 0.5 | 1.2E-02 | AA756018.1 | EST_HUMAN | al29f10.s1 Soares testis_NHT Homo sapiens cDNA clone 1344235 3' |
| 5846 | 18936 | 32120 | 1.72 | 1.2E-02 | D78589.1 | NT | Rana rugosa mRNA for calreticulin, complete cds |
| 6238 | 19311 | 32543 | 0.58 | 1.2E-02 | AF045555.1 | NT | Homo sapiens wbscr1 (WBSCR1) and wbscr5 (WBSCR5) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds |
| 7203 | 20227 | 33560 | 5.57 | 1.2E-02 | AF175412.1 | NT | Mus musculus DNA methyltransferase (Dnm1) gene, exons 2, 3, 4, and 5 |
| 7510 | 20475 | 33836 | 1.07 | 1.2E-02 | H02187.1 | EST_HUMAN | y34h12.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:150695 3' |
| 7534 | 20497 | 33858 | 8.5 | 1.2E-02 | AV732093.1 | EST_HUMAN | AV732093 HTF Homo sapiens cDNA clone HTFBHQ9 5' |
| 7805 | 20755 | 34131 | 0.54 | 1.2E-02 | BF216650.1 | EST_HUMAN | 601882949F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095253 5' |
| 8330 | 21299 | 34715 | 2.28 | 1.2E-02 | Q11205 | SWISSPROT | GMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYL TRANSFERASE (BETA-GALACTOSIDE ALPHA-2,3-SIALYL TRANSFERASE) (ALPHA 2,3-ST) (GAL-NAC6S) (GAL-BETA-1,3-GALNAC-ALPHA-2,3-SIALYL TRANSFERASE) (ST3GALA.2) (SIAT4-B) |
| 8534 | 21502 | 34919 | 1.31 | 1.2E-02 | AF193612.1 | NT | Homo sapiens fringe protein mRNA, partial cds |
| 8534 | 21502 | 34920 | 1.31 | 1.2E-02 | AF193612.1 | NT | Homo sapiens fringe protein mRNA, partial cds |
| 9242 | 22208 | | 1.1 | 1.2E-02 | T76987.1 | EST_HUMAN | yf72d08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:113774 3' |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 9997 | 22924 | 36389 | 2.63 | 1.2E-02 | AB031013.1 | NT | Norwalk-like virus genogroup 2 gene for capsid protein, complete cds |
| 10030 | 22957 | 36425 | 1.29 | 1.2E-02 | AJ246003.1 | NT | Homo sapiens Spesi gene for apelin protein |
| 12310 | 25118 | 31841 | 2.74 | 1.2E-02 | O15634 | SWISSPROT | PERIOD CIRCADIAN PROTEIN 1 (CIRCADIAN PACEMAKER PROTEIN RIGU1) (HPER) |
| 12896 | 25482 | | 5.61 | 1.2E-02 | C18119.1 | EST_HUMAN | C18119 Human placenta cDNA (Tfujwara) Homo sapiens cDNA clone GEN-557G06 5' |
| 1274 | 14309 | 27270 | 1.14 | 1.1E-02 | AA070364.1 | EST_HUMAN | zm60e1.s1 Stratiogene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:530924 3' |
| 1719 | 14749 | 27734 | 1.8 | 1.1E-02 | X75491.1 | NT | H. sapiens LIPA gene, exon 4 |
| 1719 | 14749 | 27735 | 1.8 | 1.1E-02 | X75491.1 | NT | H. sapiens LIPA gene, exon 4 |
| 2054 | 15073 | 28092 | 4.08 | 1.1E-02 | BF345263.1 | EST_HUMAN | 602018037F1 NCI CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4153808 5' |
| 2889 | 15948 | | 3.91 | 1.1E-02 | N99523.1 | EST_HUMAN | z440e05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:295040 5' |
| 3535 | 16581 | 28505 | 2.75 | 1.1E-02 | A1653508.1 | EST_HUMAN | tg95b10.x1 NCI CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2216539 3' similar to SW:XP_F_HUMAN |
| 4051 | 17088 | | 1.52 | 1.1E-02 | BE144637.1 | EST_HUMAN | Q92889 DNA-REPAIR PROTEIN COMPLEMENTING XP-F CELL ; |
| 4133 | 17165 | | 0.71 | 1.1E-02 | AW813796.1 | EST_HUMAN | PN3-HT0175-300999-001-h08 HT0175 Homo sapiens cDNA |
| 4887 | 17884 | 30772 | 2.22 | 1.1E-02 | AL048383.2 | EST_HUMAN | RC3-ST0197-120200-015-g11 ST0197 Homo sapiens cDNA |
| | | | | | | | DKFZ586E0924 .s1 586 (synonym: huter) Homo sapiens cDNA clone DKFZp586E0924 |
| 6272 | 18345 | 32578 | 1.02 | 1.1E-02 | U66480.1 | NT | Bacillus subtilis SpoVK (spovK), YnaA (ynaA), YnaB (ynbB), GlnR (glnR), glutamine synthetase (glnA), YnaA (ynaA), YnaB (ynbB), YnaC (ynaC), YnaD (ynad), YnaE (ynae), YnaF (ynaf), YnaG (ynag), YnaH (ynah), YnaI (ynai), YnaJ (ynaj), YnaK (ynak), YnaL (ynal), YnaM (ynam), YnaN (ynan), YnaO (ynao), YnaP (ynap), YnaQ (ynaq), YnaR (ynar), YnaS (ynas), YnaT (ynat), YnaU (ynau), YnaV (ynav), YnaW (ynaw), YnaX (ynax), YnaY (ynay), YnaZ (ynaz), Ynaa (ynaA), Ynab (ynbB), Ynac (ynac), Ynad (ynad), Ynae (ynae), Ynaf (ynaf), Ynag (ynag), Ynah (ynah), Ynai (ynai), Ynaj (ynaj), Ynak (ynak), Ynal (ynal), Ynam (ynam), Ynan (ynan), Ynao (ynao), Ynap (ynap), Ynaq (ynaq), Ynar (ynar), Ynas (ynas), Ynat (ynat), Ynau (ynau), Ynav (ynav), Ynaw (ynaw), Ynax (ynax), Ynay (ynay), Ynaz (ynaz), Ynaa (ynaA), Ynab (ynbB), Ynac (ynac), Ynad (ynad), Ynae (ynae), Ynaf (ynaf), Ynag (ynag), Ynah (ynah), Ynai (ynai), Ynaj (ynaj), Ynak (ynak), Ynal (ynal), Ynam (ynam), Ynan (ynan), Ynao (ynao), Ynap (ynap), Ynaq (ynaq), Ynar (ynar), Ynas (ynas), Ynat (ynat), Ynau (ynau), Ynav (ynav), Ynaw (ynaw), Ynax (ynax), Ynay (ynay), Ynaz (ynaz) |
| 7855 | 20800 | 34176 | 2.47 | 1.1E-02 | BE149611.1 | EST_HUMAN | RC1-HT0256-100300-016-h07 HT0256 Homo sapiens cDNA |
| 8105 | 21042 | 34441 | 3.79 | 1.1E-02 | 9631294 | NT | Melanoplus sanguinipes entomopoxvirus, complete genome |
| 8987 | 21953 | 35377 | 0.7 | 1.1E-02 | AW996160.1 | EST_HUMAN | QV3-BN0045-220300-128-h02 BN0045 Homo sapiens cDNA |
| 9174 | 22140 | 35566 | 0.68 | 1.1E-02 | C04803.1 | EST_HUMAN | C04803 Human heart cDNA (Ynakamura) Homo sapiens cDNA clone 3NHC4040 |
| 9253 | 22219 | 35650 | 7.21 | 1.1E-02 | Q61982 | SWISSPROT | NEUROGENIC LOCUS NOTCH 3 PROTEIN |
| 10289 | 23214 | 36698 | 2.1 | 1.1E-02 | AA082578.1 | EST_HUMAN | zn24a01.r1 Stratiogene neuroepithelium NT2RAM1 937234 Homo sapiens cDNA clone IMAGE:548328 5' |
| 10454 | 23376 | 36869 | 3.79 | 1.1E-02 | AA314665.1 | EST_HUMAN | EST188494 Colon carcinoma (HCC) cell line II Homo sapiens cDNA 5' end |
| 11324 | 24274 | 37802 | 2.01 | 1.1E-02 | 11435505 | NT | Homo sapiens T-box 5 (TBX5), mRNA |
| 12194 | 25039 | | 3.52 | 1.1E-02 | AA668239.1 | EST_HUMAN | ab77f11.s1 Stratiogene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853005 3' similar to contains |
| 12960 | 17165 | | 1.67 | 1.1E-02 | AW813796.1 | EST_HUMAN | Alu repetitive element |
| 7 | 13127 | 26027 | 6.08 | 1.0E-02 | AW846120.1 | EST_HUMAN | RC3-ST0197-120200-015-g11 ST0197 Homo sapiens cDNA |
| 1526 | 14559 | 27530 | 1.07 | 1.0E-02 | AW368128.1 | EST_HUMAN | MR3-CT0176-111099-003-e10 CT0176 Homo sapiens cDNA |
| 2578 | 15579 | | 1.26 | 1.0E-02 | AA060389.1 | EST_HUMAN | CM2-HT0177-041099-017-h12 HT0177 Homo sapiens cDNA |
| 3106 | 16163 | 28075 | 2.7 | 1.0E-02 | BE835556.1 | EST_HUMAN | cc22h08.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1350495 3' |
| 3276 | 16330 | 29251 | 1.33 | 1.0E-02 | BE869899.1 | EST_HUMAN | RC0-FN0025-250500-021-d02 FN0025 Homo sapiens cDNA |
| | | | | | | | 601649967R1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3633689 3' |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 3520 | 16566 | | 0.65 | 1.0E-02 | AW845621.1 | EST_HUMAN | MR0-CT0060-081099-003-h10 CT0060 Homo sapiens cDNA |
| 3895 | 16935 | 28845 | 0.75 | 1.0E-02 | AI065086.1 | EST_HUMAN | HA0921 Human fetal liver cDNA library Homo sapiens cDNA |
| 3911 | 16951 | 28862 | 1.06 | 1.0E-02 | AL163302.2 | NT | Homo sapiens chromosome 21 segment HS21C102 |
| 4811 | 17828 | 30725 | 4.97 | 1.0E-02 | 6753521 | NT | Mus musculus corticotropin releasing hormone receptor 2 (Chr2), mRNA |
| 4881 | 17888 | 30787 | 5.01 | 1.0E-02 | R96567.1 | EST_HUMAN | yq54h01.1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:199633 5' |
| 5036 | 18049 | 30929 | 0.63 | 1.0E-02 | AL161593.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 89 |
| 5490 | 18590 | 31501 | 0.86 | 1.0E-02 | H52681.1 | EST_HUMAN | yu38h11.1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:235941 5' |
| 5840 | 18830 | 32114 | 0.82 | 1.0E-02 | AF309388.1 | NT | Mus musculus transcription complex subunit NF-ATc4 (Nfatc4) gene, exons 1 and 2 |
| 6237 | 19310 | 32542 | 1.02 | 1.0E-02 | AF257303.1 | NT | Mus musculus synaptotagmin II (Syx2) gene, complete cds |
| 6305 | 19376 | 32614 | 2.49 | 1.0E-02 | AW577113.1 | EST_HUMAN | MR4-BT0356-070100-201-h01 BT0356 Homo sapiens cDNA |
| 6305 | 19376 | 32615 | 2.49 | 1.0E-02 | AW577113.1 | EST_HUMAN | MR4-BT0356-070100-201-h01 BT0356 Homo sapiens cDNA |
| 6926 | 20150 | 33470 | 2.15 | 1.0E-02 | Z29642.1 | NT | Z mays U3snRNA pseudogene |
| 8748 | 22689 | 36145 | 4.19 | 1.0E-02 | BF036331.1 | EST_HUMAN | 601459570F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863177 5' |
| 8748 | 22689 | 36146 | 4.19 | 1.0E-02 | BF036331.1 | EST_HUMAN | 601459570F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863177 5' |
| 11594 | 24532 | | 1.96 | 1.0E-02 | AF157559.1 | NT | Citridia fasciculata 27 kDa guide RNA-binding protein mRNA, complete cds, mitochondrial gene for |
| 11695 | 24660 | 38238 | 2.05 | 1.0E-02 | AV760016.1 | EST_HUMAN | AV760016 MDS Homo sapiens cDNA clone MDSBDC10 5' |
| 12091 | 24962 | | 1.47 | 1.0E-02 | AL163282.2 | NT | Homo sapiens chromosome 21 segment HS21C082 |
| 12276 | 25990 | | 1.99 | 1.0E-02 | O62203 | SWISSPROT | SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66) |
| 12337 | 25757 | 31518 | 3.9 | 1.0E-02 | AW935521.1 | EST_HUMAN | RC2-DT0007-120200-016-h02 DT0007 Homo sapiens cDNA |
| 12356 | 25816 | | 5.66 | 1.0E-02 | S70330.1 | NT | Homo sapiens renal dipeptidase (RDP) gene, complete cds |
| 12722 | 25789 | | 2.07 | 1.0E-02 | AJ276505.1 | NT | Mus musculus genomic fragment, 279 Kb, chromosome 7 |
| 12873 | 25873 | | 4.76 | 1.0E-02 | X62654.1 | NT | H.sapiens gene for Me491/CD63 antigen |
| 13094 | 25620 | 31676 | 1.7 | 1.0E-02 | AB039887.1 | NT | Homo sapiens WDR4 gene for WD repeat protein, complete cds |
| 884 | 13949 | 26907 | 1.77 | 9.0E-03 | AJ796126.1 | EST_HUMAN | wh42f09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2383433 3' similar to contains element |
| 1269 | 14304 | | 1.88 | 9.0E-03 | BE781889.1 | EST_HUMAN | MER22 MER22 repetitive element |
| 1476 | 14510 | 27485 | 0.97 | 9.0E-03 | AE001270.1 | NT | 601470242F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873346 5' |
| 2405 | 15412 | 28436 | 2.87 | 9.0E-03 | AL161559.2 | NT | Trepotema pallidum section 86 of 87 of the complete genome |
| 2413 | 15420 | 28444 | 0.95 | 9.0E-03 | AF099334.1 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59 |
| 2917 | 15975 | 28898 | 0.69 | 9.0E-03 | AI251744.1 | EST_HUMAN | Mus musculus MHC class III protein RP1 (Rp1) mRNA, partial cds |
| 2917 | 15975 | 28899 | 0.69 | 9.0E-03 | AI251744.1 | EST_HUMAN | qh90f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3' |
| 3682 | 16725 | 29638 | 0.87 | 9.0E-03 | J05184.1 | NT | qh90f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3' |
| 5061 | 18071 | 30950 | 1.01 | 9.0E-03 | T70044.1 | EST_HUMAN | S.acidocalcarius thermophilus gene, complete cds |
| | | | | | | | yc17b03.s1 Stratogene lung (#837210) Homo sapiens cDNA clone IMAGE:80919 3' |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 5061 | 18071 | 30951 | 1.01 | 9.0E-03 | T70044.1 | EST_HUMAN | yc17b08.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:80919 3' |
| 5280 | 18298 | 31136 | 0.95 | 9.0E-03 | 6753521 | NT | Mus musculus corticotropin releasing hormone receptor 2 (Chr2), mRNA |
| 5908 | 18994 | | 1.2 | 9.0E-03 | AI809792.1 | EST_HUMAN | wf7704.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2361631 3' |
| 6785 | 19840 | | 4 | 9.0E-03 | BE745988.1 | EST_HUMAN | 601573438F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834782 5' |
| 7698 | 20656 | 34020 | 0.63 | 9.0E-03 | AI242219.1 | EST_HUMAN | qh87c12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1853974 3' |
| 7712 | 20686 | 34036 | 0.81 | 9.0E-03 | 8922570 | NT | Homo sapiens hypothetical protein FLJ10650 (FLJ10650), mRNA |
| 8207 | 21177 | | 0.99 | 9.0E-03 | AL039991.1 | EST_HUMAN | DKFZp434L0412.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L0412 5' |
| 8592 | 21560 | | 0.55 | 9.0E-03 | AF223391.1 | NT | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced |
| 10221 | 23146 | 36635 | 1.42 | 9.0E-03 | P20908 | SWISSPROT | COLLAGEN ALPHA 1(V) CHAIN PRECURSOR |
| 11331 | 24281 | | 1.6 | 9.0E-03 | Y18000.1 | NT | Homo sapiens NF2 gene |
| 12690 | 25985 | | 2.12 | 9.0E-03 | BE348385.1 | EST_HUMAN | hw77b09.x1 NCI_OGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183161 3' |
| 12989 | 25549 | | 15.47 | 9.0E-03 | BF351141.1 | EST_HUMAN | PM1-HT0452-291298-001-e09 HT0452 Homo sapiens cDNA |
| 502 | 13574 | | 3.01 | 8.0E-03 | AA723007.1 | EST_HUMAN | zh30a03.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:413596 3' similar to contains Alu repetitive element |
| 991 | 14043 | 28997 | 19.52 | 8.0E-03 | AF106656.1 | NT | Homo sapiens adenylosuccinate lyase gene, complete cds |
| 2166 | 15182 | 28202 | 1.66 | 8.0E-03 | AL163283.2 | NT | Homo sapiens chromosome 21 segment HS21C083 |
| 3321 | 16372 | 29293 | 1.12 | 8.0E-03 | BE171225.1 | EST_HUMAN | RC1-HT0545-120200-011-b09 HT0545 Homo sapiens cDNA |
| 3370 | 16420 | 29345 | 0.93 | 8.0E-03 | AJ131016.1 | NT | Homo sapiens SCL gene locus |
| 3689 | 16732 | 29644 | 1.25 | 8.0E-03 | P32644 | SWISSPROT | HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION |
| 3689 | 16732 | 29644 | 1.25 | 8.0E-03 | P32644 | SWISSPROT | HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION |
| 4285 | 17314 | 30193 | 1.08 | 8.0E-03 | BE840049.1 | EST_HUMAN | QV0-FN0181-140700-304-g10 FN0181 Homo sapiens cDNA |
| 4410 | 17438 | 30326 | 5.3 | 8.0E-03 | BF363327.1 | EST_HUMAN | CM4-NN0119-300600-223-b05 NN0119 Homo sapiens cDNA |
| 4747 | 17767 | 30662 | 0.65 | 8.0E-03 | P03181 | SWISSPROT | HYPOTHETICAL BHLF1 PROTEIN |
| 4747 | 17767 | 30663 | 0.65 | 8.0E-03 | P03181 | SWISSPROT | HYPOTHETICAL BHLF1 PROTEIN |
| 5601 | 18697 | 31698 | 2.68 | 8.0E-03 | AF110520.1 | NT | Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial> |
| 6323 | 25658 | 32635 | 1.39 | 8.0E-03 | AP000002.1 | NT | Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt. position (27) |
| 6913 | 16965 | 33261 | 4.24 | 8.0E-03 | P55577 | SWISSPROT | PROBABLE PEPTIDASE Y4NA |
| 7104 | 20038 | | 1.4 | 8.0E-03 | V01109.1 | NT | Human BK virus (strain MM) genome. (Closely related to SV40.) |
| 7415 | 20382 | 33733 | 1.88 | 8.0E-03 | M17197.1 | NT | A. californica (marine gastropod mollusc) neuropeptide gene (bag cell), exon 1, 5' end |
| 7790 | 20743 | | 1.81 | 8.0E-03 | AB038267.1 | NT | Tursiops truncatus mRNA for p40-phox, complete cds |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 9235 | 22201 | 35631 | 0.58 | 8.0E-03 | P98160 | SWISSPROT | BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN |
| 9261 | 22227 | 35657 | 3.77 | 8.0E-03 | AW809692.1 | EST_HUMAN | PRECURSOR (HSPG) (PERLECAN) (PLC) |
| 9270 | 22236 | 35665 | 0.52 | 8.0E-03 | AL139075.2 | NT | MR1-ST0111-111196-011-106 ST0111 Homo sapiens cDNA |
| 9331 | 22296 | 35726 | 0.58 | 8.0E-03 | 9789956 | NT | Campylobacter jejuni NCTC11168 complete genome; segment 2/6 |
| 10308 | 23232 | | 5.16 | 8.0E-03 | BE086509.1 | EST_HUMAN | Mus musculus fusion 2 (human) (Fus2), mRNA |
| 11118 | 24078 | 37602 | 1.96 | 8.0E-03 | BE788441.1 | EST_HUMAN | QV1-BT0677-040400-131-g03 BT0677 Homo sapiens cDNA |
| 11330 | 24280 | | 2.66 | 8.0E-03 | Z49652.1 | NT | 601475619F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3878405 5' |
| 11649 | 24586 | 38156 | 2.59 | 8.0E-03 | BF383327.1 | EST_HUMAN | S.cerevisiae chromosome X reading frame ORF YJR152w |
| 11710 | 24675 | 38252 | 1.55 | 8.0E-03 | AA828817.1 | EST_HUMAN | CM4-NN0119-300600-223-b05 NN0119 Homo sapiens cDNA |
| 11710 | 24675 | 38253 | 1.55 | 8.0E-03 | AA828817.1 | EST_HUMAN | cd80a09.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1374232 |
| 12024 | 24900 | 38495 | 3.74 | 8.0E-03 | AF064589.1 | NT | cd80a09.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1374232 |
| 12205 | 25047 | | 2.04 | 8.0E-03 | M69035.1 | NT | Homo sapiens melanoma-associated antigen (MAGE-C1) gene, complete cds |
| 12249 | 25077 | | 2.6 | 8.0E-03 | AB038161.1 | NT | Oryctolagus cuniculus eIF-2a kinase mRNA, complete cds |
| 695 | 13757 | 26687 | 18.14 | 7.0E-03 | AF097183.1 | NT | Homo sapiens ABCG1 gene for ABC transporter (ATP-binding cassette, sub-family G (WHITE), member 1), complete cds |
| 695 | 13757 | 26688 | 18.14 | 7.0E-03 | AF097183.1 | NT | Cryptosporidium parvum HC-10 gene, complete cds |
| 978 | 14029 | 26983 | 4.68 | 7.0E-03 | AF243376.1 | NT | Cryptosporidium parvum HC-10 gene, complete cds |
| 1118 | 14182 | 27113 | 4.38 | 7.0E-03 | AV731712.1 | EST_HUMAN | Glycine max glutathione S-transferase GST 21 mRNA, partial cds |
| 1366 | 14400 | | 1.16 | 7.0E-03 | Q61060 | SWISSPROT | AV731712 HTF Homo sapiens cDNA clone HTFAZF10 5' |
| 1396 | 14430 | 27399 | 3.03 | 7.0E-03 | AA688298.1 | EST_HUMAN | FORKHEAD BOX PROTEIN D3 (HNF3FH TRANSCRIPTION FACTOR GENESIS) (HEPATOCTE |
| 1502 | 14535 | 27506 | 3.04 | 7.0E-03 | AW303599.1 | EST_HUMAN | NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 2) (HFH-2) |
| 1756 | 14785 | 27769 | 1.03 | 7.0E-03 | AW950556.1 | EST_HUMAN | ab79b09.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853145 3' |
| 2287 | 15898 | 28307 | 2.08 | 7.0E-03 | P04929 | SWISSPROT | xx21b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813739 3' |
| 3571 | 16616 | 29537 | 0.67 | 7.0E-03 | AI150273.1 | EST_HUMAN | EST362626 MAGE resequences; MAGE Homo sapiens cDNA |
| 3778 | 16820 | 29728 | 0.93 | 7.0E-03 | AW44463.1 | EST_HUMAN | EST362626 MAGE resequences; MAGE Homo sapiens cDNA |
| 3825 | 16885 | 29769 | 1.45 | 7.0E-03 | AF196344.1 | NT | HISTIDINE-RICH GLYCOPROTEIN PRECURSOR |
| 4048 | 16820 | 29728 | 0.83 | 7.0E-03 | AW44463.1 | EST_HUMAN | q34h02.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1751955 3' |
| 4366 | 17393 | | 0.66 | 7.0E-03 | U60086.1 | NT | UI-H-B13-akb-c-10-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733691 3' |
| | | | | | | | Rattus norvegicus neuronal nicotinic acetylcholine receptor subunit (Alpha10) mRNA, complete cds |
| | | | | | | | UI-H-B13-akb-c-10-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733691 3' |
| | | | | | | | Dichytellum discoidium multidrug resistance transporter/Ser protease (tagC) mRNA, complete cds |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 4565 | 17588 | | 1 | 7.0E-03 | AW117711.1 | EST_HUMAN | xe34f09.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2609033 3' similar to TR:Q12987 Q12987 |
| 4629 | 17650 | | 1.47 | 7.0E-03 | AW630888.1 | EST_HUMAN | ACIDIC 82 KDA PROTEIN. ; |
| 5024 | 18038 | | 1.81 | 7.0E-03 | AL169278.2 | NT | hh89a05.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2969936 5' |
| 5226 | 18234 | 31108 | 1.4 | 7.0E-03 | AV724419.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C078 |
| 5228 | 18234 | 31108 | 1.4 | 7.0E-03 | AV724419.1 | EST_HUMAN | AV724419 HTB Homo sapiens cDNA clone HTBCE08 5' |
| 5918 | 19004 | | 0.83 | 7.0E-03 | H71106.1 | EST_HUMAN | AV724419 HTB Homo sapiens cDNA clone HTBCE08 5' |
| 6233 | 25656 | | 5.11 | 7.0E-03 | AW861059.1 | EST_HUMAN | y82g01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211824 5' similar to |
| 6447 | 19512 | 32762 | 1.38 | 7.0E-03 | W68251.1 | EST_HUMAN | gbX14723 CLUSTERIN PRECURSOR (HUMAN); |
| 6687 | 19744 | 33019 | 3.16 | 7.0E-03 | AA327129.1 | EST_HUMAN | RC1-CT0286-050400-018-c08 CT0286 Homo sapiens cDNA |
| 6717 | 19773 | 33052 | 0.91 | 7.0E-03 | BE857385.1 | EST_HUMAN | z633f10.1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:342475 5' |
| 7284 | 20061 | 33367 | 1.92 | 7.0E-03 | BE928133.1 | EST_HUMAN | EST30674 Codon 1 Homo sapiens cDNA 5' end |
| 7763 | 20716 | 34098 | 5.31 | 7.0E-03 | Z35838.1 | NT | 7g34b10.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3308347 3' similar to TR:Q13387 |
| 7763 | 20716 | 34098 | 5.31 | 7.0E-03 | Z35838.1 | NT | Q13387 HYPOTHETICAL PROTEIN 384D8_2 ; contains TAR1.12 TAR1 repetitive element ; |
| 8180 | 21150 | 34557 | 0.45 | 7.0E-03 | AJ229043.1 | NT | CM2-CT0478-230800-347-411 CT0478 Homo sapiens cDNA |
| 8180 | 21150 | 34558 | 0.45 | 7.0E-03 | AJ229043.1 | NT | S.cerevisiae chromosome II reading frame ORF YBL077w |
| 8448 | 21417 | 34830 | 2.46 | 7.0E-03 | BE175667.1 | EST_HUMAN | S.cerevisiae chromosome II reading frame ORF YBL077w |
| 8961 | 21827 | 35354 | 0.49 | 7.0E-03 | AF281074.1 | NT | Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3 |
| 9752 | 22693 | | 0.71 | 7.0E-03 | AF111168.2 | NT | Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3 |
| 9953 | 22880 | 36344 | 0.85 | 7.0E-03 | N52378.1 | EST_HUMAN | RC6-HT0582-160300-011-D02 HT0582 Homo sapiens cDNA |
| 10078 | 23005 | 36475 | 2.84 | 7.0E-03 | P48992 | SWISSPROT | Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced |
| 10078 | 23005 | 36476 | 2.84 | 7.0E-03 | P48992 | SWISSPROT | Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes |
| 10668 | 23590 | | 1.06 | 7.0E-03 | AV887379.1 | EST_HUMAN | yw49c10.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:246066 3' similar to contains |
| 10853 | 23773 | | 0.95 | 7.0E-03 | AI799734.1 | EST_HUMAN | Alu repetitive element |
| 11175 | 24132 | 37662 | 2.23 | 7.0E-03 | AB008852.1 | NT | BETA-GALACTOSIDASE PRECURSOR (LACTASE) |
| 11248 | 24201 | 37722 | 1.51 | 7.0E-03 | AJ004862.1 | NT | BETA-GALACTOSIDASE PRECURSOR (LACTASE) |
| 11248 | 24201 | 37723 | 1.51 | 7.0E-03 | AJ004862.1 | NT | BETA-GALACTOSIDASE PRECURSOR (LACTASE) |
| 12734 | 25977 | | 1.53 | 7.0E-03 | H94065.1 | EST_HUMAN | AV887379 GKC Homo sapiens cDNA clone GKCAFC07 5' |
| 12741 | 25391 | | 1.91 | 7.0E-03 | BE263253.1 | EST_HUMAN | wc37e09.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2320840 3' |
| 12834 | 25451 | | 1.99 | 7.0E-03 | Y17455.1 | NT | Bos taurus mRNA for NDP52, complete cds |
| | | | | | | | Bos taurus partial MUC5B gene, exon 1-29 |
| | | | | | | | Homo sapiens partial MUC5B gene, exon 1-29 |
| | | | | | | | Homo sapiens partial MUC5B gene, exon 1-29 |
| | | | | | | | yw15h01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:242833 3' similar to contains |
| | | | | | | | Alu repetitive element |
| | | | | | | | 601145154F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160476 5' |
| | | | | | | | Homo sapiens LSFR2 gene, penultimate exon |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 1245 | 14282 | 27244 | 9.96 | 6.0E-03 | AW511148.1 | EST_HUMAN | hd22a05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2810224 3' similar to SW:PXN_HUMAN O75469 ORPHAN NUCLEAR RECEPTOR PXR ; |
| 1245 | 14282 | 27245 | 9.96 | 6.0E-03 | AW511148.1 | EST_HUMAN | hd22a05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2810224 3' similar to SW:PXN_HUMAN O75469 ORPHAN NUCLEAR RECEPTOR PXR ; |
| 2762 | 15774 | 28793 | 1.32 | 6.0E-03 | AF112374.1 | NT | Danio rerio odorant receptor gene cluster |
| 2901 | 15960 | 28879 | 4.82 | 6.0E-03 | AA759135.1 | EST_HUMAN | ah78e11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1321772 3' |
| 2901 | 15960 | 28880 | 4.82 | 6.0E-03 | AA759135.1 | EST_HUMAN | ah78e11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1321772 3' |
| 3280 | 16314 | | 2.26 | 6.0E-03 | H75690.1 | EST_HUMAN | y77h04.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:211351 5' |
| 3393 | 16442 | 29368 | 1.3 | 6.0E-03 | U90880.1 | NT | Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, sepiapterin reductase and vasotocin genes, complete cds |
| 3393 | 16442 | 29369 | 1.3 | 6.0E-03 | U90880.1 | NT | Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, sepiapterin reductase and vasotocin genes, complete cds |
| 3557 | 16603 | | 1.28 | 6.0E-03 | W37985.1 | EST_HUMAN | zz13a11.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:322172 5' |
| 3672 | 16715 | 29629 | 4.48 | 6.0E-03 | BF510986.1 | EST_HUMAN | UHH-B14-qpm-c-06-0-UI.s1 NCI CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3087754 3' |
| 3708 | 16751 | 29667 | 1.21 | 6.0E-03 | BE077356.1 | EST_HUMAN | RC1-BT0606-280400-014-a07 BT0606 Homo sapiens cDNA |
| 3790 | 16831 | 29737 | 1.19 | 6.0E-03 | 6754028 | NT | Mus musculus glucosamine-6-phosphate deaminase (Gnpl), mRNA |
| 3944 | 16984 | 29900 | 0.87 | 6.0E-03 | AW847284.1 | EST_HUMAN | RC0-CT0204-240998-021-b10 CT0204 Homo sapiens cDNA |
| 3979 | 17019 | | 0.9 | 6.0E-03 | BE250108.1 | EST_HUMAN | 600942904F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959513 5' |
| 4391 | 17419 | | 1.81 | 6.0E-03 | A018833.1 | EST_HUMAN | ov33c11.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1639124 3' |
| 4724 | 17744 | 30635 | 5.97 | 6.0E-03 | AA324242.1 | EST_HUMAN | EST27116 Cerebellum II Homo sapiens cDNA 5' end similar to EST containing Alu repeat |
| 6276 | 25657 | 32581 | 0.9 | 6.0E-03 | 9827521 | NT | Varidola virus, complete genome |
| 6969 | 20212 | 33541 | 0.87 | 6.0E-03 | O14994 | SWISSPROT | SYNAPSIN III |
| 7034 | 18396 | 31253 | 0.64 | 6.0E-03 | BE253748.1 | EST_HUMAN | 601112353F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3353172 5' |
| 7461 | 20427 | 33783 | 0.83 | 6.0E-03 | AA299442.1 | EST_HUMAN | EST11949 Uterus tumor I Homo sapiens cDNA 5' end |
| 7461 | 20427 | 33784 | 0.83 | 6.0E-03 | AA299442.1 | EST_HUMAN | EST11949 Uterus tumor I Homo sapiens cDNA 5' end |
| 7808 | 20851 | 34238 | 0.63 | 6.0E-03 | AF128894.1 | NT | Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 7-16 and complete cds |
| 8100 | 21036 | 34436 | 0.62 | 6.0E-03 | P17964 | SWISSPROT | RAS-RELATED PROTEIN RAP-28 |
| 8136 | 21073 | 34473 | 0.5 | 6.0E-03 | AJ243211.1 | NT | Homo sapiens DMBT1 candidate tumor suppressor gene, exons 1 to 55 |
| 8191 | 21161 | 34571 | 6.56 | 6.0E-03 | A1033980.1 | EST_HUMAN | ow13a04.x1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1648670 3' similar to contains MER10.b1 MER10 repetitive element ; |
| 8307 | 21276 | 34687 | 2.54 | 6.0E-03 | AW799337.1 | EST_HUMAN | RC0-UM0051-210300-032-g02 UM0051 Homo sapiens cDNA |
| 8381 | 21350 | | 1.51 | 6.0E-03 | BF038198.1 | EST_HUMAN | 601454915F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3658628 5' |
| 9912 | 22733 | 36188 | 8.57 | 6.0E-03 | D10548.1 | NT | Subacute sclerosing panencephalitis (SSPE) virus mRNA for fusion protein |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 10403 | 23325 | | 2.08 | 6.0E-03 | AI432661.1 | EST_HUMAN | 122c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2131202 3' similar to SW:R13A_HUMAN |
| 10523 | 23445 | 36943 | 0.87 | 6.0E-03 | AJ011849.1 | NT | P40428 60S RIBOSOMAL PROTEIN L13A ; Bacillus subtilis fenD gene |
| 10659 | 23581 | | 1.03 | 6.0E-03 | AF084555.1 | NT | Homo sapiens dksale acid-inducible and cAMP-regulated phosphoprotein 19 (ARPP-19) mRNA, complete cds |
| 10769 | 23690 | 37187 | 0.68 | 6.0E-03 | X68360.1 | NT | M.thermophilum complete plasmid pFV1 DNA |
| 11096 | 24056 | 37590 | 1.61 | 6.0E-03 | AW062184.1 | EST_HUMAN | EST1374237 MAGE resequences, MAGG Homo sapiens cDNA |
| 11162 | 24120 | | 1.55 | 6.0E-03 | 11545814 | NT | Homo sapiens hypothetical zinc finger protein FLJ14011 (FLJ14011), mRNA |
| 11327 | 24277 | | 3.99 | 6.0E-03 | U14556.1 | NT | Mus musculus zinc-finger protein mRNA, complete cds |
| 11328 | 24278 | 37805 | 2.55 | 6.0E-03 | BE737895.1 | EST_HUMAN | 601572746F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839747 5' |
| 12319 | 25123 | | 2.28 | 6.0E-03 | AF010486.1 | NT | Rhodobacter capsulatus strain SB1003, partial genome |
| 12422 | 25812 | | 1.52 | 6.0E-03 | BF071185.1 | EST_HUMAN | 602151024F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4292212 5' |
| 12446 | 25744 | | 5.26 | 6.0E-03 | AE000833.1 | NT | Methanobacterium thermoautotrophicum from bases 428192 to 450286 (section 39 of 148) of the complete genome |
| 12525 | 25807 | | 2.71 | 6.0E-03 | U30790.1 | NT | Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds |
| 12576 | 25285 | | 1.48 | 6.0E-03 | Q62209 | SWISSPROT | SYNAPTONEMAL COMPLEX PROTEIN 1 (SCP-1) PROTEIN |
| 12850 | 25459 | | 2.16 | 6.0E-03 | BE788019.1 | EST_HUMAN | 601482821F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3885388 5' |
| 12869 | 25471 | | 1.53 | 6.0E-03 | AJ245480.1 | NT | Brassica napus slg gene for S-locus glycoprotein, cultivar T2 |
| 13043 | 25584 | | 1.76 | 6.0E-03 | BF110298.1 | EST_HUMAN | 7n36b11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3566564 3' |
| 670 | 13735 | 26661 | 2.34 | 5.0E-03 | L25105.1 | NT | Chlamydia trachomatis partial ORF8; aminoacyl-tRNA synthase, complete cds; complete ORF8, and grpE-like protein, complete cds |
| 670 | 13735 | 26662 | 2.34 | 5.0E-03 | L25105.1 | NT | Chlamydia trachomatis partial ORF8; aminoacyl-tRNA synthase, complete cds; complete ORF8, and grpE-like protein, complete cds |
| 671 | 13735 | 26661 | 3.43 | 5.0E-03 | L25105.1 | NT | Chlamydia trachomatis partial ORF8; aminoacyl-tRNA synthase, complete cds; complete ORF8, and grpE-like protein, complete cds |
| 671 | 13735 | 26662 | 3.43 | 5.0E-03 | L25105.1 | NT | Chlamydia trachomatis partial ORF8; aminoacyl-tRNA synthase, complete cds; complete ORF8, and grpE-like protein, complete cds |
| 1114 | 14158 | 27109 | 1.03 | 5.0E-03 | AJ010457.1 | NT | Arabidopsis thaliana mRNA for DEAD box RNA helicase, RH3 |
| 1574 | 14607 | | 1.02 | 5.0E-03 | A1138977.1 | EST_HUMAN | qd79d05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1735689 3' |
| 2690 | 15686 | 28703 | 2.63 | 5.0E-03 | AB033008.1 | NT | Homo sapiens mRNA for KIAA1180 protein, partial cds |
| 2947 | 16005 | 28930 | 3.66 | 5.0E-03 | BE266057.1 | EST_HUMAN | 601194796F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538799 5' |
| 3153 | 16210 | 29125 | 3.96 | 5.0E-03 | T87623.1 | EST_HUMAN | yc81f09.31 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:22395 3' |
| 3169 | 16224 | | 3.05 | 5.0E-03 | AL161491.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 3 |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 3181 | 16236 | 29153 | 1.22 | 5.0E-03 | R71794.1 | EST_HUMAN | y86g02.s1 Soares breast 2NHBst Homo sapiens cDNA clone IMAGE:155668 3' |
| 3291 | 16344 | | 0.94 | 5.0E-03 | AJ297357.1 | NT | Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene |
| 3679 | 16722 | 29635 | 0.97 | 5.0E-03 | AL163285.2 | NT | Homo sapiens chromosome 21 segment HS21C085 |
| 3713 | 16766 | 29670 | 4.03 | 5.0E-03 | AF147449.2 | NT | Pseudomonas aeruginosa strain PAO1 penicillin-binding protein 1B (ponB) gene, complete cds |
| 3771 | 16813 | 29722 | 1 | 5.0E-03 | U38914.1 | NT | Citrus sinensis seed storage protein citrin mRNA, complete cds |
| 3995 | 17035 | | 2 | 5.0E-03 | AA296675.1 | EST_HUMAN | EST12218 Uterus tumor 1 Homo sapiens cDNA 5' end |
| 4333 | 17361 | 30246 | 0.69 | 5.0E-03 | H78355.1 | EST_HUMAN | y179g10.r1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:240066 5' |
| 4335 | 16813 | 29722 | 1.02 | 5.0E-03 | U38914.1 | NT | Citrus sinensis seed storage protein citrin mRNA, complete cds |
| 4601 | 17622 | 30515 | 1.02 | 5.0E-03 | U46691.1 | NT | Human putative chromatin structure regulator (SUPT6H) mRNA, complete cds |
| 4638 | 17659 | 30546 | 1.13 | 5.0E-03 | AJ131016.1 | NT | Homo sapiens SCL gene locus |
| 4749 | 17769 | 30665 | 1.34 | 5.0E-03 | AJ752367.1 | EST_HUMAN | cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC.cn15c02 random |
| 4970 | 17985 | 30875 | 1.08 | 5.0E-03 | P15265 | SWISSPROT | SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS) |
| 5222 | 18230 | 31105 | 1.69 | 5.0E-03 | 6754029 | NT | Mus musculus glucosamine-6-phosphate deaminase (Gnpi) mRNA |
| 5893 | 18981 | 32172 | 5.69 | 5.0E-03 | P35600 | SWISSPROT | SODIUM CHANNEL PROTEIN PARA (PARALYTIC PROTEIN) |
| 6162 | 19237 | 32468 | 2.97 | 5.0E-03 | O09507 | SWISSPROT | PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF-Y (UBIQUITIN THIOLESTERASE FAF-Y) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE FAF-Y) (DEUBIQUITINATING ENZYME FAF-Y) (FAT FACETS PROTEIN RELATED, Y-LINKED) (UBIQUITIN-SPECIFIC PROTEASE 8, Y CHROMOSOME) |
| 6198 | 19272 | | 0.89 | 5.0E-03 | AE002234.2 | NT | Chlamydia pneumoniae AR39, section 62 of 94 of the complete genome |
| 6747 | 19601 | | 7.44 | 5.0E-03 | BE300091.1 | EST_HUMAN | 600944564T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860871 3' |
| 7023 | 18355 | 31274 | 7.12 | 5.0E-03 | AB025024.1 | NT | Mus musculus AMD1 gene for S-adenosylmethionine decarboxylase, complete cds |
| 7240 | 19575 | | 0.82 | 5.0E-03 | AB038267.1 | NT | Tursiops truncatus mRNA for p40-phox, complete cds |
| 7295 | 20267 | 33602 | 0.57 | 5.0E-03 | 6753651 | NT | Mus musculus dynein, exon, heavy chain 11 (Dnahe11), mRNA |
| 7727 | 20683 | 34047 | 0.62 | 5.0E-03 | T06124.1 | EST_HUMAN | EST03012 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCR93 similar to EST containing Alu repeat |
| 7856 | 20801 | | 1.17 | 5.0E-03 | AW854327.1 | EST_HUMAN | RC3-CT0255-031099-011-f07 CT0255 Homo sapiens cDNA |
| 8044 | 20981 | 34378 | 6.8 | 5.0E-03 | AB016816.1 | NT | Homo sapiens MASL1 mRNA, complete cds |
| 8097 | 21033 | 34431 | 0.49 | 5.0E-03 | Q9R001 | SWISSPROT | ADAM-TS 5 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 5) (ADAMTS-5) (ADAM-TS5) (AGGRECANASE-2) (ADMP-2) (IMPLANTIN) |
| 8097 | 21033 | 34432 | 0.49 | 5.0E-03 | Q9R001 | SWISSPROT | ADAM-TS 5 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 5) (ADAMTS-5) (ADAM-TS5) (AGGRECANASE-2) (ADMP-2) (IMPLANTIN) |
| 8581 | 21549 | 34967 | 2.12 | 5.0E-03 | P48982 | SWISSPROT | BETA-GALACTOSIDASE PRECURSOR (LACTASE) |
| 8959 | 21925 | | 5.83 | 5.0E-03 | M61132.1 | NT | Mouse complement receptor (CR2) mRNA, 3' end |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 9159 | 22125 | 35554 | 1.08 | 5.0E-03 | D90723.1 | NT | Escherichia coli genomic DNA. (19.1 - 19.4 min) |
| 9292 | 22258 | 35698 | 0.61 | 5.0E-03 | M25090.1 | NT | Rabbit uteroglobin (UGL) gene, exon 1 |
| 10199 | 23124 | 36611 | 0.97 | 5.0E-03 | L21710.1 | NT | Plasmodium berghei 58 kDa phosphoprotein mRNA, partial cds |
| 10330 | 23254 | 36732 | 0.68 | 5.0E-03 | AW821888.1 | EST_HUMAN | RC0-ST0379-210100-032-c02 ST0379 Homo sapiens cDNA |
| 10518 | 23440 | 36938 | 0.44 | 5.0E-03 | AA533143.1 | EST_HUMAN | h48h10.s1 NCI_CGAP_P78 Homo sapiens cDNA clone IMAGE:995587 |
| 10698 | 23618 | 37112 | 0.47 | 5.0E-03 | 7662557 | NT | Homo sapiens PRO0471 protein (PRO0471), mRNA |
| 10844 | 23764 | | 0.51 | 5.0E-03 | AA653261.1 | EST_HUMAN | ag49c10.s1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1126290 3' |
| 11075 | 24037 | | 4.17 | 5.0E-03 | T19596.1 | EST_HUMAN | 694F Heart Homo sapiens cDNA clone 694 |
| 11287 | 24237 | 37764 | 2.15 | 5.0E-03 | AW170334.1 | EST_HUMAN | xr59g05.x1 Soares_NHCeC_cervical_tumor Homo sapiens cDNA clone IMAGE:2698040 3' similar to contains L1.12 L1 repetitive element ; |
| 11287 | 24237 | 37765 | 2.15 | 5.0E-03 | AW170334.1 | EST_HUMAN | xr59g05.x1 Soares_NHCeC_cervical_tumor Homo sapiens cDNA clone IMAGE:2698040 3' similar to contains L1.12 L1 repetitive element ; |
| 11391 | 24328 | 37857 | 1.55 | 5.0E-03 | T49153.1 | EST_HUMAN | y09e04.r1 Stratagene placenta (#937225) Homo sapiens cDNA clone IMAGE:70698 5' |
| 11659 | 24595 | | 3.62 | 5.0E-03 | BE048055.1 | EST_HUMAN | tz46c04.y1 NCI_CGAP_Brm52 Homo sapiens cDNA clone IMAGE:2291622 5' |
| 12463 | 25938 | | 5.42 | 5.0E-03 | AF047874.1 | NT | Gallus gallus glyceraldehyde-3-phosphate dehydrogenase mRNA, complete cds |
| 12595 | 25298 | | 3.7 | 5.0E-03 | AF067253.1 | NT | Brugia malayi Y chromosome marker |
| 12688 | 25355 | | 3.19 | 5.0E-03 | L10347.1 | NT | Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds |
| 12718 | 25372 | | 1.89 | 5.0E-03 | AA456597.1 | EST_HUMAN | zx75a03.s1 Soares ovary tumor NBH07 Homo sapiens cDNA clone IMAGE:809648 3' similar to |
| 12743 | 25752 | | 5.67 | 5.0E-03 | BF572332.1 | EST_HUMAN | SW_DXA2_MOUSE P14685 PROBABLE DIPHENOL OXIDASE A2 COMPONENT ; |
| 12922 | 25498 | 31702 | 3.21 | 5.0E-03 | AW449109.1 | EST_HUMAN | 60207774F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4252002 5' |
| 235 | 13335 | 26259 | 2.6 | 4.0E-03 | AW500196.1 | EST_HUMAN | UI-P-819-akt-f08-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734216 3' |
| 321 | 13413 | 26337 | 2.12 | 4.0E-03 | R46482.1 | EST_HUMAN | UI-HF-BN0-akt-h-04-0-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076831 5' |
| 443 | 13516 | 26449 | 1.15 | 4.0E-03 | P54675 | SWISSPROT | y051e04.s1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:35988 3' |
| 605 | 13872 | 26586 | 4.63 | 4.0E-03 | AA039339.1 | EST_HUMAN | PHOSPHATIDYLINOSITOL 3-KINASE 3 (PI3-KINASE) (PTDINS-3-KINASE) (PI3K) |
| 878 | 13933 | 26893 | 1.9 | 4.0E-03 | R46482.1 | EST_HUMAN | on75g12.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1562566 3' |
| 912 | 13967 | | 3.64 | 4.0E-03 | AW749101.1 | EST_HUMAN | y051e04.s1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:35988 3' |
| 1153 | 14195 | 27147 | 27.01 | 4.0E-03 | AA09977.1 | EST_HUMAN | RC3-BT0333-110100-012-f01 BT0333 Homo sapiens cDNA |
| 1173 | 14214 | 27169 | 1.92 | 4.0E-03 | AW794740.1 | EST_HUMAN | 2181a08.r1 Siratogene colon (#937204) Homo sapiens cDNA clone IMAGE:510988 5' |
| 1306 | 14342 | 27306 | 1.5 | 4.0E-03 | AA284374.1 | EST_HUMAN | RC6-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA |
| 1590 | 14622 | | 1.64 | 4.0E-03 | AV708305.1 | EST_HUMAN | zs59a01.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701736 5' |
| 1758 | 14787 | 27772 | 2.38 | 4.0E-03 | U33472.1 | NT | AV708305 ADC Homo sapiens cDNA clone ADCAKB08 5' |
| 2034 | 15053 | 28070 | 11.42 | 4.0E-03 | AA069777.1 | EST_HUMAN | Rattus norvegicus type 1 astrocyte and olfactory-limbic associated protein AT1-46 mRNA, complete cds |
| | | | | | | | 2181a08.r1 Siratogene colon (#937204) Homo sapiens cDNA clone IMAGE:510988 5' |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 2259 | 15273 | | 1.68 | 4.0E-03 | BE410586.1 | EST_HUMAN | 601304161F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:36388510 5' |
| 2286 | 15299 | 28323 | 1.53 | 4.0E-03 | AW794740.1 | EST_HUMAN | RC8-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA |
| 2579 | 15580 | 28598 | 1.75 | 4.0E-03 | U52111.2 | NT | Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenergic dystrophy protein > |
| 2579 | 15580 | | 1.75 | 4.0E-03 | U52111.2 | NT | Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenergic dystrophy protein > |
| 2701 | 15697 | 28712 | 3.92 | 4.0E-03 | AJ277365.1 | NT | Homo sapiens polyglutamine-containing C14ORF4 gene |
| 2701 | 15697 | 28713 | 3.92 | 4.0E-03 | AJ277365.1 | NT | Homo sapiens polyglutamine-containing C14ORF4 gene |
| 2707 | 15702 | 28716 | 1.68 | 4.0E-03 | AL163284.2 | NT | Homo sapiens chromosome 21 segment HS21C084 |
| 3239 | 16294 | 29217 | 1.04 | 4.0E-03 | BE154134.1 | EST_HUMAN | PM1-HT0340-151298-003-t08 HT0340 Homo sapiens cDNA |
| 3239 | 16294 | 29218 | 1.04 | 4.0E-03 | BE154134.1 | EST_HUMAN | PM1-HT0340-151298-003-t08 HT0340 Homo sapiens cDNA |
| 3541 | 16587 | 29510 | 0.8 | 4.0E-03 | AW188426.1 | EST_HUMAN | x98f04.x1 NCI_CGAP_Cot18 Homo sapiens cDNA clone IMAGE:2665279 3' |
| 3541 | 16587 | 29511 | 0.8 | 4.0E-03 | AW188426.1 | EST_HUMAN | x98f04.x1 NCI_CGAP_Cot18 Homo sapiens cDNA clone IMAGE:2665279 3' |
| 3639 | 16682 | 29597 | 0.64 | 4.0E-03 | Q13606 | SWISSPROT | OLFACTORY RECEPTOR 511 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1) |
| 4020 | 17058 | | 2.14 | 4.0E-03 | AJ011712.1 | NT | Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS) |
| 4643 | 17664 | 30553 | 1.1 | 4.0E-03 | AI732764.1 | EST_HUMAN | ab18a08.x5 Stragene lung (#837210) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains Alu repetitive element |
| 4805 | 17822 | 30717 | 3.73 | 4.0E-03 | AL163284.2 | NT | Homo sapiens chromosome 21 segment HS21C084 |
| 5173 | 18182 | 31059 | 0.98 | 4.0E-03 | AW103719.1 | EST_HUMAN | x983d03.x1 NCI_CGAP_Bin35 Homo sapiens cDNA clone IMAGE:2614469 3' similar to contains L1.t1 L1 |
| 5220 | 18228 | 31102 | 0.63 | 4.0E-03 | AA699995.1 | EST_HUMAN | L1 repetitive element |
| 5272 | 18278 | 31142 | 0.93 | 4.0E-03 | J02187.1 | NT | Foot and mouth disease virus serotype A-12 119ab capsid protein VP3 |
| 5348 | 18453 | 31324 | 1.56 | 4.0E-03 | AF005859.1 | NT | Drosophila melanogaster anon2D7 (anon2D7) mRNA, complete cds |
| 5473 | 18574 | 31482 | 23.1 | 4.0E-03 | AF189825.1 | NT | Rattus norvegicus beta-catenin binding protein mRNA, complete cds |
| 5891 | 18979 | 32171 | 2.72 | 4.0E-03 | P04196 | SWISSPROT | (HPRG) |
| 5895 | 18983 | 32173 | 1.63 | 4.0E-03 | P21849 | SWISSPROT | MAJOR SURFACE-LABELLED TROPHOZOITE ANTIGEN PRECURSOR |
| 5983 | 19068 | 32266 | 0.87 | 4.0E-03 | AL133871.1 | EST_HUMAN | DKF2p7611014.J1 761 (synonym: hamy2) Homo sapiens cDNA clone DKF2p7611014 5' |
| 6203 | 19277 | | 3.56 | 4.0E-03 | U22180.1 | NT | Rattus norvegicus opsin gene, complete cds |
| 6361 | 19430 | 32673 | 1 | 4.0E-03 | AW590572.1 | EST_HUMAN | hg46c07.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2849652 3' |
| 6442 | 19507 | 32757 | 1.78 | 4.0E-03 | BE548453.1 | EST_HUMAN | 601076015F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3481954 5' |
| 6827 | 19881 | 33172 | 0.87 | 4.0E-03 | AA813222.1 | EST_HUMAN | aj3211.s1 Soares_testis_NHT Homo sapiens cDNA clone 1392045 3' |
| 6942 | 20166 | 33489 | 1.5 | 4.0E-03 | U76408.1 | NT | Lycopodium esculentum knotted 3 protein (TKn3) mRNA, complete cds |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 7273 | 20008 | 33308 | 1.22 | 4.0E-03 | AL163278.2 | NT | Homo sapiens chromosome 21 segment HS21C078 |
| 7273 | 20008 | 33309 | 1.22 | 4.0E-03 | AL163278.2 | NT | Homo sapiens chromosome 21 segment HS21C078 |
| 7404 | 20372 | 33723 | 4.12 | 4.0E-03 | Q02817 | SWISSPROT | MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2) |
| 7665 | 20624 | 33998 | 0.99 | 4.0E-03 | AI681483.1 | EST_HUMAN | bc37g12.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2271814 3' |
| 7667 | 20628 | 33990 | 0.72 | 4.0E-03 | BE670170.1 | EST_HUMAN | 7e31b02.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284043 3' |
| 7767 | 20720 | | 0.68 | 4.0E-03 | X92109.1 | NT | H. sapiens hcgIX gene |
| 8274 | 21243 | 34655 | 0.49 | 4.0E-03 | Q91T92 | SWISSPROT | ADAM-TS 5 (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 5) (ADAMTS-5) (ADAM-TS5) (AGGRECANASE-2) (ADMP-2) (ADAM-TS 11) |
| 8383 | 21352 | 34761 | 5.06 | 4.0E-03 | AF111944.1 | NT | Dicystotellum discoideum AX4 development protein DG1122 (DG1122) gene, partial cds |
| 8545 | 21513 | 34930 | 1.92 | 4.0E-03 | 7662067 | NT | Homo sapiens KIAA0345 gene product (KIAA0345), mRNA |
| 9064 | 22030 | 35453 | 7.41 | 4.0E-03 | AI553983.1 | EST_HUMAN | te49b11.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090013 3' similar to contains Alu repetitive element; |
| 9241 | 22207 | | 4.72 | 4.0E-03 | AL163209.2 | NT | Homo sapiens chromosome 21 segment HS21C009 |
| 9250 | 22216 | 35646 | 3.66 | 4.0E-03 | AL163278.2 | NT | Homo sapiens chromosome 21 segment HS21C078 |
| 10287 | 23212 | 36695 | 0.57 | 4.0E-03 | H30684.1 | EST_HUMAN | yp42g12.t1 Scores retina N2b5fHR Homo sapiens cDNA clone IMAGE:190150 5' |
| 10742 | 23664 | 37159 | 0.79 | 4.0E-03 | AL161555.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 55 |
| 11176 | 24133 | 37663 | 1.65 | 4.0E-03 | AW513635.1 | EST_HUMAN | xc47h04.x1 NCI CGAP_U11 Homo sapiens cDNA clone IMAGE:2707159 3' |
| 11464 | 24407 | 37954 | 4.53 | 4.0E-03 | AL163206.2 | NT | Homo sapiens chromosome 21 segment HS21C006 |
| 12431 | 25956 | | 1.52 | 4.0E-03 | BE815173.1 | EST_HUMAN | PM4-BN0738-180600-002-b08 BN0738 Homo sapiens cDNA |
| 12454 | 25213 | | 3.2 | 4.0E-03 | BE288290.1 | EST_HUMAN | 601118164F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028095 5' |
| 12533 | 25259 | | 2.13 | 4.0E-03 | AW504273.1 | EST_HUMAN | UI-HF-BN0-elp-g-04-0-J1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3080622 5' |
| 12755 | 25400 | | 7.22 | 4.0E-03 | BF224125.1 | EST_HUMAN | element; contains element MER31 repetitive element ; |
| 12801 | 25866 | | 3.31 | 4.0E-03 | AW614596.1 | EST_HUMAN | hh02c07.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2863932 3' similar to contains element |
| 12814 | 25437 | | 2.73 | 4.0E-03 | AW819141.1 | EST_HUMAN | LTR5 repetitive element ; |
| 13093 | 25919 | 31675 | 6.48 | 4.0E-03 | 11436955 | NT | RC3-ST0281-240400-015-f03 ST0281 Homo sapiens cDNA |
| 371 | 13457 | 26387 | 1.69 | 3.0E-03 | AF011920.1 | NT | Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA |
| 880 | 13935 | 26894 | 3.09 | 3.0E-03 | AF011920.1 | NT | Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1 |
| 1669 | 14701 | 27676 | 5.52 | 3.0E-03 | AA468110.1 | EST_HUMAN | Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1 |
| 2268 | 15281 | | 1.58 | 3.0E-03 | AF05066.1 | NT | nc73c05.s1 NCI CGAP_Pr2 Homo sapiens cDNA clone IMAGE:782984 similar to contains Alu repetitive element; |
| 2302 | 15314 | | 8.06 | 3.0E-03 | Z32521.1 | NT | Homo sapiens MHC class 1 region |
| 2303 | 15315 | 28334 | 1.3 | 3.0E-03 | U46858.1 | NT | S. cereale (cv. Hado) mRNA for triosephosphate isomerase |
| | | | | | | | Mus musculus intestinal trefoil factor gene, partial cds |

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Table 4
Single Exon Probes Expressed In Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 2303 | 15315 | 28335 | 1.3 | 3.0E-03 | U48858.1 | NT | Mus musculus intestinal trefoil factor gene, partial cds |
| 3008 | 16064 | | 0.8 | 3.0E-03 | Y09006.1 | NT | Arabidopsis thaliana tpom1 gene |
| 3099 | 16156 | 29069 | 4.09 | 3.0E-03 | BE379286.1 | EST_HUMAN | 601237982F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609933 5' |
| 3166 | 16221 | 29136 | 2.54 | 3.0E-03 | AW802687.1 | EST_HUMAN | IL2-UM0076-240300-056-D03 UM0076 Homo sapiens cDNA |
| 3428 | 16476 | 29395 | 1.62 | 3.0E-03 | U34606.1 | NT | Mus musculus alpha-1(XVII) collagen (COL18A1) gene, exon 1 and 2 |
| 3439 | 16486 | | 6.72 | 3.0E-03 | Y12500.1 | NT | C.elegans samdc gene |
| 4002 | 17041 | 29949 | 7.18 | 3.0E-03 | AV762392.1 | EST_HUMAN | AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5' |
| 4002 | 17041 | 29950 | 7.18 | 3.0E-03 | AV762392.1 | EST_HUMAN | AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5' |
| 4067 | 17103 | 29995 | 1.47 | 3.0E-03 | AI792278.1 | EST_HUMAN | af0409.y6 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1156689 5' |
| 4177 | 17208 | | 1.08 | 3.0E-03 | Z32521.1 | NT | S.cereale (cv. Halo) mRNA for triosephosphate isomerase |
| 4424 | 17451 | 30342 | 3.8 | 3.0E-03 | AJ011432.1 | NT | Rattus norvegicus gdnf gene |
| 4546 | 17568 | 30458 | 5.58 | 3.0E-03 | AI536141.1 | EST_HUMAN | xu8.P10.H3 conorm Homo sapiens cDNA 3' |
| 4871 | 17888 | 30776 | 1.74 | 3.0E-03 | AI732754.1 | EST_HUMAN | ab18a08.x5 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains Alu repetitive element |
| 4890 | 17907 | 30796 | 5.49 | 3.0E-03 | BE787945.1 | EST_HUMAN | 601482715F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3885483 5' |
| 5338 | 18443 | 31196 | 3.42 | 3.0E-03 | 8922489 | NT | Homo sapiens hypothetical protein FLJ10539 (FLJ10539), mRNA |
| 5535 | 18731 | 31893 | 1.22 | 3.0E-03 | AJ249881.1 | NT | Mus musculus mRNA for hypothetical protein (ORF2 ortholog) |
| 5708 | 18803 | 31980 | 0.95 | 3.0E-03 | U35323.1 | NT | Mus musculus H2-M alpha chain (H2-Ma) gene, H2-M beta 2 chain (H2-Mb2) gene, H2-M beta 1 chain (H2-Mb1) gene, low molecular weight protein 2 Lmp2 (Lmp2) gene, complete cds |
| 6705 | 19761 | 33040 | 10.04 | 3.0E-03 | AA456701.1 | EST_HUMAN | aa13f10.f1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:813163 5' |
| 7224 | 20246 | 33580 | 0.65 | 3.0E-03 | D37977.1 | NT | Fugu rubripes mRNA for sodium channel alpha subunit, partial cds |
| 7412 | 20379 | 33730 | 1.37 | 3.0E-03 | AJ011419.1 | NT | Kluyveromyces fragilis pop3 gene for purine-cytosine permease |
| 7755 | 20718 | 34091 | 3.16 | 3.0E-03 | AB021736.1 | NT | Oryza sativa gene for bZIP protein, complete cds |
| 8145 | 21082 | 34481 | 0.49 | 3.0E-03 | P26659 | SWISSPROT | DNA REPAIR HELICASE RAD15 (RHP3) |
| 8270 | 21239 | 34650 | 0.91 | 3.0E-03 | BF333058.1 | EST_HUMAN | RCO-BT0812-250900-032-e07 BT0812 Homo sapiens cDNA |
| 8270 | 21239 | 34651 | 0.91 | 3.0E-03 | BF333058.1 | EST_HUMAN | RCO-BT0812-250900-032-e07 BT0812 Homo sapiens cDNA |
| 8496 | 21464 | 34880 | 1.31 | 3.0E-03 | N92580.1 | EST_HUMAN | zb27b04.s1 Soares_parrathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:304783 3' |
| 8658 | 21626 | | 0.77 | 3.0E-03 | M63408.1 | NT | S.cerevisiae UGA35 gene, complete cds |
| 8804 | 21771 | 35197 | 1.16 | 3.0E-03 | P51989 | SWISSPROT | HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A)) |
| 8827 | 21794 | 35217 | 1.34 | 3.0E-03 | AL163268.2 | NT | Homo sapiens chromosome 21 segment HS21C068 |
| 8933 | 21899 | | 1.25 | 3.0E-03 | Q9QM81 | SWISSPROT | NONSTRUCTURAL PROTEIN V |
| 9343 | 22308 | | 10.07 | 3.0E-03 | AW613774.1 | EST_HUMAN | hh80f10.x1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2969131 3' similar to contains L1.1 L1 repetitive element; |
| 9400 | 22365 | 35797 | 4.01 | 3.0E-03 | AL161589.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85 |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 9424 | 22388 | 35827 | 4.74 | 3.0E-03 | AI016731.1 | EST_HUMAN | ow03d12.x1 NCI CGAP_K1d3 Homo sapiens cDNA clone IMAGE:1636247 3' similar to gb:X57138_rna1 |
| 9434 | 22398 | 35836 | 0.83 | 3.0E-03 | BF339078.1 | EST_HUMAN | HISTONE H2B.2 (HUMAN); |
| 9764 | 22705 | | 0.95 | 3.0E-03 | D90901.1 | NT | 602035980F1 NCI CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4183938 5' |
| 9802 | 21125 | 34529 | 0.61 | 3.0E-03 | BE154670.1 | EST_HUMAN | Synchoecysis sp. PCC8803 complete genome, 3/27, 271600-402289 |
| 9894 | 22921 | | 0.82 | 3.0E-03 | P03355 | SWISSPROT | PM3-HT0344-071299-003-d07 HT0344 Homo sapiens cDNA |
| 10065 | 22892 | | 5.33 | 3.0E-03 | P08672 | SWISSPROT | POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H] |
| | | | | | | | CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS) |
| | | | | | | | RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; |
| 10255 | 23180 | 36867 | 1.56 | 3.0E-03 | P11369 | SWISSPROT | ENDONUCLEASE) |
| 10355 | 23279 | 36755 | 1.15 | 3.0E-03 | P51989 | SWISSPROT | HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A)) |
| 10499 | 23421 | 36920 | 4.39 | 3.0E-03 | AL163303.2 | NT | Homo sapiens chromosome 21 segment HS21C103 |
| 11194 | 24149 | | 1.62 | 3.0E-03 | 5803028 | NT | Homo sapiens ATP/GTP-binding protein (HEAB), mRNA |
| 11708 | 24673 | 38250 | 1.47 | 3.0E-03 | AF008222.1 | NT | Pneumocystis carinii kexin-like serine endoprotease mRNA, partial cds |
| 11775 | 23930 | 37451 | 1.86 | 3.0E-03 | AF268285.1 | NT | Homo sapiens golgin-like protein (GLP) gene, complete cds |
| 11810 | 24695 | 38275 | 2.27 | 3.0E-03 | AF094481.1 | NT | Homo sapiens trinuclotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds |
| 11810 | 24695 | 38276 | 2.27 | 3.0E-03 | AF094481.1 | NT | Homo sapiens trinuclotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds |
| | | | | | | | RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; |
| 11881 | 24763 | 38348 | 1.47 | 3.0E-03 | P11369 | SWISSPROT | ENDONUCLEASE) |
| 12199 | 25765 | | 4.08 | 3.0E-03 | AI525056.1 | EST_HUMAN | promina-5.E07.r bvtumor Homo sapiens cDNA 5' |
| | | | | | | | ct77b10.s1 Soares_tetal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1622779 3' similar to |
| 12232 | 25064 | 38162 | 1.83 | 3.0E-03 | AA963154.1 | EST_HUMAN | contains L1.13 MER26 repetitive element; |
| 12292 | 25895 | | 2.42 | 3.0E-03 | AB009668.1 | NT | Homo sapiens gene for CMP-N-acetylneuraminic acid hydroxylase, partial cds |
| 12478 | 25226 | 31794 | 2.01 | 3.0E-03 | AJ296282.1 | NT | Rattus norvegicus mRNA for connexin36 (cx36 gene) |
| 516 | 13587 | 26506 | 0.92 | 2.0E-03 | Q04652 | SWISSPROT | RING CANAL PROTEIN (KELCH PROTEIN) |
| 516 | 13587 | 26507 | 0.92 | 2.0E-03 | Q04652 | SWISSPROT | RING CANAL PROTEIN (KELCH PROTEIN) |
| 786 | 15851 | | 12.64 | 2.0E-03 | T70874.1 | EST_HUMAN | yd15h03.1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:108341 5' |
| 1365 | 14399 | 27370 | 1.9 | 2.0E-03 | M20783.1 | NT | Human alpha-2-plasmin inhibitor gene, exons 6 and 7 |
| 1368 | 14402 | 27372 | 1.34 | 2.0E-03 | AA661605.1 | EST_HUMAN | nu66f01.s1 NCI CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1217593 |
| 1376 | 14410 | 27380 | 12.34 | 2.0E-03 | AF284446.1 | NT | Homo sapiens tumor-related protein DRC2 (DRC2) gene, complete cds |
| | | | | | | | Homo sapiens tumor-related protein DRC2 (DRC2) gene, complete cds |
| 1486 | 14519 | 27492 | 1.63 | 2.0E-03 | P48509 | SWISSPROT | PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN |
| | | | | | | | SFA-1) (CD151 ANTIGEN) |
| 1519 | 14551 | 27522 | 3.03 | 2.0E-03 | | NT | Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 1519 | 14551 | 27523 | 3.03 | 2.0E-03 | 4557836 | NT | Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA |
| 1595 | 14627 | | 8.7 | 2.0E-03 | P29400 | SWISSPROT | COLLAGEN ALPHA 5(IV) CHAIN PRECURSOR |
| 1766 | 14815 | 27800 | 1.26 | 2.0E-03 | AA450138.1 | EST_HUMAN | z42a10.t1 Soares_total_fetus Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789114 5' |
| 2011 | 15032 | 28042 | 1.52 | 2.0E-03 | AF302691.1 | NT | Mus musculus myelin expression factor-3-like protein gene, partial cds |
| 2261 | 15275 | 28299 | 1.02 | 2.0E-03 | AL163302.2 | NT | Homo sapiens chromosome 21 segment HS21C102 |
| 2584 | 15585 | | 4.02 | 2.0E-03 | AW137782.1 | EST_HUMAN | UI-H-B11-edi-g-10-Q-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717010 3' |
| 3427 | 16475 | 29394 | 4.82 | 2.0E-03 | AA450138.1 | EST_HUMAN | z42a10.t1 Soares_total_fetus Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789114 5' |
| 3434 | 16481 | 29400 | 0.8 | 2.0E-03 | BF588995.1 | EST_HUMAN | 602183960T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300070 3' |
| 3680 | 16723 | 28638 | 6.1 | 2.0E-03 | X87344.1 | NT | H. sapiens DMA, DMB, HLA-z1, IP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes |
| 3973 | 17013 | 29927 | 0.65 | 2.0E-03 | AB040802.1 | NT | Rattus norvegicus mRNA for SREB1, complete cds |
| 4140 | 17171 | 30059 | 2.1 | 2.0E-03 | P03374 | SWISSPROT | ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP38] |
| 4203 | 17234 | 30122 | 1.29 | 2.0E-03 | AA176993.1 | EST_HUMAN | zp13h01.r1 Strategene fetal retina 837202 Homo sapiens cDNA clone IMAGE:609361 5' |
| 4248 | 17277 | | 9.31 | 2.0E-03 | U68491.1 | NT | Rattus norvegicus 5-hydroxytryptamine/ receptor gene, partial cds |
| 4458 | 17494 | | 1.01 | 2.0E-03 | AW297380.1 | EST_HUMAN | UI-H-BW0-air-g-03-Q-UI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2730413 3' |
| 4482 | 17488 | 30375 | 1.11 | 2.0E-03 | A1084746.1 | EST_HUMAN | HA0507 Human fetal liver cDNA library Homo sapiens cDNA |
| 4577 | 17599 | 30493 | 1.99 | 2.0E-03 | L42512.1 | NT | Drosophila melanogaster shortighted class 2 (shs) mRNA, complete cds |
| 4577 | 17599 | 30494 | 1.99 | 2.0E-03 | L42512.1 | NT | Drosophila melanogaster shortighted class 2 (shs) mRNA, complete cds |
| 4735 | 17755 | 30649 | 1.09 | 2.0E-03 | AF223391.1 | NT | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced |
| 4740 | 17760 | | 1.84 | 2.0E-03 | R87773.1 | EST_HUMAN | yo45602.s1 Soares adult brain N2b-4H55Y Homo sapiens cDNA clone IMAGE:180890 3' |
| 5054 | 18066 | 30945 | 0.75 | 2.0E-03 | AF003528.1 | NT | Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions |
| 5163 | 18172 | 31051 | 1.02 | 2.0E-03 | AF187974.1 | NT | 8 Homo sapiens concentrative nucleoside transporter (CNT1) gene, exon 12 |
| 5281 | 18287 | 31149 | 2.26 | 2.0E-03 | D85606.1 | NT | Homo sapiens gene for cholesterylkinin type-A receptor, complete cds |
| 5564 | 18661 | 31607 | 1.33 | 2.0E-03 | BF241410.1 | EST_HUMAN | 601876385F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104692 5' |
| 5709 | 25643 | 31981 | 2.18 | 2.0E-03 | AB074593.1 | NT | Homo sapiens mRNA for KIAA0693 protein, partial cds |
| 5795 | 18887 | 32068 | 0.61 | 2.0E-03 | AW796111.1 | EST_HUMAN | MR2-UM0025-300300-102-402 UM0025 Homo sapiens cDNA |
| 5795 | 18887 | 32069 | 0.61 | 2.0E-03 | AW796111.1 | EST_HUMAN | MR2-UM0025-300300-102-402 UM0025 Homo sapiens cDNA |
| 5797 | 18899 | 32071 | 1.73 | 2.0E-03 | U63711.1 | NT | Xenopus laevis xefilin mRNA, complete cds |
| 6231 | 19305 | 32538 | 3.79 | 2.0E-03 | P23477 | SWISSPROT | ATP-DEPENDENT NUCLEASE SUBUNIT B |
| 6231 | 19305 | 32537 | 3.79 | 2.0E-03 | P23477 | SWISSPROT | ATP-DEPENDENT NUCLEASE SUBUNIT B |
| 6480 | 19545 | 32793 | 15.16 | 2.0E-03 | Q95203 | SWISSPROT | CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-RP II) (CA-XI) |

Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 6480 | 19545 | 32794 | 15.16 | 2.0E-03 | Q95203 | SWISSPROT | CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-RP II) (CA-XI) |
| 6482 | 19547 | 32798 | 7.38 | 2.0E-03 | BF308187.1 | EST_HUMAN | 601887434F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4121408 5' |
| 6521 | 19584 | 32842 | 2.26 | 2.0E-03 | Q9UKP4 | SWISSPROT | ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7) |
| 6522 | 19585 | 32843 | 0.77 | 2.0E-03 | AV709075.1 | EST_HUMAN | AV709075 ADC Homo sapiens cDNA clone ADCAEF09 5' |
| 6554 | 19614 | 32879 | 1.36 | 2.0E-03 | X94451.1 | NT | L. esculentum mRNA for lysyl-tRNA synthetase (LysRS) |
| 6756 | 19810 | | 1.25 | 2.0E-03 | A1991089.1 | EST_HUMAN | wu38h09.x1 Soares_Dieckgreffe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522177 3' similar to SW_RL29_HUMAN P47914 60S RIBOSOMAL PROTEIN L29 ; contains element MSR1 repetitive element ; |
| 6794 | 19848 | 33133 | 0.71 | 2.0E-03 | AA677831.1 | EST_HUMAN | zh13a11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:430652 3' |
| 7151 | 18383 | 31271 | 1.08 | 2.0E-03 | AB038502.1 | NT | Caenorhabditis elegans mRNA for galectin LEC-11, complete cds |
| 7287 | 20064 | 33371 | 2.86 | 2.0E-03 | BE067986.1 | EST_HUMAN | CM4-BT0368-061299-054-d01 BT0368 Homo sapiens cDNA |
| 7351 | 20321 | 33668 | 0.64 | 2.0E-03 | A1298883.1 | EST_HUMAN | gm99d11.x1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1896885 3' |
| 7511 | 20476 | 33837 | 0.77 | 2.0E-03 | T86598.1 | EST_HUMAN | yt77g10.r1 Soares_fetal_liver_spleen_1NFLS_Homo sapiens cDNA clone IMAGE:114306 6' |
| 7877 | 20821 | 34198 | 1.55 | 2.0E-03 | P07354 | SWISSPROT | PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP) |
| 8386 | 21355 | 34763 | 1.95 | 2.0E-03 | AW592004.1 | EST_HUMAN | h137b06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2834035 3' similar to TR-Q60976 Q60976 JERKY ; |
| 8560 | 21528 | 34947 | 6.01 | 2.0E-03 | N20287.1 | EST_HUMAN | yx42g06.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:264442 3' similar to contains L1.b2 L1 repetitive element ; |
| 8560 | 21528 | 34948 | 6.01 | 2.0E-03 | N20287.1 | EST_HUMAN | yx42g06.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:264442 3' similar to contains L1.b2 L1 repetitive element ; |
| 8607 | 21575 | 34990 | 0.57 | 2.0E-03 | Q92350 | SWISSPROT | HYPOTHEICAL 32.8 KD PROTEIN C6G9.05 IN CHROMOSOME 1 |
| 8628 | 21597 | 35018 | 1.23 | 2.0E-03 | P19137 | SWISSPROT | LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN) |
| 8684 | 21652 | 35074 | 0.77 | 2.0E-03 | 6005855 | NT | Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA |
| 8684 | 21652 | 35075 | 0.77 | 2.0E-03 | 6005855 | NT | Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA |
| 8709 | 21677 | 35102 | 0.81 | 2.0E-03 | AU136679.1 | EST_HUMAN | AU136679 PLACE1 Homo sapiens cDNA clone PLACE1004839 5' |
| 8762 | 21729 | | 0.67 | 2.0E-03 | AJ400677.1 | NT | Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene |
| 9550 | 18887 | 32098 | 0.66 | 2.0E-03 | AW796111.1 | EST_HUMAN | MR2-UM0025-300300-102-702 UM0025 Homo sapiens cDNA |
| 9550 | 18887 | 32099 | 0.66 | 2.0E-03 | AW796111.1 | EST_HUMAN | MR2-UM0025-300300-102-702 UM0025 Homo sapiens cDNA |
| 9595 | 22557 | 36007 | 0.66 | 2.0E-03 | AF224869.1 | NT | Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds |
| 9884 | 22837 | 36291 | 0.97 | 2.0E-03 | H50832.1 | EST_HUMAN | yp88a09.s1 Soares_fetal_liver_spleen_1NFLS_Homo sapiens cDNA clone IMAGE:194296 3' |
| 9884 | 22837 | 36292 | 0.97 | 2.0E-03 | H50832.1 | EST_HUMAN | yp88a09.s1 Soares_fetal_liver_spleen_1NFLS_Homo sapiens cDNA clone IMAGE:194296 3' |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 9916 | 22737 | 36190 | 3.31 | 2.0E-03 | P24821 | SWISSPROT | TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (GMEIN) (JI) (MOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR MATRIX ANTIGEN) (GP 150-225) (TENASCIN-C) (TN-C) |
| 10026 | 22963 | 36421 | 1.02 | 2.0E-03 | P48982 | SWISSPROT | BETA-GALACTOSIDASE PRECURSOR (LACTASE) |
| 10026 | 22963 | 36422 | 1.02 | 2.0E-03 | P48982 | SWISSPROT | BETA-GALACTOSIDASE PRECURSOR (LACTASE) |
| 10081 | 23008 | 36479 | 0.65 | 2.0E-03 | AF097732.1 | NT | Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds |
| 10081 | 23008 | 36480 | 0.65 | 2.0E-03 | AF097732.1 | NT | Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds |
| 10275 | 23200 | 36684 | 0.94 | 2.0E-03 | AW884269.1 | EST_HUMAN | QV3-OT0064-060400-144-e01 OT0064 Homo sapiens cDNA |
| 10402 | 23324 | | 6.44 | 2.0E-03 | AA251376.1 | EST_HUMAN | zs10a06.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684754.3 |
| 10781 | 23702 | 37200 | 0.45 | 2.0E-03 | BF367386.1 | EST_HUMAN | MR2-GN0030-140900-001-e05 GN0030 Homo sapiens cDNA |
| 10969 | 23889 | 37401 | 0.43 | 2.0E-03 | AW361176.1 | EST_HUMAN | RC1-CT0251-141099-012-401 CT0251 Homo sapiens cDNA |
| 10969 | 23889 | 37402 | 0.43 | 2.0E-03 | AW361176.1 | EST_HUMAN | RC1-CT0251-141099-012-401 CT0251 Homo sapiens cDNA |
| 11356 | 24306 | | 2.4 | 2.0E-03 | M86824.1 | NT | Human dystrophin gene |
| 11817 | 20821 | 34196 | 2.2 | 2.0E-03 | P07354 | SWISSPROT | PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP) |
| 11870 | 24752 | | 1.87 | 2.0E-03 | BF330909.1 | EST_HUMAN | RC3-BT0333-310800-115-g04 BT0333 Homo sapiens cDNA |
| 11876 | 24758 | 38342 | 10.47 | 2.0E-03 | Z11740.1 | NT | H sapiens variable number tandem repeat (VNTR) locus DNA |
| | | | | | | | ty65h03.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2283989.3 similar to SW:VATG_MANSE |
| 12180 | 25028 | | 2.99 | 2.0E-03 | A1625745.1 | EST_HUMAN | Q25532 VACUOLAR ATP SYNTHASE SUBUNIT G ; |
| 12197 | 25042 | 38623 | 2.41 | 2.0E-03 | AF157516.2 | NT | Homo sapiens SEL1L (SEL1L) gene, partial cds |
| 12220 | 25057 | 38627 | 1.75 | 2.0E-03 | A1084325.1 | EST_HUMAN | oy43g06.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1668634.3 similar to TR:P97535 P97535 PS-PLA1 PRECURSOR ; |
| 12241 | 18349 | | 11.57 | 2.0E-03 | AJ245167.1 | NT | Camelus dromedarius cyhp19 gene for immunoglobulin heavy chain variable region |
| 12459 | 25892 | | 2.03 | 2.0E-03 | AV697966.1 | EST_HUMAN | AV697966 GKC Homo sapiens cDNA clone GKCXGD05.5 |
| 12550 | 25273 | 31777 | 1.93 | 2.0E-03 | Y00503.1 | NT | H sapiens M1 gene for muscarinic acetylcholine receptor |
| 12683 | 25341 | | 1.33 | 2.0E-03 | AL163203.2 | NT | Homo sapiens chromosome 21 segment HS21C003 |
| 12710 | 25795 | | 1.55 | 2.0E-03 | A1375037.1 | EST_HUMAN | ta66f02.x1 Soares_tet_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2049051.3 similar to contains Alu repetitive element; |
| | | | | | | | Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds |
| 12826 | 25445 | | 1.6 | 2.0E-03 | AF128756.1 | NT | |
| 13002 | 25745 | | 1.95 | 2.0E-03 | AV697966.1 | EST_HUMAN | AV697966 GKC Homo sapiens cDNA clone GKCXGD05.5 |
| 13095 | 25621 | | 1.44 | 2.0E-03 | P04787 | SWISSPROT | GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE (GAPDH) |
| 439 | 13513 | 26444 | 1.72 | 1.0E-03 | H86471.1 | EST_HUMAN | y88c08.r1 Soares_pituitary_gland_NbHPG Homo sapiens cDNA clone IMAGE:232334.5 |

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Table 4
Single Exon Probes Expressed In Bone Marrow

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 830 | 13887 | 26842 | 2.08 | 1.0E-03 | A1720263.1 | EST_HUMAN | as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825 Q13825 AU-BINDING PROTEINENOVYL-COA HYDRATASE. ; |
| 830 | 13887 | 26843 | 2.09 | 1.0E-03 | A1720263.1 | EST_HUMAN | as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825 Q13825 AU-BINDING PROTEINENOVYL-COA HYDRATASE. ; |
| 1097 | 14141 | 27091 | 3.37 | 1.0E-03 | A1865788.1 | EST_HUMAN | wk66606.x1 NCI CGAP Part1 Homo sapiens cDNA clone IMAGE:2422258 3' |
| 1117 | 14161 | 27112 | 1.69 | 1.0E-03 | A1854572.1 | EST_HUMAN | wx93e10.x1 NCI CGAP_Mel15 Homo sapiens cDNA clone IMAGE:2551242 3' |
| 1170 | 14211 | 27165 | 1.5 | 1.0E-03 | A1692616.1 | EST_HUMAN | wd86a01.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2338440 3' similar to contains Alu repetitive element. |
| 2042 | 15081 | 28082 | 3.08 | 1.0E-03 | P47808 | SWISSPROT | HIGH MOLECULAR WEIGHT FORM OF MYOSIN I (HMMMI) |
| 2163 | 15179 | 28199 | 9.01 | 1.0E-03 | AJ131016.1 | NT | Homo sapiens SCL gene locus |
| 2893 | 16051 | 28972 | 1.42 | 1.0E-03 | AB033117.1 | NT | Homo sapiens mRNA for KIAA1291 protein, partial cds |
| 3205 | 16280 | 29179 | 2.08 | 1.0E-03 | P18915 | SWISSPROT | CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED CARBONIC ANHYDRASE) (SALIVARY CARBONIC ANHYDRASE) |
| 3205 | 16260 | 29180 | 2.08 | 1.0E-03 | P18915 | SWISSPROT | CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED CARBONIC ANHYDRASE) (SALIVARY CARBONIC ANHYDRASE) |
| 3313 | 16368 | 29286 | 1.23 | 1.0E-03 | P08547 | SWISSPROT | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| 3553 | 16598 | 29524 | 0.92 | 1.0E-03 | U68061.1 | NT | Human MUC2 gene, promoter region |
| 3553 | 16598 | 29525 | 0.92 | 1.0E-03 | U68061.1 | NT | Human MUC2 gene, promoter region |
| 3678 | 16721 | | 1.49 | 1.0E-03 | AB044400.1 | NT | Homo sapiens SVMT gene for synaptic vesicle monoamine transporter, exons 14, 15 |
| 3946 | 16988 | 29901 | 0.64 | 1.0E-03 | AW170552.1 | EST_HUMAN | xr63d07.x1 Soares NHCC cervical tumor Homo sapiens cDNA clone IMAGE:2698381 3' similar to contains TAR1.11 TAR1 repetitive element ; |
| 3954 | 16984 | 29910 | 1.11 | 1.0E-03 | Z49649.1 | NT | S. cerevisiae chromosome X reading frame ORF YJR149w |
| 4464 | 17490 | 30377 | 2.27 | 1.0E-03 | BE939162.1 | EST_HUMAN | RC1-TN0128-160800-021-g01 TN0128 Homo sapiens cDNA |
| 4502 | 17527 | 30412 | 4.39 | 1.0E-03 | BE246536.1 | EST_HUMAN | TCBAP1D4909 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HQSC project=TCBA Homo sapiens cDNA clone TCBAP1909 |
| 4892 | 17713 | 30608 | 0.79 | 1.0E-03 | U29449.1 | NT | Caenorhabditis elegans spliced leader RNA (SL4), and (SL5) genes |
| 4861 | 17878 | 30765 | 2.07 | 1.0E-03 | A1073485.1 | EST_HUMAN | ov45c04.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1640262 3' |
| 4861 | 17878 | 30766 | 2.07 | 1.0E-03 | A1073485.1 | EST_HUMAN | ov45c04.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1640262 3' |
| 4862 | 17879 | | 4.33 | 1.0E-03 | BE154067.1 | EST_HUMAN | PMO-HT0339-200400-010-D02 HT0339 Homo sapiens cDNA |
| 5113 | 18123 | 30998 | 9.53 | 1.0E-03 | O46409 | SWISSPROT | APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV) |
| 5202 | 18211 | 31085 | 1.03 | 1.0E-03 | AV685870.1 | EST_HUMAN | AV685870 GK Homo sapiens cDNA clone GKCDME11 5' |
| 5381 | 18485 | 31360 | 1.74 | 1.0E-03 | AA290951.1 | EST_HUMAN | zs44f01.1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700345 5' |
| 5476 | 18577 | 31486 | 2.98 | 1.0E-03 | AJ006345.1 | NT | Homo sapiens KVLQ11 gene |
| 5531 | 18628 | 31565 | 1.77 | 1.0E-03 | K03332.1 | NT | Epstein-Barr virus (AG876 isolate) U2-LR2 domain encoding nuclear protein EBNA2, complete cds |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 5531 | 18629 | 31566 | 1.77 | 1.0E-03 | K03332.1 | NT | Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds |
| 5652 | 18748 | 31916 | 0.93 | 1.0E-03 | BE796491.1 | EST_HUMAN | 601589841F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943954 5' |
| 5658 | 18754 | 31921 | 1.76 | 1.0E-03 | Q02388 | SWISSPROT | COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN) |
| 5716 | 18810 | 31988 | 0.7 | 1.0E-03 | N41974.1 | EST_HUMAN | W07h06.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:270587 5' similar to contains element MER6 repetitive element; |
| 5716 | 18810 | 31989 | 0.7 | 1.0E-03 | N41974.1 | EST_HUMAN | W07h06.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:270587 5' similar to contains element MER6 repetitive element; |
| 5965 | 19079 | 32276 | 0.56 | 1.0E-03 | AA773352.1 | EST_HUMAN | ab65g12.s1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:845734 3' |
| 6018 | 19101 | | 0.52 | 1.0E-03 | BF541639.1 | EST_HUMAN | 602068042F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4066907 5' |
| 6136 | 19213 | | 2.57 | 1.0E-03 | X07699.1 | NT | Mouse nucleolin gene |
| 6177 | 19252 | 32485 | 1.06 | 1.0E-03 | BE963939.2 | EST_HUMAN | 601657519R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875693 3' |
| 6316 | 19387 | | 8.39 | 1.0E-03 | 11626176 | NT | Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA |
| 6468 | 19533 | 32781 | 1.05 | 1.0E-03 | T87761.1 | EST_HUMAN | x493a11.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:115772 5' |
| 8549 | 19610 | | 1.69 | 1.0E-03 | AW902585.1 | EST_HUMAN | QV3-NN1024-260400-171-g05 NN1024 Homo sapiens cDNA |
| 6919 | 19970 | 33266 | 1.18 | 1.0E-03 | L77570.1 | NT | Homo sapiens DiGeorge syndrome critical region, centromeric end |
| 7359 | 20329 | 33678 | 2.43 | 1.0E-03 | D16926.1 | NT | Human gene for fourth somatostatin receptor subtype |
| 7729 | 20885 | | 2.36 | 1.0E-03 | AJ229042.1 | NT | Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3 |
| 7901 | 20844 | 34228 | 1.71 | 1.0E-03 | U52111.2 | NT | Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 8 (DUSP8), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRT), CDM protein (CDM), adrenergic dystrophy protein > |
| 7975 | 20914 | 34305 | 3.18 | 1.0E-03 | M63376.1 | NT | Human TRPM2 protein gene, exons 1, 2 and 3 |
| 8033 | 20970 | 34364 | 0.87 | 1.0E-03 | BE880044.1 | EST_HUMAN | 601491081F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3893276 5' |
| 8221 | 21190 | 34599 | 0.55 | 1.0E-03 | AF274591.1 | NT | Homo sapiens prolactin-releasing peptide receptor gene, 5' flanking region |
| 8282 | 21251 | 34663 | 5.32 | 1.0E-03 | AJ251973.1 | NT | Homo sapiens partial steerin-1 gene |
| 8483 | 21451 | 34869 | 1.01 | 1.0E-03 | AA122270.1 | EST_HUMAN | z497c09.s1 Soares_pregnant_uterus_NbhPU Homo sapiens cDNA clone IMAGE:490768 3' similar to contains L1.11 L1 repetitive element; |
| 8588 | 21554 | 34970 | 2.42 | 1.0E-03 | AF153980.1 | NT | Homo sapiens exostosin-like protein 1 (EXTL1) gene, exons 2 through 11, and complete cds |
| 8773 | 21740 | 35161 | 0.7 | 1.0E-03 | U29397.1 | NT | Rattus norvegicus plasma membrane Ca2+ ATPase isoform 3 (PMCA3) gene, 5' flanking region |
| 8941 | 21907 | 35331 | 0.53 | 1.0E-03 | AA001613.1 | EST_HUMAN | zh82e08.s1 Soares_fetal_liver_spleen_1NfLS_S1 Homo sapiens cDNA clone IMAGE:427810 3' |
| 8941 | 21907 | 35332 | 0.53 | 1.0E-03 | AA001613.1 | EST_HUMAN | zh82e08.s1 Soares_fetal_liver_spleen_1NfLS_S1 Homo sapiens cDNA clone IMAGE:427810 3' |
| 9295 | 22261 | | 1.37 | 1.0E-03 | Y11204.1 | NT | V. carteri gene encoding volvoxpsin |
| 9321 | 22286 | 35716 | 0.6 | 1.0E-03 | AW840353.1 | EST_HUMAN | CM8-LT0079-170200-092-e07 LT0079 Homo sapiens cDNA |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|-----------------------------|-------------------------------|---|
| 9435 | 22389 | | 0.65 | 1.0E-03 | U52111.2 | NT | Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein > |
| 9474 | 22438 | 35877 | 3.71 | 1.0E-03 | M30471.1 | NT | Human class III alcohol dehydrogenase (ADH5) chi subunit mRNA, complete cds |
| 9474 | 22438 | 35878 | 3.71 | 1.0E-03 | M30471.1 | NT | Human class III alcohol dehydrogenase (ADH5) chi subunit mRNA, complete cds |
| 9855 | 22682 | | 0.45 | 1.0E-03 | A1247482.1 | EST_HUMAN | qh56d01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848873 3' similar to gb:M97388 TATA-BINDING PROTEIN-ASSOCIATED PHOSPHOPROTEIN (HUMAN); |
| 9866 | 22693 | 36354 | 1.77 | 1.0E-03 | AF011400.1 | NT | Thermotoga neapolitana alpha-1,6-galactosidase (aglA) gene, complete cds |
| 9866 | 22693 | 36355 | 1.77 | 1.0E-03 | AF011400.1 | NT | Thermotoga neapolitana alpha-1,6-galactosidase (aglA) gene, complete cds |
| 10179 | 23104 | 36585 | 0.8 | 1.0E-03 | Q01129 | SWISSPROT | BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN) (PG40) (DERMATAN SULFATE |
| 10524 | 23446 | 36944 | 1.55 | 1.0E-03 | AF03529.1 | NT | Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions |
| 10529 | 23451 | | 0.79 | 1.0E-03 | AF097485.1 | NT | Homo sapiens transducin beta-like 2 (TBL2) gene, complete cds |
| 10879 | 23601 | 37096 | 1.12 | 1.0E-03 | A1024350.1 | EST_HUMAN | ov75f08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1643175.3' similar to contains MER39.b1 |
| 11025 | 23990 | 37516 | 1.65 | 1.0E-03 | AW362393.1 | EST_HUMAN | MER39 MER39 repetitive element; |
| 11025 | 23990 | 37517 | 1.65 | 1.0E-03 | AW362393.1 | EST_HUMAN | RC1-CT0278-181099-011-a09 CT0278 Homo sapiens cDNA |
| 11102 | 24082 | 37585 | 2.91 | 1.0E-03 | BE170859.1 | EST_HUMAN | RC1-CT0278-181099-011-a09 CT0278 Homo sapiens cDNA |
| 11172 | 24129 | | 2.21 | 1.0E-03 | A1583847.1 | EST_HUMAN | QV3-HT0543-220300-130-a03 HT0543 Homo sapiens cDNA |
| 11491 | 24434 | | 2.59 | 1.0E-03 | AV755949.1 | EST_HUMAN | tt73a12.x1 NCI_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246446 3' similar to TR:Q26185 Q26185 PVA1 GENE; |
| 11662 | 24598 | 38171 | 6.18 | 1.0E-03 | AA122270.1 | EST_HUMAN | AV755949 MDS Homo sapiens cDNA clone MDSDDF11 5' |
| 12176 | 25024 | 38621 | 6.74 | 1.0E-03 | BE894488.1 | EST_HUMAN | z497c09.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:490768 3' similar to contains L1.1 L1 repetitive element; |
| 12653 | 25915 | | 1.53 | 1.0E-03 | A1347355.1 | EST_HUMAN | 601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5' |
| 12753 | 25938 | 31311 | 7.37 | 1.0E-03 | BE780572.1 | EST_HUMAN | tc05h11.x1 NCI_CGAP_Cot6 Homo sapiens cDNA clone IMAGE:2063013 3' similar to contains Aliu repetitive element; |
| 5765 | 18957 | | 1.76 | 9.0E-04 | P06727 | SWISSPROT | 801468879F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872035 5' |
| 6388 | 19456 | | 0.81 | 9.0E-04 | AJ006345.1 | NT | APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV) |
| 6633 | 19691 | 32970 | 1.08 | 9.0E-04 | P02381 | SWISSPROT | Homo sapiens KVLQ1 gene |
| 10001 | 22928 | | 1.39 | 9.0E-04 | AB037203.1 | NT | MITOCHONDRIAL RIBOSOMAL PROTEIN VAR1 |
| 1484 | 14517 | | 1.04 | 8.0E-04 | X96465.1 | NT | Glycylthiaz alabra GbAS1 mRNA for beta-amylin synthase, complete cds |
| 3339 | 16979 | 28894 | 0.64 | 8.0E-04 | R07008.1 | EST_HUMAN | X laevis mRNA for C4SR protein |
| 4209 | 17238 | | 4.49 | 8.0E-04 | P08547 | SWISSPROT | yf12h10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:128691 5' |
| | | | | | | | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 4798 | 17815 | 30709 | 2.7 | 8.0E-04 | U29185.1 | NT | Homo sapiens prion protein (PrP) gene, complete cds |
| 11480 | 24423 | | 2.01 | 8.0E-04 | AA77084.1 | EST_HUMAN | z24c10.s1 Soares fetal heart_NbH19W Homo sapiens cDNA clone IMAGE:377874 3' |
| 11627 | 24565 | | 2.02 | 8.0E-04 | AI571099.1 | EST_HUMAN | tr85a08.x1 NCL CGAP_U12 Homo sapiens cDNA clone IMAGE:2176310 3' |
| 1844 | 14870 | 27868 | 1.17 | 7.0E-04 | L41825.1 | NT | Homo sapiens CYP17 gene, 5' end |
| 2408 | 15415 | 28439 | 1.01 | 7.0E-04 | U29185.1 | NT | Homo sapiens prion protein (PrP) gene, complete cds |
| 2728 | 15720 | 28737 | 1.22 | 7.0E-04 | AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C010 |
| 3293 | 16346 | 28266 | 1.13 | 7.0E-04 | 4885170 | NT | Homo sapiens chromosome X open reading frame 6 (GXORF6) mRNA |
| 6215 | 19289 | 32522 | 1.02 | 7.0E-04 | AA516212.1 | EST_HUMAN | ng65g12.s1 NCL CGAP_Lip2 Homo sapiens cDNA clone IMAGE:939718 similar to contains L1.b3 L1 L1 |
| 6962 | 19719 | | 2.3 | 7.0E-04 | AI769331.1 | EST_HUMAN | repetitive element; |
| 7438 | 20405 | | 0.78 | 7.0E-04 | AK024445.1 | NT | Homo sapiens mRNA for FLJ00335 protein, partial cds |
| 10163 | 23088 | 36565 | 0.48 | 7.0E-04 | P13497 | SWISSPROT | BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1) |
| 10163 | 23088 | 36566 | 0.48 | 7.0E-04 | P13497 | SWISSPROT | BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1) |
| 11892 | 24773 | | 1.98 | 7.0E-04 | U78027.1 | NT | Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds |
| 11920 | 24801 | 38392 | 2.41 | 7.0E-04 | Z40561.1 | EST_HUMAN | HSC28A072 normalized infant brain cDNA Homo sapiens cDNA clone c-28a07 3' |
| 12921 | 25497 | | 4.1 | 7.0E-04 | R17336.1 | EST_HUMAN | y913c06.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:32288 5' |
| 12952 | 25527 | | 3.97 | 7.0E-04 | 6005855 | NT | Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA |
| 2706 | 15701 | | 1.03 | 6.0E-04 | BF341380.1 | EST_HUMAN | 60201339F1 NCL CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4149297 5' |
| 3984 | 17024 | 29935 | 1.78 | 6.0E-04 | AI862525.1 | EST_HUMAN | w15a11.x1 NCL CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402876 3' |
| 4214 | 17243 | 30128 | 3.15 | 6.0E-04 | U45983.1 | NT | Homo sapiens COR8 chemokine receptor (CMKBR8) gene, complete cds |
| 7830 | 20778 | 34156 | 0.59 | 6.0E-04 | Q15034 | SWISSPROT | HYPOTHETICAL PROTEIN KIAA0032 |
| 8198 | 21188 | | 3.16 | 6.0E-04 | P46408 | SWISSPROT | GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE (FRUCTOSE TRANSPORTER) |
| 8349 | 21318 | | 0.69 | 6.0E-04 | H92947.1 | EST_HUMAN | y94c11.s1 Soares pituitary gland_N3HPG Homo sapiens cDNA clone IMAGE:231956 3' similar to contains LOR1 repetitive element; |
| 10339 | 23263 | | 3.99 | 6.0E-04 | ALD48507.2 | EST_HUMAN | DKFZp586M2024_r1 596 (synonym: huter1) Homo sapiens cDNA clone DKFZp586M2024 |
| 10440 | 23362 | 36852 | 2.19 | 6.0E-04 | BE005850.1 | EST_HUMAN | RC2-BN0120-250400-012-h11 BN0120 Homo sapiens cDNA |
| 10704 | 23626 | | 0.65 | 6.0E-04 | AF287478.1 | NT | Lytechinus variegatus embryonic blastocoel extracellular matrix protein precursor (ECM3) mRNA, complete cds |
| 11814 | 24696 | 38280 | 2.11 | 6.0E-04 | AJ229042.1 | NT | Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21 q22, segment 2/3 |
| 11893 | 24774 | 38360 | 3.12 | 6.0E-04 | AW013847.1 | EST_HUMAN | U1H-B10-aab-e-09-0-U1.s1 NCL CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3' |
| 12364 | 25820 | | 5.73 | 6.0E-04 | AW380519.1 | EST_HUMAN | RC1-H10269-261198-012-d08 HT0269 Homo sapiens cDNA |
| 652 | 13718 | 26640 | 8.71 | 5.0E-04 | O10341 | SWISSPROT | HYPOTHETICAL 29.3 KD PROTEIN (ORF92) |
| 1501 | 14534 | | 1.88 | 5.0E-04 | AW851844.1 | EST_HUMAN | QV0-CT0225-021099-030-a07 CT0225 Homo sapiens cDNA |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 3424 | 16472 | 29391 | 1.28 | 5.0E-04 | AA548931.1 | EST_HUMAN | nk27e11.s1 NCI_CGAP_Cor11 Homo sapiens cDNA clone IMAGE:1014764.3' similar to contains Alu repetitive element |
| 3728 | 16770 | 29682 | 0.95 | 5.0E-04 | Q9UKP4 | SWISSPROT | ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7) |
| 5549 | 18946 | 31598 | 2.37 | 5.0E-04 | AF248054.1 | NT | Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds |
| 6784 | 19839 | 33124 | 5.64 | 5.0E-04 | AA156080.1 | EST_HUMAN | zo33b08.r1 Stratiogene colon (#837204) Homo sapiens cDNA clone IMAGE:588663.5' |
| 7602 | 20563 | 33924 | 10.72 | 5.0E-04 | M23604.1 | NT | Gorilla gorilla involucrin gene medium allele, complete cds |
| 8289 | 21258 | 34669 | 4.95 | 5.0E-04 | A1186382.1 | EST_HUMAN | gd113f06.x1 Soares placenta_8to9weeks_2NbpHP8t9W Homo sapiens cDNA clone IMAGE:1723619.3' similar to gb:X51602.cds1 VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 1 (HUMAN); contains Alu repetitive element |
| 8546 | 21614 | 35036 | 0.92 | 5.0E-04 | AA814519.1 | EST_HUMAN | ab96e02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1339226.3' similar to contains element |
| 8632 | 22576 | 36026 | 1.57 | 5.0E-04 | AA846545.1 | EST_HUMAN | MER22 repetitive element; |
| 8726 | 22754 | 36207 | 0.62 | 5.0E-04 | N83765.1 | EST_HUMAN | aj56h03.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1394357.3' |
| 9876 | 22829 | 36283 | 0.54 | 5.0E-04 | P29126 | SWISSPROT | KK2745F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone KK2745.5' similar to REPETITIVE ELEMENT |
| 9968 | 22895 | 36358 | 4.55 | 5.0E-04 | AW270938.1 | EST_HUMAN | BIFUNCTIONAL ENDO-1,4-BETA-XYLANASE XYLA PRECURSOR |
| 10640 | 23562 | | 0.47 | 5.0E-04 | U50871.1 | NT | xs05e02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2768858.3' |
| 11320 | 24270 | | 1.94 | 5.0E-04 | AL048507.2 | EST_HUMAN | Human familial Alzheimer's disease (STM2) gene, complete cds |
| 12022 | 18946 | 31598 | 10.61 | 5.0E-04 | AF248054.1 | NT | DKFZp586M2024_t1 586 (synonym: huter1) Homo sapiens cDNA clone DKFZp586M2024 |
| 12298 | 25753 | | 4.4 | 5.0E-04 | AA568513.1 | EST_HUMAN | Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds |
| 674 | 13738 | 26665 | 1.48 | 4.0E-04 | U32748.1 | NT | trf15h02.s1 NCI_CGAP_Pt1 Homo sapiens cDNA clone IMAGE:913875 |
| 848 | 13904 | 26862 | 1.8 | 4.0E-04 | A1720263.1 | EST_HUMAN | Haemophilus influenzae Rd section 63 of 163 of the complete genome |
| 848 | 13904 | 26863 | 1.6 | 4.0E-04 | A1720263.1 | EST_HUMAN | as70b08.x1 Barehead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039.3' similar to TR:Q13825 |
| 1461 | 14494 | 27458 | 2.76 | 4.0E-04 | AW753356.1 | EST_HUMAN | Q13825 AU-BINDING PROTEIN/ENOVYL-COA HYDRATASE. ; |
| 2095 | 15112 | 28133 | 1.57 | 4.0E-04 | AL163278.2 | NT | RC3-CT0254-130100-023-f01 CT0254 Homo sapiens cDNA |
| 2143 | 15160 | | 0.89 | 4.0E-04 | AL046704.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C078 |
| 2635 | 15634 | 28659 | 1.66 | 4.0E-04 | O96615 | SWISSPROT | DKFZp434D059_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D059.5' |
| 3178 | 16233 | 29150 | 1.8 | 4.0E-04 | AF281074.1 | NT | SERPIN-2 (SILK GUM PROTEIN 2) |
| | | | | | | | Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 4351 | 17378 | 30257 | 3.23 | 4.0E-04 | AA576331.1 | EST_HUMAN | nh10a10.s1 NCL_CGAP_Cot1 Homo sapiens cDNA clone IMAGE:951930 3' similar to gb:M21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN); |
| 4351 | 17378 | 30258 | 3.23 | 4.0E-04 | AA576331.1 | EST_HUMAN | nh10a10.s1 NCL_CGAP_Cot1 Homo sapiens cDNA clone IMAGE:951930 3' similar to gb:M21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN); |
| 4568 | 17591 | 30484 | 1.4 | 4.0E-04 | AA086324.1 | EST_HUMAN | SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN); |
| 5124 | 18133 | 31010 | 4.37 | 4.0E-04 | BE560660.1 | EST_HUMAN | zn61c08.s1 Stralagene muscle 937209 Homo sapiens cDNA clone IMAGE:662870 3' |
| 5288 | 16921 | | 1.02 | 4.0E-04 | AL163267.2 | NT | 601345895.F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3678910 5' |
| | | | | | | | Homo sapiens chromosome 21 segment HS21C067 |
| 7483 | 20449 | 33806 | 1.26 | 4.0E-04 | P48442 | SWISSPROT | EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID CELL CALCIUM-SENSING RECEPTOR) |
| 7780 | 20733 | | 0.78 | 4.0E-04 | AL161566.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68 |
| 7987 | 20928 | 34321 | 0.56 | 4.0E-04 | AU122079.1 | EST_HUMAN | AU122079 MAMMA1 Homo sapiens cDNA clone MAMMA1001620 5' |
| 8881 | 21848 | 35269 | 1.07 | 4.0E-04 | BF240712.1 | EST_HUMAN | 601875885.F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099700 5' |
| 8889 | 21855 | 35275 | 1.56 | 4.0E-04 | N2507.1 | EST_HUMAN | yx39e12.r1 Soares melanocyte 2NBM Homo sapiens cDNA clone IMAGE:284142 5' |
| 10049 | 22976 | 36442 | 3.11 | 4.0E-04 | AJ025699.1 | EST_HUMAN | ov87h03.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1644341 3' |
| 10200 | 23125 | | 1.11 | 4.0E-04 | AF022855.1 | NT | Mus musculus neuropilin-2(a17) mRNA, alternatively spliced, complete cds |
| 12684 | 25728 | | 2.42 | 4.0E-04 | AF254822.1 | NT | Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced |
| 157 | 13260 | 26187 | 3.45 | 3.0E-04 | AL119426.1 | EST_HUMAN | DKFZp761J221.1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761J221 5' |
| 197 | 13298 | 26226 | 1.65 | 3.0E-04 | P49259 | SWISSPROT | 180 KD SECRETORY PHOSPHOLIPASE A2 RECEPTOR PRECURSOR (PLA2-R) |
| 881 | 13938 | 26895 | 1.64 | 3.0E-04 | U83991.1 | NT | Human short chain acyl CoA dehydrogenase gene, exons 1 and 2 |
| 1856 | 14882 | 27878 | 1.65 | 3.0E-04 | AJ262100.1 | EST_HUMAN | q28d03.y1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2028197 5' |
| 1871 | 14886 | | 1.43 | 3.0E-04 | AJ399674.1 | EST_HUMAN | th23a02.x1 NCL_CGAP_P28 Homo sapiens cDNA clone IMAGE:2119082 3' |
| 3319 | 16371 | 29291 | 3.17 | 3.0E-04 | P25147 | SWISSPROT | INTERNALIN B PRECURSOR |
| 3987 | 17027 | 29938 | 2.72 | 3.0E-04 | P49448 | SWISSPROT | GLUTAMATE DEHYDROGENASE 2 PRECURSOR (GDH) |
| 4086 | 17120 | | 1.21 | 3.0E-04 | AJ271735.1 | NT | Homo sapiens Xq pseudautosomal region; segment 1/2 |
| 4120 | 17153 | | 1.33 | 3.0E-04 | BE140609.1 | EST_HUMAN | RCO-HT0014-310598-028 HT0014 Homo sapiens cDNA |
| 4854 | 17871 | | 5.28 | 3.0E-04 | BE153778.1 | EST_HUMAN | PMO-HT0339-190200-007-g12 HT0339 Homo sapiens cDNA |
| 5248 | 18256 | | 1.02 | 3.0E-04 | AJ271735.1 | NT | Homo sapiens Xq pseudautosomal region; segment 1/2 |
| 6256 | 19339 | | 5.73 | 3.0E-04 | AL163261.2 | NT | Homo sapiens chromosome 21 segment HS21C081 |
| 6993 | 20119 | 33432 | 1.62 | 3.0E-04 | AL163278.2 | NT | Homo sapiens chromosome 21 segment HS21C078 |
| 7183 | 18414 | 31216 | 0.71 | 3.0E-04 | AW593981.1 | EST_HUMAN | RC4-NN0027-060400-011-508 NN0027 Homo sapiens cDNA |
| 7847 | 20794 | 34171 | 0.77 | 3.0E-04 | P23468 | SWISSPROT | PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (R-PTP-DELTA) |
| 8602 | 21570 | 34988 | 5.18 | 3.0E-04 | P22607 | SWISSPROT | FIBROBLAST GROWTH FACTOR RECEPTOR 3 PRECURSOR (FGFR-3) |
| | | | | | | | zn48c08.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:795471 5' similar to gb:M62762 |
| 10280 | 23205 | 36689 | 1.44 | 3.0E-04 | AA454055.1 | EST_HUMAN | VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (HUMAN); |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 10538 | 23460 | 36957 | 0.56 | 3.0E-04 | A1992139.1 | EST_HUMAN | wt75at11.x1 Soares_thymus_NHFT1 Homo sapiens cDNA clone IMAGE:2513276 3' |
| 10825 | 23746 | 37247 | 7.72 | 3.0E-04 | AA781201.1 | EST_HUMAN | aj24g05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391288 3' similar to gb:M36072.60S RIBOSOMAL PROTEIN L7A (HUMAN); |
| 12245 | 25957 | 31315 | 3.98 | 3.0E-04 | AA228301.1 | EST_HUMAN | nc38a04.r1 NCI_CGAP_Pr2 Homo sapiens cDNA clone IMAGE:1010430 similar to contains L1 L2 L1 repetitive element; |
| 12623 | 25902 | 31525 | 5.33 | 3.0E-04 | AB018292.1 | NT | Homo sapiens mRNA for KIAA0749 protein, partial cds |
| 13014 | 25584 | | 4.33 | 3.0E-04 | AL134483.1 | EST_HUMAN | DKFZp547L185_r1 547 (synonym: hfrt1) Homo sapiens cDNA clone DKFZp547L185 5' |
| 177 | 13278 | 26204 | 1.29 | 2.0E-04 | AF217796.1 | NT | Homo sapiens SCG10 like-protein, helicase-like protein NHL, M88, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds |
| 479 | 13551 | 26479 | 3.55 | 2.0E-04 | AU146707.1 | EST_HUMAN | AU146707 HEMBB1 Homo sapiens cDNA clone HEMBB1001253 3' |
| 908 | 13963 | 26919 | 4.01 | 2.0E-04 | M86524.1 | NT | Human dystrophin gene |
| 908 | 13963 | 26920 | 4.01 | 2.0E-04 | M86524.1 | NT | Human dystrophin gene |
| 1183 | 14224 | | 2.52 | 2.0E-04 | AI286021.1 | EST_HUMAN | qh98e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains MER3 b2 MER3 repetitive element; |
| 1190 | 14230 | | 2.5 | 2.0E-04 | AL163203.2 | NT | Homo sapiens chromosome 21 segment HS21C003 |
| 1849 | 14875 | | 1.19 | 2.0E-04 | AF224268.1 | NT | Mus musculus 5' flanking region of Plk3 gene |
| 2194 | 15209 | | 1.03 | 2.0E-04 | AA479980.1 | EST_HUMAN | zu39b05.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740337 3' similar to contains Alu repetitive element; |
| 2581 | 15582 | 28601 | 4.05 | 2.0E-04 | U66061.1 | NT | Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV19S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2, > |
| 3000 | 16058 | 28977 | 1.13 | 2.0E-04 | A1124529.1 | EST_HUMAN | am58c09.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539760 3' |
| 3449 | 16496 | 29413 | 2.44 | 2.0E-04 | BE082317.1 | EST_HUMAN | QV2-BT0636-070500-194-b07 BT0636 Homo sapiens cDNA |
| 3932 | 16972 | 29886 | 1.21 | 2.0E-04 | AW978441.1 | EST_HUMAN | EST390550 IMAGE resequences, MAGP Homo sapiens cDNA |
| 4167 | 17198 | | 5.41 | 2.0E-04 | U01029.1 | NT | Phaeosolus vulgaris nitrate reductase (PNR2) gene, complete cds |
| 4696 | 17717 | 30612 | 1.21 | 2.0E-04 | H96265.1 | EST_HUMAN | yu01e11.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5' |
| 4696 | 17717 | 30613 | 1.21 | 2.0E-04 | H96265.1 | EST_HUMAN | yu01e11.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5' |
| 4834 | 17851 | | 1.46 | 2.0E-04 | U09226.1 | NT | Gallus gallus proteasome 28 kDa subunit homolog mRNA, complete cds |
| 5070 | 18080 | 30961 | 1.21 | 2.0E-04 | H85683.1 | EST_HUMAN | ys68b08.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:219927 5' similar to contains L1 repetitive element; |
| 5098 | 18108 | 30981 | 1.85 | 2.0E-04 | AB037997.1 | NT | Danio rerio hagaromo gene, exons 1 to 6, partial cds |
| 5623 | 18719 | 31878 | 1.23 | 2.0E-04 | AV654352.1 | EST_HUMAN | AV654352 GLC Homo sapiens cDNA clone GLCDUH10 3' |
| 5636 | 18732 | 31894 | 1.78 | 2.0E-04 | AI680862.1 | EST_HUMAN | tq03b11.x1 NCI_CGAP_U03 Homo sapiens cDNA clone IMAGE:2207709 3' |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 5843 | 18933 | 32117 | 1.15 | 2.0E-04 | AA206652.1 | EST_HUMAN | EST11191 Uterus Homo sapiens cDNA 5' end similar to EST containing O family repeat |
| 6057 | 19138 | 32349 | 0.88 | 2.0E-04 | 4758179 | NT | Homo sapiens cell cycle progression 3 protein (DNJ3) mRNA |
| 6366 | 19435 | 32678 | 0.8 | 2.0E-04 | AF140708.1 | NT | Mus musculus G protein coupled receptor gene, complete cds; and unknown gene |
| 7440 | 20407 | | 2.54 | 2.0E-04 | AU121712.1 | EST_HUMAN | AU121712 MAMMA1 Homo sapiens cDNA clone MAMMA1000798 5' |
| 7546 | 20509 | | 0.61 | 2.0E-04 | AW860963.1 | EST_HUMAN | QV0-CT0387-180300-167-e10 CT0387 Homo sapiens cDNA |
| 7882 | 20826 | | 15.1 | 2.0E-04 | P08548 | SWISSPROT | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| 7892 | 20835 | 34215 | 1.21 | 2.0E-04 | P54296 | SWISSPROT | MYOMESIN 2 (M-PROTEIN) (165 KD TITIN-ASSOCIATED PROTEIN) (165 KD CONNECTIN-ASSOCIATED PROTEIN) |
| 8170 | 21109 | 34508 | 0.53 | 2.0E-04 | AL043272.2 | EST_HUMAN | DKFZp434L2023_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L2023 5' |
| 8170 | 21109 | 34509 | 0.53 | 2.0E-04 | AL043272.2 | EST_HUMAN | DKFZp434L2023_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L2023 5' |
| 8288 | 21257 | 34667 | 2.13 | 2.0E-04 | U32444.2 | NT | Solanum lycopersicum phytochrome F (PHYF) gene, partial cds |
| 8288 | 21257 | 34668 | 2.13 | 2.0E-04 | U32444.2 | NT | Solanum lycopersicum phytochrome F (PHYF) gene, partial cds |
| 8627 | 21595 | 35015 | 1.21 | 2.0E-04 | AB026898.1 | NT | Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds) |
| 8627 | 21595 | 35016 | 1.21 | 2.0E-04 | AB026898.1 | NT | Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds) |
| 8911 | 21877 | 35303 | 1.9 | 2.0E-04 | AF020503.1 | NT | Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5 |
| 9095 | 22061 | 35486 | 0.56 | 2.0E-04 | X57331.1 | NT | Human Immunoglobulin C(mu) and C(delta) heavy chain genes (constant regions) |
| 9699 | 22642 | 36100 | 0.51 | 2.0E-04 | AA726700.1 | EST_HUMAN | ai22a12.s1 Soares testis_NHT Homo sapiens cDNA clone 1343518 3' |
| 9774 | 22715 | 36170 | 0.65 | 2.0E-04 | P18716 | SWISSPROT | GASTRULA ZINC FINGER PROTEIN XLCGF26.1 |
| 10334 | 23258 | 36735 | 1.21 | 2.0E-04 | BE149303.1 | EST_HUMAN | RC3-HT0254-151099-011-b05 HT0254 Homo sapiens cDNA |
| 10377 | 23300 | 36776 | 2.74 | 2.0E-04 | AA405777.1 | EST_HUMAN | zu68c11.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:742984 5' |
| 11197 | 24132 | 37683 | 3.56 | 2.0E-04 | AV730373.1 | EST_HUMAN | AV730373 HTF Homo sapiens cDNA clone HTFAA01 5' |
| 11510 | 24451 | | 2.59 | 2.0E-04 | AJ243213.1 | NT | Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5 |
| 11635 | 24572 | 38136 | 2.95 | 2.0E-04 | AI440282.1 | EST_HUMAN | J01111.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140269 3' similar to contains Alu repetitive element |
| 11755 | 24693 | 38262 | 2.49 | 2.0E-04 | AW136740.1 | EST_HUMAN | UI-H-B1-adm-c-04-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717190 3' |
| 768 | 13827 | 26771 | 0.81 | 1.0E-04 | H99546.1 | EST_HUMAN | yx26c09.s1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:262864 3' similar to contains L1.1 L1 repetitive element |
| 951 | 14004 | 26956 | 2.03 | 1.0E-04 | P48725 | SWISSPROT | PERICENTRIN |
| 1076 | 14121 | 27072 | 2.61 | 1.0E-04 | P11369 | SWISSPROT | RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ; ENDONUCLEASE] |
| 1116 | 14160 | 27110 | 4.21 | 1.0E-04 | AW013947.1 | EST_HUMAN | UI-H-B10-aab-e-09-0-UI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3' |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 1118 | 14180 | 27111 | 4.21 | 1.0E-04 | AW013847.1 | EST_HUMAN | UI-H-BD-aab-09-0-UI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3' |
| 1335 | 14386 | | 3.08 | 1.0E-04 | U62818.1 | NT | Anguilla anguilla dopamine D1A1 receptor (d1A1) gene, complete cds |
| | | | | | | | Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds |
| 1632 | 14685 | 27640 | 3.19 | 1.0E-04 | AF148805.1 | NT | Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds |
| 1632 | 14685 | 27641 | 3.19 | 1.0E-04 | AF148805.1 | NT | Equus caballus DNA, chromosome 24q14, microsatellite TKY36 |
| 1878 | 14903 | 27903 | 2.37 | 1.0E-04 | AB048342.1 | NT | h45c08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176366 3' |
| 2698 | 15694 | 28710 | 1.05 | 1.0E-04 | BE218833.1 | EST_HUMAN | h45c08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176366 3' |
| 2698 | 15694 | 28711 | 1.05 | 1.0E-04 | BE218833.1 | EST_HUMAN | h45c08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176366 3' |
| 3297 | 16350 | 28270 | 1.14 | 1.0E-04 | Q62203 | SWISSPROT | SPLICING FACTOR 3A SUBUNIT 2 (SF3A66) |
| | | | | | | | 901f11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140269 3' similar to contains Alu repetitive element; |
| 3748 | 16790 | 29702 | 0.93 | 1.0E-04 | AI440282.1 | EST_HUMAN | Mouse alpha 1 type-IV collagen mRNA |
| 4089 | 17123 | 30017 | 2.07 | 1.0E-04 | M14042.1 | NT | AV647727 GLC Homo sapiens cDNA clone GLCBB04 3' |
| 4109 | 17143 | 30037 | 1.04 | 1.0E-04 | AV647727.1 | EST_HUMAN | Homo sapiens KIAA0237 gene product (KIAA0237), mRNA |
| 5132 | 18141 | 31019 | 1.87 | 1.0E-04 | 7662015 | NT | Homo sapiens KIAA0237 gene product (KIAA0237), mRNA |
| 5132 | 18141 | 31020 | 1.87 | 1.0E-04 | 7662015 | NT | Homo sapiens KIAA0237 gene product (KIAA0237), mRNA |
| 5137 | 18146 | 31026 | 0.92 | 1.0E-04 | A1357156.1 | EST_HUMAN | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| 5980 | 18045 | 32244 | 1.19 | 1.0E-04 | P08547 | SWISSPROT | 753F Heart Homo sapiens cDNA clone 753 |
| 6033 | 19116 | 32319 | 0.52 | 1.0E-04 | T19615.1 | EST_HUMAN | 753F Heart Homo sapiens cDNA clone 753 |
| 6033 | 19116 | 32320 | 0.52 | 1.0E-04 | T19615.1 | EST_HUMAN | 753F Heart Homo sapiens cDNA clone 753 |
| 6579 | 19639 | 32805 | 0.9 | 1.0E-04 | AA177111.1 | EST_HUMAN | nc02612.s1 NCI_CGAP_P33 Homo sapiens cDNA clone IMAGE:252 |
| | | | | | | | h25a04.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:993486 3' similar to gb.M97252 |
| 7012 | 20138 | 33455 | 0.68 | 1.0E-04 | AA564561.1 | EST_HUMAN | KALLMANN SYNDROME PROTEIN PRECURSOR (HUMAN); contains Alu repetitive element; |
| 7392 | 20361 | 33713 | 12.86 | 1.0E-04 | A1251980.1 | EST_HUMAN | q57d10.x1 NCI_CGAP_Ov32 Homo sapiens cDNA clone IMAGE:1985683 3' |
| 7821 | 20361 | 33713 | 12.73 | 1.0E-04 | A1251980.1 | EST_HUMAN | q57d10.x1 NCI_CGAP_Ov32 Homo sapiens cDNA clone IMAGE:1985683 3' |
| 8328 | 21297 | 34712 | 0.89 | 1.0E-04 | AA630453.1 | EST_HUMAN | ab94q08.s1 Stratagene lung (R937210) Homo sapiens cDNA clone IMAGE:854654 3' |
| 9692 | 22845 | 36102 | 2.18 | 1.0E-04 | A1806220.1 | EST_HUMAN | wf26a08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356742 3' |
| 9703 | 22856 | 36111 | 1.47 | 1.0E-04 | O88969 | SWISSPROT | CYSTATIN-RELATED EPIDIDYMAL SPERMATOGENIC PROTEIN PRECURSOR (CYSTATIN 8) |
| 9790 | 22721 | | 0.63 | 1.0E-04 | T77153.1 | EST_HUMAN | y472c08.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:113774 5' |
| 10004 | 22831 | 36394 | 1.89 | 1.0E-04 | 10863876 | NT | Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA |
| 10539 | 23481 | | 9.91 | 1.0E-04 | P08547 | SWISSPROT | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| 10578 | 23488 | 36990 | 0.91 | 1.0E-04 | P08548 | SWISSPROT | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |

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Table 4
Single Exon Probes Expressed In Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 11667 | 24603 | | 1.74 | 1.0E-04 | M28587.1 | NT | Mouse alpha leukocyte interferon gene, complete cds |
| 11961 | 24840 | 38433 | 1.5 | 1.0E-04 | AB032968.1 | NT | Homo sapiens mRNA for KIAA1142 protein, partial cds |
| 11999 | 24876 | 38472 | 1.46 | 1.0E-04 | AW269061.1 | EST_HUMAN | xy49g12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2816518 3' |
| 12032 | 24908 | 38502 | 1.81 | 1.0E-04 | Q03696 | SWISSPROT | NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM) |
| 12032 | 24908 | 38503 | 1.81 | 1.0E-04 | Q03696 | SWISSPROT | NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM) |
| 12413 | 25770 | | 2.4 | 1.0E-04 | BE676399.1 | EST_HUMAN | 722a10.x1 NCI_CGAP_GLI1 Homo sapiens cDNA clone IMAGE:3296058 3' similar to contains L1.13 L1 repetitive element; |
| 13081 | 25597 | | 1.38 | 1.0E-04 | BE700353.1 | EST_HUMAN | PM4-NN0091-190700-004-f11 NN0091 Homo sapiens cDNA |
| 699 | 13781 | 26693 | 2.39 | 9.0E-05 | AA718933.1 | EST_HUMAN | ah45c11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1292468 3' |
| 2020 | 15041 | 28052 | 1.09 | 9.0E-05 | AW866218.1 | EST_HUMAN | QV4-SN0023-070400-166-504 SN0023 Homo sapiens cDNA |
| 6074 | 19155 | 32367 | 1.58 | 9.0E-05 | Q60716 | SWISSPROT | PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR |
| 7828 | 20776 | 34153 | 0.67 | 9.0E-05 | AW204958.1 | EST_HUMAN | U1-H-B11-aer-d-05-Q-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2720289 3' |
| 7828 | 20776 | 34154 | 0.67 | 9.0E-05 | AW204958.1 | EST_HUMAN | U1-H-B11-aer-d-05-Q-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2720289 3' |
| 9831 | 22690 | | 2.89 | 9.0E-05 | D85606.1 | NT | Homo sapiens gene for cholecystikinin type-A receptor, complete cds |
| 9833 | 22692 | 36137 | 3.13 | 9.0E-05 | AF120982.1 | NT | Homo sapiens methyl-CpG binding protein 1 (MBD1) gene, exon 15b |
| 11472 | 24415 | 37984 | 2.03 | 9.0E-05 | AW073078.1 | EST_HUMAN | xs34g05.x1 NCI_CGAP_B18 Homo sapiens cDNA clone IMAGE:2568728 3' similar to contains L1.12 L1 repetitive element; |
| 11938 | 19155 | 32367 | 3.21 | 9.0E-05 | Q60716 | SWISSPROT | PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR |
| 12485 | 25832 | | 3.02 | 9.0E-05 | AF129756.1 | NT | Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G8c, G5b, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds |
| 822 | 13890 | 26831 | 1.79 | 8.0E-05 | AJ251646.1 | NT | Pisum sativum mRNA for beta-1,3 glucanase (gns2 gene) |
| 885 | 13921 | | 7.38 | 8.0E-05 | AJ251646.1 | NT | Pisum sativum mRNA for beta-1,3 glucanase (gns2 gene) |
| 2961 | 16019 | | 0.91 | 8.0E-05 | MB3575.1 | NT | Human platelet-derived growth factor A chain (PDGFA) gene, exons only |
| 4507 | 17532 | 30415 | 0.87 | 8.0E-05 | AW044605.1 | EST_HUMAN | wy78a04.x1 Soares_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2554638 3' |
| 9101 | 22087 | 35493 | 0.48 | 8.0E-05 | Y11666.1 | NT | Mus musculus gene for hexokinase II, exon 1 (and joined CDS) |
| 11485 | 24428 | 37979 | 3.06 | 8.0E-05 | M69197.1 | NT | Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds |
| 13050 | 25815 | | 2.74 | 8.0E-05 | AA279333.1 | EST_HUMAN | zs88h01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704593 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element; |
| 347 | 13436 | 26358 | 6.11 | 7.0E-05 | AW847445.1 | EST_HUMAN | RC3-CT0208-220999-011-E04 CT0208 Homo sapiens cDNA |
| 347 | 13436 | 26359 | 6.11 | 7.0E-05 | AW847445.1 | EST_HUMAN | RC3-CT0208-220999-011-E04 CT0208 Homo sapiens cDNA |
| 569 | 13639 | 26553 | 1 | 7.0E-05 | L49075.1 | EST_HUMAN | HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST HFD072014 |
| 569 | 13639 | 26554 | 1 | 7.0E-05 | L49075.1 | EST_HUMAN | HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST HFD072014 |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 1058 | 14104 | 27055 | 1.47 | 7.0E-05 | Q22949 | SWISSPROT | PROBABLE GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (GPAT) |
| 2730 | 15724 | 28740 | 4.26 | 7.0E-05 | AL163278.2 | NT | Homo sapiens chromosome 21 segment HS21C078 |
| 3172 | 16227 | 29143 | 4.21 | 7.0E-05 | AB009080.1 | NT | Dichysetellum discoideum gene for TRFA, complete cds |
| 3714 | 16757 | | 0.9 | 7.0E-05 | AI432413.1 | EST_HUMAN | ig73c09.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:21144183 |
| 4400 | 17428 | 30313 | 1.53 | 7.0E-05 | AL163201.2 | NT | Homo sapiens chromosome 21 segment HS21C001 |
| 4962 | 17977 | 30867 | 0.69 | 7.0E-05 | 9845300 | NT | Rat cytomegalovirus Measricht, complete genome |
| 8567 | 21535 | 34955 | 1.27 | 7.0E-05 | AA505582.1 | EST_HUMAN | nt93g01.s1 NCL_CGAP_Br2 Homo sapiens cDNA clone IMAGE:9680983 |
| 9911 | 22732 | 36187 | 3.34 | 7.0E-05 | T07095.1 | EST_HUMAN | EST04984 Fetal brain, Stragene (ca1836206) Homo sapiens cDNA clone HFBED80 |
| 10982 | 23902 | 37415 | 0.44 | 7.0E-05 | AL163249.2 | NT | Homo sapiens chromosome 21 segment HS21C049 |
| 10982 | 23902 | 37416 | 0.44 | 7.0E-05 | AL163249.2 | NT | Homo sapiens chromosome 21 segment HS21C049 |
| 11485 | 24438 | | 9 | 7.0E-05 | 10835048 | NT | Homo sapiens chromosome 21 segment HS21C049 |
| 2041 | 15060 | 28080 | 1.6 | 6.0E-05 | 4885170 | NT | Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA |
| 2041 | 15060 | 28081 | 1.6 | 6.0E-05 | 4885170 | NT | Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA |
| 2594 | 15595 | 28613 | 1.05 | 6.0E-05 | AI655241.1 | EST_HUMAN | wb54h06.x1 NCL_CGAP_G06 Homo sapiens cDNA clone IMAGE:23095313 similar to gb:J03250 DNA TOPOISOMERASE I (HUMAN); |
| 2694 | 15690 | 28707 | 1.3 | 6.0E-05 | Z84506.1 | NT | H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA28B10 |
| 2694 | 15690 | 28708 | 1.3 | 6.0E-05 | Z84506.1 | NT | H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA28B10 |
| 2825 | 13743 | 26669 | 3.23 | 6.0E-05 | AF053630.1 | NT | Homo sapiens monocyte/neutrophil elastase inhibitor gene, complete cds |
| 5107 | 18117 | 30960 | 0.93 | 6.0E-05 | AV722942.1 | EST_HUMAN | AV722942 HTB Homo sapiens cDNA clone HTBBED12 5' |
| 5107 | 18117 | 30991 | 0.93 | 6.0E-05 | AV722942.1 | EST_HUMAN | AV722942 HTB Homo sapiens cDNA clone HTBBED12 5' |
| 6019 | 19102 | 32303 | 3.06 | 6.0E-05 | Q12860 | SWISSPROT | CONTACTIN PRECURSOR (GLYCOPROTEIN GP135) |
| 6019 | 19102 | 32304 | 3.06 | 6.0E-05 | Q12860 | SWISSPROT | CONTACTIN PRECURSOR (GLYCOPROTEIN GP135) |
| 6543 | 19605 | 32867 | 1.45 | 6.0E-05 | N72829.1 | EST_HUMAN | y60g11.17 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:246212 5' |
| 7119 | 20053 | 33357 | 0.77 | 6.0E-05 | AA897680.1 | EST_HUMAN | qj80a03.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:15045883 |
| 8421 | 21390 | 34800 | 0.71 | 6.0E-05 | BE064410.1 | EST_HUMAN | RC4-BT0311-141199-011-h08 BT0311 Homo sapiens cDNA |
| 8421 | 21390 | 34801 | 0.71 | 6.0E-05 | BE064410.1 | EST_HUMAN | RC4-BT0311-141199-011-h08 BT0311 Homo sapiens cDNA |
| 8786 | 21753 | 35175 | 0.68 | 6.0E-05 | AA150482.1 | EST_HUMAN | z08c08.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:4917263 similar to contains element MER28 repetitive element; |
| 8791 | 21758 | 35180 | 2.37 | 6.0E-05 | AW896829.1 | EST_HUMAN | PM4-NN0050-310300-001-f10 NN0050 Homo sapiens cDNA |
| 8927 | 21993 | 35321 | 0.61 | 6.0E-05 | Q60401 | SWISSPROT | COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR |
| 9507 | 22811 | 36063 | 1.11 | 6.0E-05 | P08607 | SWISSPROT | C4B-BINDING PROTEIN PRECURSOR (C4BP) |
| 9607 | 22811 | 36064 | 1.11 | 6.0E-05 | P08607 | SWISSPROT | C4B-BINDING PROTEIN PRECURSOR (C4BP) |
| 9879 | 22832 | 36286 | 1.05 | 6.0E-05 | T94149.1 | EST_HUMAN | y628c12.17 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:1190625 |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 10079 | 23006 | 36477 | 0.71 | 6.0E-05 | AW627985.1 | EST_HUMAN | h37a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2974444 3' |
| 11100 | 24060 | 37584 | 2.27 | 6.0E-05 | R75639.1 | EST_HUMAN | y69d08.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:143535 3' similar to contains Alu repetitive element; contains LTR7 repetitive element; |
| 11847 | 24730 | 38316 | 2.71 | 6.0E-05 | AA040415.1 | EST_HUMAN | zk58f02.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487035 5' |
| 12670 | 25813 | 31529 | 16.08 | 6.0E-05 | AW890110.1 | EST_HUMAN | MRO-NT0038-250400-001-009 NT0038 Homo sapiens cDNA |
| 1403 | 14436 | 27404 | 16.34 | 5.0E-05 | AW392086.1 | EST_HUMAN | QV4-ST0234-241199-040-h11 ST0234 Homo sapiens cDNA |
| 1880 | 14805 | | 1.15 | 5.0E-05 | 8923891 | NT | Homo sapiens 22kDa peroxisomal membrane protein-like (LOC55895), mRNA |
| 4004 | 17043 | 29951 | 3.54 | 5.0E-05 | AJ251884.1 | NT | Homo sapiens partial SLCO2A3 gene for extraneuronal monoamine transporter (EMT), exon 1 |
| 5603 | 18699 | 31870 | 11.74 | 5.0E-05 | X58855.1 | NT | Human MLC1emb gene for embryonic myosin alkaline light chain, 3'UTR |
| 6107 | 19186 | 32405 | 3.22 | 5.0E-05 | AV653544.1 | EST_HUMAN | AV653544 GLC Homo sapiens cDNA clone GLCDMA06 3' |
| 6292 | 19364 | 32603 | 0.84 | 5.0E-05 | AF260225.1 | NT | Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced |
| 7553 | 20516 | | 1.18 | 5.0E-05 | AB037964.1 | NT | Mus musculus gene for calretinin, exon 1 |
| 12462 | 25371 | | 5.88 | 5.0E-05 | P49193 | SWISSPROT | RETINAL-BINDING PROTEIN (RALBP) |
| 12717 | 25371 | | 4.8 | 5.0E-05 | P49193 | SWISSPROT | RETINAL-BINDING PROTEIN (RALBP) |
| 2818 | 13329 | | 4.95 | 4.0E-05 | U12821.1 | NT | Human renin (REN) gene, 5' flanking region |
| 4508 | 17533 | 30416 | 1.68 | 4.0E-05 | P49193 | SWISSPROT | RETINAL-BINDING PROTEIN (RALBP) |
| 4508 | 17533 | 30417 | 1.68 | 4.0E-05 | P49193 | SWISSPROT | RETINAL-BINDING PROTEIN (RALBP) |
| 4910 | 17827 | | 0.99 | 4.0E-05 | AF164488.1 | NT | Cryptosporidium parvum isolate Zaire 15 kDa glycoprotein gp15 gene, partial cds |
| 7127 | 20060 | 33366 | 0.71 | 4.0E-05 | U01947.1 | NT | Macaca mulatta haptoglobin (HP) gene, 5' region |
| 9881 | 22834 | | 8.43 | 4.0E-05 | AF202635.1 | NT | Homo sapiens PP1200 mRNA, complete cds |
| 10360 | 23283 | 36760 | 0.51 | 4.0E-05 | P11369 | SWISSPROT | RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE] |
| 10771 | 23692 | 37189 | 0.66 | 4.0E-05 | P23780 | SWISSPROT | BETA-GALACTOSIDASE PRECURSOR (LACTASE) (ACID BETA-GALACTOSIDASE) |
| 11120 | 24080 | 37604 | 3.91 | 4.0E-05 | AW627946.1 | EST_HUMAN | h36c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2805192 3' |
| 12423 | 25182 | | 2.48 | 4.0E-05 | AW117580.1 | EST_HUMAN | xd99e09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:748252 3' |
| 13081 | 25612 | | 2.29 | 4.0E-05 | AA417756.1 | EST_HUMAN | z01e11.s1 NCJ_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:2814100 3' |
| 681 | 13744 | 26671 | 0.78 | 3.0E-05 | AJ248061.1 | EST_HUMAN | qf84c10.x1 Soares_fetal_liver_spleen_TNFRS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element; contains element KER repetitive element; |
| 1061 | 14107 | 27057 | 1.89 | 3.0E-05 | AW273851.1 | EST_HUMAN | xx24g03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814100 3' |
| 1133 | 14176 | 27125 | 0.82 | 3.0E-05 | BF037898.1 | EST_HUMAN | 601461463F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3865142 5' |
| 1133 | 14176 | 27126 | 0.82 | 3.0E-05 | BF037898.1 | EST_HUMAN | 601461463F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3865142 5' |
| 4409 | 17437 | 30324 | 8.15 | 3.0E-05 | BE169211.1 | EST_HUMAN | PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA |
| 4409 | 17437 | 30325 | 8.15 | 3.0E-05 | BE169211.1 | EST_HUMAN | PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA |

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Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 4493 | 17518 | 30405 | 2.41 | 3.0E-05 | AA368679.1 | EST_HUMAN | EST79996 Placenta Homo sapiens cDNA similar to p53-associated protein |
| 4493 | 17518 | 30406 | 2.41 | 3.0E-05 | AA368679.1 | EST_HUMAN | EST79996 Placenta Homo sapiens cDNA similar to p53-associated protein |
| 4820 | 17641 | | 0.7 | 3.0E-05 | AL163302.2 | NT | Homo sapiens chromosome 21 segment HS21C102 |
| 5637 | 18733 | 31895 | 1.76 | 3.0E-05 | 11072102 | NT | Mus musculus myosin light chain 2, precursor lymphocyte-specific (Myhc2pl), mRNA |
| 6921 | 19971 | 33267 | 1.18 | 3.0E-05 | AJ225782.1 | NT | Homo sapiens SYBL1 gene, exons 6-8 |
| 6921 | 19971 | 33268 | 1.18 | 3.0E-05 | AJ225782.1 | NT | Homo sapiens SYBL1 gene, exons 6-8 |
| 8230 | 21199 | 34606 | 2.48 | 3.0E-05 | BE733157.1 | EST_HUMAN | 601567451F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842292 5' |
| 8895 | 21683 | 35087 | 1.68 | 3.0E-05 | AA284049.1 | EST_HUMAN | z360b05.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:701841 3' |
| 9244 | 22210 | 35641 | 1.54 | 3.0E-05 | AW770982.1 | EST_HUMAN | h184e08.x1 NCJ_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3009638 3' |
| 9248 | 22214 | 35644 | 1.37 | 3.0E-05 | 8912431 | NT | Homo sapiens interleukin-1 receptor antagonist homolog 1 (IL1HY1), mRNA |
| 9252 | 22218 | 35649 | 0.59 | 3.0E-05 | P43361 | SWISSPROT | MELANOMA-ASSOCIATED ANTIGEN 8 (MAGE-8 ANTIGEN) |
| 9486 | 22450 | | 0.51 | 3.0E-05 | X03273.1 | NT | Human ALU-family cluster 5' of alpha(1)-acid glycoprotein gene |
| 9675 | 22628 | 36081 | 1.2 | 3.0E-05 | AA372562.1 | EST_HUMAN | EST84475 Colon adenocarcinoma IV Homo sapiens cDNA 5' end |
| 10021 | 22948 | | 3.24 | 3.0E-05 | AJ769331.1 | EST_HUMAN | wg36f09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367209 3' |
| 10901 | 23821 | 37330 | 0.89 | 3.0E-05 | Q62918 | SWISSPROT | PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NELL-LIKE PROTEIN 2) |
| 10901 | 23821 | 37331 | 0.89 | 3.0E-05 | Q62918 | SWISSPROT | PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NELL-LIKE PROTEIN 2) |
| 12353 | 25147 | | 1.49 | 3.0E-05 | L77570.1 | NT | Homo sapiens DiGeorge syndrome critical region, centromeric end |
| 2332 | 15343 | 28365 | 1.32 | 2.0E-05 | AJ286021.1 | EST_HUMAN | qh98e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains |
| 2587 | 15588 | 28605 | 2.2 | 2.0E-05 | M13792.1 | NT | MER3.b2 MER3 repetitive element ; Human adenosine deaminase (ADA) gene, complete cds |
| 2725 | 15719 | | 7.98 | 2.0E-05 | AA160362.1 | EST_HUMAN | zq48a12.f1 Stratagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:632734 5' similar to contains Alu repetitive element; contains element L1 repetitive element ; |
| 3154 | 18211 | 29126 | 1.15 | 2.0E-05 | BE066036.1 | EST_HUMAN | RC3-BT0319-120200-014-h08 BT0319 Homo sapiens cDNA |
| 3359 | 18409 | 28331 | 0.88 | 2.0E-05 | AF184614.1 | NT | Homo sapiens p47-phox (NCF1) gene, complete cds |
| 3382 | 18431 | 28359 | 1.35 | 2.0E-05 | X89211.1 | NT | H. sapiens DNA for endogenous retroviral like element |
| 3505 | 16552 | | 0.7 | 2.0E-05 | X95465.1 | NT | S. cerevisiae 12.8 Kbp fragment of the left arm of chromosome XV |
| 3820 | 16860 | | 0.69 | 2.0E-05 | AL039107.1 | EST_HUMAN | DKFZp566l064.j1 566 (synonym: hfkd2) Homo sapiens cDNA clone DKFZp566l064 5' |
| 4720 | 17740 | | 1 | 2.0E-05 | BE378471.1 | EST_HUMAN | 601238455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608653 5' |
| 5952 | 18943 | 32126 | 1.57 | 2.0E-05 | AJ011712.1 | NT | Homo sapiens TNNT1 gene, exons 1-11 (and joined ODS) |
| 6024 | 19107 | | 0.65 | 2.0E-05 | AF026308.1 | NT | Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families |
| 6082 | 19162 | 32373 | 0.86 | 2.0E-05 | Q13183 | SWISSPROT | RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER) |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptbr |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 6082 | 19182 | 32374 | 0.86 | 2.0E-05 | Q13183 | SWISSPROT | RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER) |
| 6281 | 19353 | 32589 | 0.68 | 2.0E-05 | A1149272.1 | EST_HUMAN | q72a02.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1715114 3' |
| 6356 | 19425 | 32667 | 0.49 | 2.0E-05 | P35085 | SWISSPROT | similar to contains L1 L3 L1 repetitive element; |
| 6778 | 19833 | 33116 | 2.32 | 2.0E-05 | AA714330.1 | EST_HUMAN | CALCIUM-BINDING PROTEIN |
| 7086 | 20020 | 33322 | 1.52 | 2.0E-05 | Y08926.1 | NT | hw06d12.s1 NCL_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238519 3' |
| 7099 | 20033 | 33336 | 0.94 | 2.0E-05 | A1492960.1 | EST_HUMAN | P. falciparum mRNA for AARP1 protein, partial |
| 7108 | 20042 | | 8.62 | 2.0E-05 | A1991025.1 | EST_HUMAN | q47b06.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2030003 3' similar to TR:O02711 |
| 7360 | 20330 | 33679 | 2.22 | 2.0E-05 | AF224262.1 | NT | Q02711 PRO-POL-DUTPASE POLYPROTEIN; |
| 7360 | 20330 | 33680 | 2.22 | 2.0E-05 | AF224262.1 | NT | wd35h07.x1 Soares_Dieckgraefe_cdon_NHCD Homo sapiens cDNA clone IMAGE:2522077 3' |
| 7592 | 20553 | | 0.81 | 2.0E-05 | AF128847.1 | NT | Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), and HoxA1 (HoxA1) genes, complete cds |
| 8157 | 21095 | 34494 | 0.5 | 2.0E-05 | U68061.1 | NT | Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), and HoxA1 (HoxA1) genes, complete cds |
| 8217 | 21186 | 34596 | 1.25 | 2.0E-05 | A1381040.1 | EST_HUMAN | Homo sapiens Indolethylamine N-methyltransferase (INMT) mRNA, INMT-2 allele, complete cds |
| 9477 | 22441 | 35881 | 0.52 | 2.0E-05 | BE244840.1 | EST_HUMAN | Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV19S1P, TCRBV16S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY6, TRY8, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2, > |
| 9477 | 22441 | 35882 | 0.52 | 2.0E-05 | BE244840.1 | EST_HUMAN | tg20h05.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2709369 3' |
| 9622 | 22566 | 36015 | 0.57 | 2.0E-05 | P49457 | SWISSPROT | TCBAP2E1590 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP1590 |
| 9622 | 22566 | 36016 | 0.57 | 2.0E-05 | P49457 | SWISSPROT | TCBAP2E1590 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP1590 |
| 10283 | 23208 | 36693 | 0.57 | 2.0E-05 | AL163207.2 | NT | COMPLEMENT DECAY-ACCELERATING FACTOR (CD55) |
| 10494 | 23416 | 36914 | 0.87 | 2.0E-05 | BF055939.1 | EST_HUMAN | COMPLEMENT DECAY-ACCELERATING FACTOR (CD55) |
| 10954 | 23874 | 37387 | 2.1 | 2.0E-05 | N41751.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C007 |
| 10954 | 23874 | 37388 | 2.1 | 2.0E-05 | N41751.1 | EST_HUMAN | 775g09.y1 NCL_CGAP_Brn20 Homo sapiens cDNA clone IMAGE:3340576 5' |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 11006 | 20042 | | 2.01 | 2.0E-05 | A1991026.1 | EST_HUMAN | vu35h07.x1 Soares_Dickgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522077 3' |
| 11781 | 23936 | 37457 | 1.9 | 2.0E-05 | BE175901.1 | EST_HUMAN | RCS-HT0582-280300-012-E12 HT0582 Homo sapiens cDNA |
| 12473 | 25740 | | 6.5 | 2.0E-05 | BE348229.1 | EST_HUMAN | hw21a03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3183532 3' similar to TR:Q12832 |
| 12626 | 25727 | | 1.54 | 2.0E-05 | AF275948.1 | NT | Q12832 GLYCOPHORIN HEP2: |
| 12768 | 25409 | 31759 | 1.49 | 2.0E-05 | AU131513.1 | EST_HUMAN | Homo sapiens ABCA1 (ABCA1) gene, complete cds |
| 2705 | 15902 | 28715 | 3.2 | 1.0E-05 | AL163282.2 | NT | AU131513 NT2RP3 Homo sapiens cDNA clone NT2RP3002707 5' |
| 3663 | 16706 | 29621 | 1.86 | 1.0E-05 | AF088273.1 | NT | Homo sapiens chromosome 21 segment HS21C082 |
| 3826 | 16968 | | 1.17 | 1.0E-05 | AF223391.1 | NT | Drosophila melanogaster strain Larito 120 Suppressor of Hairless (Su(H)) gene, partial cds |
| 3991 | 17031 | 29940 | 10.43 | 1.0E-05 | P81274 | SWISSPROT | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced |
| 4201 | 17232 | 30119 | 1.52 | 1.0E-05 | AL163203.2 | NT | MOSAIC PROTEIN LGN |
| 4306 | 17335 | 30213 | 1.77 | 1.0E-05 | AA431119.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C003 |
| 4887 | 17904 | 30793 | 1.82 | 1.0E-05 | AW419134.1 | EST_HUMAN | zw68g04.t1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781494 5' |
| 5005 | 18019 | 30907 | 0.94 | 1.0E-05 | Z18943.1 | NT | xy49g11.x1 NCI_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2856548 3' |
| 6915 | 19967 | 33262 | 1.03 | 1.0E-05 | AJ246003.1 | NT | H. sapiens repeat region |
| 7028 | 18360 | 31281 | 0.52 | 1.0E-05 | P08548 | SWISSPROT | Homo sapiens Spast gene for spastin protein |
| 7286 | 20063 | 33370 | 3.02 | 1.0E-05 | AA641846.1 | EST_HUMAN | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| 7288 | 20260 | 33594 | 8.81 | 1.0E-05 | 4505844 | NT | ns19g02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1184114 3' similar to contains L1.t1 L1 |
| 7921 | 20864 | 34252 | 0.66 | 1.0E-05 | BF222646.1 | EST_HUMAN | Homo sapiens phospholipase A2, group X (PLA2G10) mRNA, and translated products |
| 8057 | 20964 | | 1.5 | 1.0E-05 | P19474 | SWISSPROT | 7p57d01.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:3649945 3' similar to contains MER10.b3 |
| 9268 | 22232 | | 2.45 | 1.0E-05 | AL163227.2 | NT | MER10 repetitive element; |
| 9415 | 22380 | 35818 | 2.22 | 1.0E-05 | AA452578.1 | EST_HUMAN | 52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) |
| 9642 | 22596 | 36035 | 14.03 | 1.0E-05 | AA236110.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C027 |
| 9721 | 22749 | 36201 | 0.82 | 1.0E-05 | AV732190.1 | EST_HUMAN | zx35h12.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:788519 3' similar to |
| 10198 | 23123 | 36609 | 0.79 | 1.0E-05 | AW510902.1 | EST_HUMAN | gb:L029932 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN); |
| 10198 | 23123 | 36610 | 0.79 | 1.0E-05 | AW510902.1 | EST_HUMAN | zs05e11.t1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:984332 5' similar to contains Alu |
| 10276 | 23201 | 36685 | 1.11 | 1.0E-05 | AW291521.1 | EST_HUMAN | repetitive element; contains element TAR1 repetitive element; |
| | | | | | | | AV732190 HTF Homo sapiens cDNA clone HTFBIH01 5' |
| | | | | | | | hd41b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912043 3' similar to contains |
| | | | | | | | OFF.t1 OFF repetitive element; |
| | | | | | | | hd41b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912043 3' similar to contains |
| | | | | | | | OFF.t1 OFF repetitive element; |
| | | | | | | | UJ-H-BI2-egk-a-08-D-UJ.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3' |

Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 10278 | 23201 | 36686 | 1.11 | 1.0E-05 | AW291521.1 | EST_HUMAN | UI-H-BI2-sagk-a-08-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3' |
| 10544 | 23466 | | 1.95 | 1.0E-05 | AW466995.1 | EST_HUMAN | ha07c10.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2873010 3' similar to contains L1.12 L1 repetitive element: |
| 11264 | 24216 | 37740 | 1.79 | 1.0E-05 | U91328.1 | NT | Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds |
| 11264 | 24216 | 37741 | 1.79 | 1.0E-05 | U91328.1 | NT | Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds |
| 12941 | 25900 | 31421 | 1.43 | 1.0E-05 | AL163303.2 | NT | Homo sapiens chromosome 21 segment HS21C103 |
| 2680 | 15678 | 28697 | 5.9 | 9.0E-06 | AI583811.1 | EST_HUMAN | it73a06.x1 NCI_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246386 3' |
| 3112 | 16169 | 29079 | 4.25 | 9.0E-06 | AI218983.1 | EST_HUMAN | gg11b08.x1 Soares_placenta_8tc9weeks_2NbHP8tc9w Homo sapiens cDNA clone IMAGE:1759191 3' |
| 3624 | 16667 | | 2.82 | 9.0E-06 | M61755.1 | NT | Human alanine:glyoxylate aminotransferase (AGXT) gene, exons 1 and 2 |
| 6008 | 19091 | 32291 | 2.31 | 9.0E-06 | L23416.1 | NT | Homo sapiens differentiation antigen CD20 gene, exons 5, 6 |
| 7047 | 20059 | 33375 | 0.73 | 9.0E-06 | BE065042.1 | EST_HUMAN | RC1-BT0313-110500-017-a07 BT0313 Homo sapiens cDNA |
| 7874 | 20632 | 33996 | 0.94 | 9.0E-06 | P08547 | SWISSPROT | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| 8053 | 20990 | 34388 | 11.84 | 9.0E-06 | AI034370.1 | EST_HUMAN | alpha20g01.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1656912 3' similar to contains Alu repetitive element: |
| 8807 | 21774 | 35200 | 1.18 | 9.0E-06 | AL163209.2 | NT | Homo sapiens chromosome 21 segment HS21C009 |
| 9334 | 22299 | 35728 | 2.51 | 9.0E-06 | Q63769 | SWISSPROT | SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC) |
| 9334 | 22299 | 35729 | 2.51 | 9.0E-06 | Q63769 | SWISSPROT | SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC) |
| 9577 | 22539 | 35990 | 4.44 | 9.0E-06 | U35114.1 | NT | Human apolipoprotein E (APOE) gene, hepatic control region HCR-2 |
| 11286 | 24236 | 37763 | 3.65 | 9.0E-06 | Q10364 | SWISSPROT | PUTATIVE SERINE/THREONINE-PROTEIN KINASE C22E12.14C |
| 2535 | 15896 | 28559 | 2.23 | 8.0E-06 | AW362539.1 | EST_HUMAN | RC3-CT0283-201199-011-111 CT0283 Homo sapiens cDNA |
| 10898 | 23818 | 37326 | 0.64 | 8.0E-06 | P34083 | SWISSPROT | FASCICLIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II) |
| 10898 | 23818 | 37327 | 0.64 | 8.0E-06 | P34083 | SWISSPROT | FASCICLIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II) |
| 980 | 14031 | | 2.14 | 7.0E-06 | AA669729.1 | EST_HUMAN | ab90f10.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:854251 3' similar to contains MER20.11 MER20 repetitive element: |
| 1433 | 14467 | 27444 | 3.05 | 7.0E-06 | 7662177 | NT | Homo sapiens KIAA0555 gene product (KIAA0555), mRNA |
| 2884 | 15943 | | 7.94 | 7.0E-06 | AI368252.1 | EST_HUMAN | qw16g09.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:1991296 3' similar to contains Alu repetitive element: |

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Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 3576 | 18621 | | 0.78 | 7.0E-06 | AA385542.1 | EST_HUMAN | EST198206 Thyroid Homo sapiens cDNA 5' end similar to EST containing L1 repeat |
| 5780 | 18872 | | 5.19 | 7.0E-06 | AW883141.1 | EST_HUMAN | QV2-OT0082-250400-173-h01 OT0062 Homo sapiens cDNA |
| 5802 | 18989 | 32179 | 0.81 | 7.0E-06 | N98645.1 | EST_HUMAN | y65c07.1 Soares_multiple_sclerosis_2NbHMSF Homo sapiens cDNA clone IMAGE:278412 5' |
| 9141 | 22107 | 35533 | 0.7 | 7.0E-06 | 11420709 | NT | Homo sapiens DNA segment, numerous copies, expressed probes (GS1 gene) (DXF68S1E), mRNA |
| 10260 | 23185 | | 0.54 | 7.0E-06 | Q61147 | SWISSPROT | CERULOPLASMIN PRECURSOR (FERROXIDASE) |
| 12202 | 25927 | 31307 | 2.83 | 7.0E-06 | BF215972.1 | EST_HUMAN | 601881522F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4093972 5' |
| 2928 | 15988 | 28907 | 1.27 | 6.0E-06 | BE089188.1 | EST_HUMAN | QV3-BT0379-010300-105-d11 BT0379 Homo sapiens cDNA |
| 3706 | 16749 | 29684 | 1.08 | 6.0E-06 | BE089188.1 | EST_HUMAN | QV3-BT0379-010300-105-d11 BT0379 Homo sapiens cDNA |
| 4785 | 16010 | 28936 | 2.35 | 6.0E-06 | Q01468 | SWISSPROT | OVARIAN ABUNDANT MESSAGE PROTEIN (OAM PROTEIN) |
| 4794 | 17811 | 30703 | 2.54 | 6.0E-06 | A1040099.1 | EST_HUMAN | ox08d02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1655738 3' similar to contains MER8.12 MER8 repetitive element ; |
| 5422 | 18525 | 31403 | 1.41 | 6.0E-06 | AF167441.1 | NT | Mus musculus E-cadherin binding protein E7 mRNA, complete cds |
| 5483 | 18583 | 31495 | 1.05 | 6.0E-06 | Q02040 | SWISSPROT | PROTEIN XE7 |
| 10215 | 23140 | | 1.52 | 6.0E-06 | AW801912.1 | EST_HUMAN | IL5-UM0070-110400-083-g02 UM0070 Homo sapiens cDNA |
| 13041 | 25582 | 31700 | 1.74 | 6.0E-06 | 11418157 | NT | Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA |
| 6179 | 19254 | 32487 | 3.86 | 5.0E-06 | AL183246.2 | NT | Homo sapiens chromosome 21 segment HS21C046 |
| 6471 | 19536 | 32784 | 3.96 | 5.0E-06 | U07561.1 | NT | Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds |
| 7444 | 20410 | 33762 | 1.14 | 5.0E-06 | AB007548.1 | NT | Homo sapiens gene for LECT2, complete cds |
| 8803 | 21770 | 35185 | 0.49 | 5.0E-06 | AW856972.1 | EST_HUMAN | RC1-CT0302-120200-013-h02 CT0302 Homo sapiens cDNA |
| 8803 | 21770 | 35186 | 0.49 | 5.0E-06 | AW856972.1 | EST_HUMAN | RC1-CT0302-120200-013-h02 CT0302 Homo sapiens cDNA |
| 10462 | 23384 | 36877 | 7.1 | 5.0E-06 | AA313620.1 | EST_HUMAN | EST185496 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end |
| 12101 | 24972 | 38569 | 2 | 5.0E-06 | Q28039 | SWISSPROT | SODIUM- AND CHLORIDE-DEPENDENT GLYCINE TRANSPORTER 1 (GLYT-1) |
| 12928 | 25512 | 31709 | 2.14 | 5.0E-06 | A1065045.1 | EST_HUMAN | HA0877 Human fetal liver cDNA library Homo sapiens cDNA |
| 648 | 13714 | 26635 | 6.59 | 4.0E-06 | R18267.1 | EST_HUMAN | ya48c03.1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:53254 5' similar to contains Alu repetitive element; contains L1 repetitive element ; |
| 847 | 13903 | 26861 | 6.33 | 4.0E-06 | AW103354.1 | EST_HUMAN | xc69g12.x1 NCL_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2589574 3' similar to contains Alu repetitive element; contains element MER21 repetitive element ; |
| 1337 | 14371 | 27340 | 4.22 | 4.0E-06 | A1834928.1 | EST_HUMAN | tb33a09.x1 NCL_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3' |
| 1337 | 14371 | 27341 | 4.22 | 4.0E-06 | A1834928.1 | EST_HUMAN | tb33a09.x1 NCL_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3' |
| 1470 | 14503 | 27477 | 2.58 | 4.0E-06 | BF365612.1 | EST_HUMAN | QV2-NT0046-200800-250-h07 NT0046 Homo sapiens cDNA |
| 2274 | 15287 | 28313 | 3.05 | 4.0E-06 | AW015401.1 | EST_HUMAN | UIH-B10-eat-f-05-0-J1.st1 NCL_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710425 3' |
| 3076 | 16133 | 29046 | 0.94 | 4.0E-06 | AF198349.1 | NT | Gallus gallus Dach2 protein (Dach2) mRNA, complete cds |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 3909 | 16949 | 29860 | 1.1 | 4.0E-06 | AWB48295.1 | EST_HUMAN | IL3-CT0214-150200-074-B03 CT0214 Homo sapiens cDNA |
| 4846 | 17863 | 30756 | 2.18 | 4.0E-06 | AI886939.1 | EST_HUMAN | w194c10.x1 NCL_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2432662 3' similar to contains element |
| 8844 | 21811 | 35230 | 0.56 | 4.0E-06 | O15393 | SWISSPROT | MER22 repetitive element; |
| 9152 | 22118 | 35545 | 3.6 | 4.0E-06 | AF009660.1 | NT | TRANSMEMBRANE PROTEASE, SERINE 2 |
| 10066 | 22993 | 36462 | 1.14 | 4.0E-06 | AJ272285.1 | NT | Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region |
| 11778 | 23933 | 37454 | 2.91 | 4.0E-06 | AB007855.1 | NT | Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8 |
| 2173 | 15189 | 28209 | 1.9 | 3.0E-06 | AA700562.1 | EST_HUMAN | Homo sapiens mRNA, chromosome 1 specific transcript KIAA0486 |
| 2173 | 15189 | 28210 | 1.9 | 3.0E-06 | AA700562.1 | EST_HUMAN | z134b08.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:432863 3' similar to contains L1.t1 L1 repetitive element; |
| 2275 | 15288 | | 1.89 | 3.0E-06 | AF202835.1 | NT | z134b08.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:432863 3' similar to contains L1.t1 L1 repetitive element; |
| 2833 | 15991 | 28911 | 0.85 | 3.0E-06 | AA4868218.1 | EST_HUMAN | Homo sapiens PP1200 mRNA, complete cds |
| 3278 | 16333 | | 2.32 | 3.0E-06 | AB57779.1 | EST_HUMAN | ak48g1.1 s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409252 3' similar to contains LTR1.t3 |
| 3797 | 18837 | 29743 | 1.12 | 3.0E-06 | BE047094.1 | EST_HUMAN | w122a05.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2425616 3' similar to TR:O60734 O60734 |
| 3797 | 18837 | 29744 | 1.12 | 3.0E-06 | BE047094.1 | EST_HUMAN | LINE-1 LIKE PROTEIN; contains L1.12 L1 repetitive element; |
| 4501 | 17526 | 30411 | 0.67 | 3.0E-06 | T50266.1 | EST_HUMAN | hg94d12.x1 NCL_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3' |
| 4594 | 17615 | 30509 | 4.02 | 3.0E-06 | X54816.1 | NT | hg94d12.x1 NCL_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3' |
| 6284 | 19356 | 32592 | 0.74 | 3.0E-06 | AU159412.1 | EST_HUMAN | yb78b10.11 Stratiogene ovary (#937217) Homo sapiens cDNA clone IMAGE:77275 5' similar to contains L1 repetitive element |
| 6874 | 20197 | 33525 | 0.56 | 3.0E-06 | Z79478.1 | NT | Homo sapiens gene for alpha-1-microglobulin-bikunin, exons 1-5 (encoding alpha-1-microglobulin, N-terminus.) |
| 6874 | 20197 | 33526 | 0.56 | 3.0E-06 | Z79478.1 | NT | AU159412 THYRO1 Homo sapiens cDNA clone THYRO1001602 3' |
| 7439 | 20406 | | 1.9 | 3.0E-06 | P08548 | SWISSPROT | H.sapiens flow-sorted chromosome 6 TaqI fragment, SC9pABE5 |
| 8419 | 21388 | 34798 | 0.76 | 3.0E-06 | BE562864.1 | EST_HUMAN | H.sapiens flow-sorted chromosome 6 TaqI fragment, SC9pABE5 |
| 9032 | 21998 | 35417 | 0.64 | 3.0E-06 | P07743 | SWISSPROT | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| 12631 | 25317 | | 6.4 | 3.0E-06 | AW385282.1 | EST_HUMAN | 601336213F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690314 5' |
| 203 | 13304 | | 3.24 | 2.0E-06 | P54366 | SWISSPROT | PAROTID SECRETORY PROTEIN PRECURSOR (PSP) |
| 1572 | 14605 | | 5.6 | 2.0E-06 | P21414 | SWISSPROT | RCO-L10001-261199-011-A03 L10001 Homo sapiens cDNA |
| 2387 | 15395 | 28420 | 2.64 | 2.0E-06 | AI672138.1 | EST_HUMAN | HOMEOBOX PROTEIN GOOSECOID |
| 2474 | 15478 | 28601 | 2.73 | 2.0E-06 | P04928 | SWISSPROT | POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE] |
| | | | | | | | w104a03.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2297068 3' similar to contains MER30.b1 |
| | | | | | | | MER30 repetitive element; |
| | | | | | | | HISTIDINE-RICH GLYCOPROTEIN PRECURSOR |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 2573 | 15574 | 28594 | 1.94 | 2.0E-06 | P08719 | SWISSPROT | KNOB-ASSOCIATED HISTIDINE-RICH PROTEIN PRECURSOR (KAHRP) |
| 3531 | 16577 | 29500 | 1.29 | 2.0E-06 | AV657555.1 | EST_HUMAN | AV657555 GLC Homo sapiens cDNA clone GLCFDB05.3' |
| 3774 | 16816 | 29725 | 1.56 | 2.0E-06 | AA173518.1 | EST_HUMAN | z02a05.11 Stragene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:595232 5' |
| 3783 | 16824 | 29732 | 0.67 | 2.0E-06 | AW450215.1 | EST_HUMAN | UI-H-B13-iky-g-05-Q-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736178 3' |
| 3789 | 16830 | 29736 | 1.74 | 2.0E-06 | AB030886.1 | NT | Mus musculus gene for odorant receptor A16, complete cds |
| 6208 | 19282 | | | 2.0E-06 | AA974932.1 | EST_HUMAN | on34h01.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1558609 3' similar to contains Alu repetitive element |
| 6241 | 19314 | 32544 | 0.93 | 2.0E-06 | AI539448.1 | EST_HUMAN | tes1f05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090241 3' similar to TR:Q13537 |
| 6581 | 19641 | 32908 | 5.37 | 2.0E-06 | AI818424.1 | EST_HUMAN | Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. . |
| 8250 | 21219 | | 0.81 | 2.0E-06 | AW869223.1 | EST_HUMAN | wj90b04.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410063 3' |
| 8426 | 21395 | 34806 | 0.63 | 2.0E-06 | T12238.1 | EST_HUMAN | MR3-SN0067-120400-002-402 SN0067 Homo sapiens cDNA |
| 9188 | 22154 | | 0.61 | 2.0E-06 | AA772497.1 | EST_HUMAN | A447R Heart Homo sapiens cDNA clone A447 |
| 9200 | 22166 | 35596 | 1.83 | 2.0E-06 | H62051.1 | EST_HUMAN | zh27c11.s1 Soares_pinea_gland_N3HPG Homo sapiens cDNA clone IMAGE:413300 3' similar to |
| 9571 | 22533 | 35983 | 0.87 | 2.0E-06 | AF003529.1 | NT | TR:P70467 P70467 REVERSE TRANSCRIPTASE ; |
| 9571 | 22533 | 35984 | 0.87 | 2.0E-06 | AF003529.1 | NT | y037c04.11 Soares ovary tumor NihOT Homo sapiens cDNA clone IMAGE:235974 5' similar to gb:X74929 |
| 9591 | 22553 | | 0.48 | 2.0E-06 | AI473450.1 | EST_HUMAN | KERATIN, TYPE II CYTOSKELETAL 8 (HUMAN); |
| 10059 | 22986 | 36454 | 0.92 | 2.0E-06 | N30576.1 | EST_HUMAN | Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions |
| 10279 | 23204 | | 0.61 | 2.0E-06 | AV748969.1 | EST_HUMAN | Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions |
| 12111 | 24981 | 36581 | 2.21 | 2.0E-06 | O15553 | SWISSPROT | y16g10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141730 3' |
| 12111 | 24981 | 36582 | 2.21 | 2.0E-06 | O15553 | SWISSPROT | yw66e03.s1 Soares_placenta_8to9weeks_2NHP8to9W Homo sapiens cDNA clone IMAGE:257212 3' |
| 12540 | 25928 | 31308 | 2.97 | 2.0E-06 | P23249 | SWISSPROT | AV748969 NPC Homo sapiens cDNA clone NPCAXD05 5' |
| 36 | 13156 | 26057 | 3.02 | 1.0E-06 | O76082 | SWISSPROT | PYRIN (MARENOSTRIN) |
| 658 | 13724 | 26949 | 1.96 | 1.0E-06 | AF084364.1 | NT | PYRIN (MARENOSTRIN) |
| 1445 | 14478 | 27454 | 1.81 | 1.0E-06 | P09125 | SWISSPROT | ORGANIC CATION/CARNITINE TRANSPORTER 2 (SOLUTE CARRIER FAMILY 22, MEMBER 5) (HIGH AFFINITY SODIUM-DEPENDENT CARNITINE COTRANSPORTER) |
| 1527 | 14560 | 27531 | 1.87 | 1.0E-06 | AL163278.2 | NT | Mus musculus D6M45E protein (D6M45e) mRNA, complete cds |
| 1576 | 14609 | 27582 | 1.22 | 1.0E-06 | AA034141.1 | EST_HUMAN | MEROZOITE SURFACE PROTEIN CMZ-8 |
| 1576 | 14609 | 27583 | 1.22 | 1.0E-06 | AA034141.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C078 |
| | | | | | | | z106a12.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429982 3' similar to |
| | | | | | | | contains Alu repetitive element; |
| | | | | | | | z106a12.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429982 3' similar to |
| | | | | | | | contains Alu repetitive element; |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 1587 | 14620 | | 1.36 | 1.0E-06 | P27625 | SWISSPROT | DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT |
| 2010 | 15031 | 28040 | 5.53 | 1.0E-06 | AF184614.1 | NT | Homo sapiens p47-phox (NCF1) gene, complete cds |
| 2010 | 15031 | 28041 | 5.53 | 1.0E-06 | AF184614.1 | NT | Homo sapiens p47-phox (NCF1) gene, complete cds |
| 4397 | 17425 | 30309 | 13.21 | 1.0E-06 | U07561.1 | NT | Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds |
| 5146 | 18155 | 31034 | 1.23 | 1.0E-06 | AL163285.2 | NT | Homo sapiens chromosome 21 segment HS21C085 |
| 5146 | 18155 | 31035 | 1.23 | 1.0E-06 | AL163285.2 | NT | Homo sapiens chromosome 21 segment HS21C085 |
| 5363 | 18468 | 31339 | 4.63 | 1.0E-06 | BF333015.1 | EST_HUMAN | MR1-BT0800-030700-002-c06 BT0800 Homo sapiens cDNA |
| 5368 | 18491 | 31367 | 1.01 | 1.0E-06 | BE834518.1 | EST_HUMAN | MR3-FN0004-090600-001-e04 FN0004 Homo sapiens cDNA |
| 5388 | 18491 | 31368 | 1.01 | 1.0E-06 | BE834518.1 | EST_HUMAN | MR3-FN0004-090600-001-e04 FN0004 Homo sapiens cDNA |
| 5552 | 18649 | 31592 | 1.24 | 1.0E-06 | O60613 | SWISSPROT | 15 KDA SELENOPROTEIN PRECURSOR |
| 5892 | 18980 | | 0.64 | 1.0E-06 | BE063527.1 | EST_HUMAN | CM0-BT0281-031199-087-h04 BT0281 Homo sapiens cDNA |
| 7056 | 20078 | 33387 | 6.4 | 1.0E-06 | P02671 | SWISSPROT | FIBRINOGEN ALPHA2(A) CHAIN PRECURSOR |
| 8018 | 26005 | | 0.56 | 1.0E-06 | BE185330.1 | EST_HUMAN | IL5-HT0730-020500-074-g01 HT0730 Homo sapiens cDNA |
| 8334 | 21303 | | 0.75 | 1.0E-06 | AA912623.1 | EST_HUMAN | cl28c08.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1524878 3' |
| 8616 | 21584 | 35000 | 1.05 | 1.0E-06 | AI347010.1 | EST_HUMAN | qp54e02.x1 NCI_CGAP_C08 Homo sapiens cDNA clone IMAGE:1926842 3' |
| 8833 | 21800 | 35219 | 1.26 | 1.0E-06 | AI287878.1 | EST_HUMAN | q23106.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1982435 3' similar to contains element |
| 9659 | 22816 | 36270 | 1.15 | 1.0E-06 | N74635.1 | EST_HUMAN | MIR repetitive element |
| 9734 | 22762 | 36217 | 0.55 | 1.0E-06 | Q39575 | SWISSPROT | z55e01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:298472 3' |
| 10041 | 22668 | 36434 | 3.97 | 1.0E-06 | U82668.1 | NT | DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM |
| 10041 | 22668 | 36435 | 3.97 | 1.0E-06 | U82668.1 | NT | Homo sapiens shox gene, alternatively spliced products, complete cds |
| 10085 | 23012 | 36485 | 4.9 | 1.0E-06 | AA132611.1 | EST_HUMAN | Homo sapiens p47-phox (NCF1) gene, complete cds |
| 10147 | 23073 | | 3.89 | 1.0E-06 | AA449257.1 | EST_HUMAN | z04411.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:587174 5' |
| 10554 | 23774 | | 2.02 | 1.0E-06 | AL163203.2 | NT | gb:26129 RIBONUCLEASE PANCREATIC PRECURSOR (HUMAN); |
| 11960 | 24839 | | 3.14 | 1.0E-06 | AW890941.1 | EST_HUMAN | g017e08.r1 Striatagene colon (#937204) Homo sapiens cDNA clone IMAGE:587174 5' |
| 12672 | 15031 | 28040 | 1.71 | 1.0E-06 | AF184614.1 | NT | RC4-NT0054-120500-012-b03 NT0054 Homo sapiens cDNA |
| 12672 | 15031 | 28041 | 1.71 | 1.0E-06 | AF184614.1 | NT | Homo sapiens p47-phox (NCF1) gene, complete cds |
| 360 | 13447 | 26374 | 1.95 | 9.0E-07 | AF003529.1 | NT | Homo sapiens p47-phox (NCF1) gene, complete cds |
| 360 | 13447 | 26375 | 1.95 | 9.0E-07 | AF003529.1 | NT | Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions |
| 8750 | 21718 | | 0.59 | 9.0E-07 | AL163280.2 | NT | Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions |
| 8898 | 21864 | | 0.43 | 9.0E-07 | AA449276.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C080 |
| 11577 | 24515 | 38070 | 4.11 | 9.0E-07 | AL163281.2 | NT | zw63h01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782833 3' |
| | | | | | | | Homo sapiens chromosome 21 segment HS21C081 |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 4804 | 17821 | 30715 | 3.87 | 8.0E-07 | A1288596.1 | EST_HUMAN | ql82g07.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1878876 3' |
| 4804 | 17821 | 30716 | 3.87 | 8.0E-07 | A1288596.1 | EST_HUMAN | ql82g07.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1878876 3' |
| 5888 | 18073 | | 8.55 | 8.0E-07 | P21414 | SWISSPROT | POLYPROTEIN[CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE] |
| 8335 | 21304 | | 11.24 | 8.0E-07 | AF135416.1 | NT | Homo sapiens UDP-glucuronosyltransferase gene, complete cds |
| 11843 | 24823 | | 5.78 | 8.0E-07 | T07770.1 | EST_HUMAN | EST05660 Fetal brain, Stragene (cat#36206) Homo sapiens cDNA clone HFBEN89 |
| 12183 | 25031 | | 9.17 | 8.0E-07 | AL163280.2 | NT | Homo sapiens chromosome 21 segment HS21C080 |
| 5597 | 18993 | 31663 | 0.73 | 7.0E-07 | 6005700 | NT | Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA |
| 5597 | 18993 | 31664 | 0.73 | 7.0E-07 | 6005700 | NT | Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA |
| 1928 | 14952 | 27948 | 4.99 | 6.0E-07 | AW855588.1 | EST_HUMAN | CM3-CT0277-221099-024-e11 CT0277 Homo sapiens cDNA |
| 2500 | 15503 | 28530 | 5.38 | 6.0E-07 | AF019413.1 | NT | Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B (Bf), and complement component C2 (C2) genes, > |
| 3898 | 17038 | | 2.25 | 6.0E-07 | P41479 | SWISSPROT | HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION |
| 9497 | 22461 | 35902 | 2.17 | 6.0E-07 | BF001887.1 | EST_HUMAN | 7q94f07.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3314149 3' similar to TR:O75920-O75920 4'5L.; |
| 12442 | 25880 | | 3.45 | 6.0E-07 | AW803222.1 | EST_HUMAN | CM4-NN1028-250300-121-h12 NN1028 Homo sapiens cDNA |
| 326 | 13417 | | 0.99 | 5.0E-07 | A1831893.1 | EST_HUMAN | wh84f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3' |
| 1060 | 14108 | | 2.45 | 5.0E-07 | AA380630.1 | EST_HUMAN | EST83615 Supr cells Homo sapiens cDNA 5' end |
| 3044 | 16101 | | 0.66 | 5.0E-07 | A1831893.1 | EST_HUMAN | wh84f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3' |
| 4878 | 17897 | 30584 | 1.16 | 5.0E-07 | AF149774.1 | NT | Homo sapiens NOD1 protein (NOD1) gene, exons 4 through 14 and complete cds |
| 6242 | 18315 | 32545 | 1.23 | 5.0E-07 | U65067.1 | NT | Mus musculus OG-2 homeodomain protein (OG-2) gene, partial cds |
| 7268 | 20001 | 33300 | 1.68 | 5.0E-07 | A1939981.1 | EST_HUMAN | tg06b05.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107853 3' similar to contains Alu repetitive element; contains element A3R repetitive element ; |
| 7268 | 20001 | 33301 | 1.68 | 5.0E-07 | A1939981.1 | EST_HUMAN | tg06b05.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107853 3' similar to contains Alu repetitive element; contains element A3R repetitive element ; |
| 7571 | 20534 | 33892 | 15.74 | 5.0E-07 | AW070885.1 | EST_HUMAN | xy31a02.x1 NCI_CGAP_Br18 Homo sapiens cDNA clone IMAGE:2568362 3' similar to gb:X16341 CYTOCHROME C OXIDASE POLYPEPTIDE VIA-LIVER (HUMAN); |
| 8618 | 21586 | 35002 | 0.87 | 5.0E-07 | Q9WUQ1 | SWISSPROT | ADAM-TS 1 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 1) (ADAMTS-1) (ADAM-TS1) |
| 8835 | 21802 | | 1.86 | 5.0E-07 | P09593 | SWISSPROT | SANTIGEN PROTEIN PRECURSOR |
| 10732 | 23654 | 37147 | 5.39 | 5.0E-07 | A1908587.1 | EST_HUMAN | CM-BT178-220469-014 BT178 Homo sapiens cDNA |
| 11845 | 24728 | 38314 | 3.52 | 5.0E-07 | P11087 | SWISSPROT | COLLAGEN ALPHA 1(I) CHAIN PRECURSOR |
| 11906 | 24787 | | 2.12 | 5.0E-07 | AJ271735.1 | NT | Homo sapiens Xq pseudautosomal region; segment 1/2 |
| 12842 | 25780 | | 4.14 | 5.0E-07 | AW862537.1 | EST_HUMAN | QV0-CT0383-210400-204-b12 CT0383 Homo sapiens cDNA |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 4024 | 17082 | 28984 | 1.81 | 4.0E-07 | AW009602.1 | EST_HUMAN | w84h05.x1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:2504697 3' |
| 7384 | 20354 | | 0.81 | 4.0E-07 | AJ272265.1 | NT | Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8 |
| 7482 | 20448 | 33804 | 1.3 | 4.0E-07 | Q8Z2V6 | SWISSPROT | HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE MHD41) |
| 7482 | 20448 | 33805 | 1.3 | 4.0E-07 | Q8Z2V6 | SWISSPROT | HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE MHD41) |
| 8255 | 21224 | 34634 | 0.53 | 4.0E-07 | AL163207.2 | NT | Homo sapiens chromosome 21 segment HS21C007 |
| 9406 | 22371 | 35806 | 5.52 | 4.0E-07 | AW419134.1 | EST_HUMAN | xy49g11.x1 NCI_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2856548 3' |
| 10486 | 23408 | 36904 | 0.46 | 4.0E-07 | BE901975.1 | EST_HUMAN | 601676748F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959651 5' |
| 10486 | 23408 | 36905 | 0.46 | 4.0E-07 | BE901975.1 | EST_HUMAN | 601676748F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959651 5' |
| 10888 | 23610 | 37105 | 0.47 | 4.0E-07 | AL163218.2 | NT | Homo sapiens chromosome 21 segment HS21C018 |
| 11284 | 24234 | 37760 | 2.6 | 4.0E-07 | A1765528.1 | EST_HUMAN | w81b08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2399703 3' |
| 11284 | 24234 | 37761 | 2.6 | 4.0E-07 | A1765528.1 | EST_HUMAN | w81b08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2399703 3' |
| 11555 | 24495 | | 2.72 | 4.0E-07 | BE001828.1 | EST_HUMAN | PM1-BN0083-030300-003-e12 BN0083 Homo sapiens cDNA |
| 441 | 13515 | 26448 | 4.77 | 3.0E-07 | U19719.1 | NT | Human microtubulin-associated glycoprotein (MFAP2) gene, putative promoter region and alternatively spliced untranslated exons |
| 585 | 13653 | 26567 | 3.11 | 3.0E-07 | AJ271735.1 | NT | Homo sapiens Xq pseudautosomal region; segment 1/2 |
| 1375 | 14409 | 27379 | 2.82 | 3.0E-07 | M89149.1 | NT | Human polymorphic microsatellite DNA |
| 1630 | 14683 | | 2.45 | 3.0E-07 | M84857.1 | NT | Human IgK subgroup I germline gene, exons 1 and 2, V-region 018 allele |
| 2062 | 15080 | | 1.01 | 3.0E-07 | AA526763.1 | EST_HUMAN | ni56b09.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:980825 similar to contains Alu repetitive element; contains L1.13 L1 repetitive element; |
| 2296 | 15308 | 28330 | 2.56 | 3.0E-07 | M99149.1 | NT | Human polymorphic microsatellite DNA |
| 2477 | 15481 | 28505 | 6.03 | 3.0E-07 | BE005077.1 | EST_HUMAN | MFO-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA |
| 2477 | 15481 | 28506 | 6.03 | 3.0E-07 | BE005077.1 | EST_HUMAN | MFO-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA |
| 3047 | 16104 | 29018 | 0.8 | 3.0E-07 | T84704.1 | EST_HUMAN | yd50f12.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:11695 5' |
| 3173 | 16228 | 29144 | 1.71 | 3.0E-07 | P38739 | SWISSPROT | HYPOTHETICAL 63.8 KD PROTEIN IN GUT1-RIM1 INTERGENIC REGION PRECURSOR |
| 4706 | 17727 | | 0.74 | 3.0E-07 | P20740 | SWISSPROT | OVOSTATIN PRECURSOR (OVOMACROGLOBULIN) |
| 4758 | 17778 | 30673 | 8.86 | 3.0E-07 | AV650201.1 | EST_HUMAN | AV650201 GLC Homo sapiens cDNA clone GLCCCD01 3' |
| 4796 | 17813 | 30706 | 0.81 | 3.0E-07 | A1797236.1 | EST_HUMAN | wa86b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347967 3' |
| 5103 | 18113 | 30985 | 2.02 | 3.0E-07 | T57850.1 | EST_HUMAN | yc14h09.s1 Stragelene lung (#837210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gb:M62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN) |
| 5103 | 18113 | 30986 | 2.02 | 3.0E-07 | T57850.1 | EST_HUMAN | yc14h09.s1 Stragelene lung (#837210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gb:M62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN) |
| 5749 | 18943 | 32026 | 9.02 | 3.0E-07 | O89807 | SWISSPROT | PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4) |
| 6085 | 19165 | 32377 | 0.73 | 3.0E-07 | O42280 | SWISSPROT | (PEPTIDYLARGININE DEIMINASE TYPE ALPHA) |

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 6861 | 19814 | | 5.12 | 3.0E-07 | AA816175.1 | EST_HUMAN | cc04c10.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1339880 3' |
| 7752 | 20705 | 34074 | 3.26 | 3.0E-07 | AW797188.1 | EST_HUMAN | QV1-UM0036-200300-115-g02 UM0036 Homo sapiens cDNA |
| 7926 | 20868 | | 1.09 | 3.0E-07 | AI591065.1 | EST_HUMAN | hw28f11.x1 NCL_CGAP_Ov45 Homo sapiens cDNA clone IMAGE:2281037 3' similar to contains Alu repetitive element; contains element MSR1 MSR1 repetitive element ; |
| 13083 | 25614 | | 7.27 | 3.0E-07 | AJ132352.1 | NT | Rattus norvegicus mRNA for 45 kDa secretory protein, partial |
| 31 | 13151 | 26051 | 4.19 | 2.0E-07 | AF262888.1 | NT | Homo sapiens TRF2-interacting telomeric RAP1 protein (RAP1) mRNA, complete cds |
| 155 | 13258 | 26185 | 6.64 | 2.0E-07 | L77569.1 | NT | Homo sapiens DiGeorge syndrome critical region, telomeric end |
| 155 | 13258 | 26186 | 6.64 | 2.0E-07 | L77569.1 | NT | Homo sapiens DiGeorge syndrome critical region, telomeric end |
| 183 | 13283 | 26209 | 152.61 | 2.0E-07 | U39849.1 | NT | Fugu rubripes beta-cytoplasmic(vascular) actin gene, complete cds |
| 749 | 13810 | 26761 | 1.29 | 2.0E-07 | AF003530.1 | NT | Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions |
| 749 | 13810 | 26762 | 1.29 | 2.0E-07 | AF003530.1 | NT | Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions |
| 760 | 13820 | | 0.87 | 2.0E-07 | P11369 | SWISSPROT | RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE] |
| 942 | 13985 | 26947 | 3.12 | 2.0E-07 | AA232260.1 | EST_HUMAN | zr08b07.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650869 3' similar to gb:L31860 GLYCOPHORIN A PRECURSOR (HUMAN); contains Alu repetitive element; |
| 943 | 13988 | 26948 | 7.18 | 2.0E-07 | T63042.1 | EST_HUMAN | yc15g04.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:80790 3' similar to contains L1 repetitive element ; |
| 1167 | 14208 | 27162 | 1.16 | 2.0E-07 | Q26768 | SWISSPROT | IIG AUTOANTIGEN |
| 1604 | 14636 | 27613 | 2.35 | 2.0E-07 | Q09701 | SWISSPROT | HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I |
| 3633 | 16676 | 29656 | 0.86 | 2.0E-07 | BF131397.1 | EST_HUMAN | 601818916F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4044881 5' |
| 3700 | 16743 | 29656 | 17.94 | 2.0E-07 | AF125348.1 | NT | Homo sapiens cavedin 1 (CAV1) gene, exon 3 and partial cds |
| 4196 | 17228 | 30115 | 1.42 | 2.0E-07 | AI873563.1 | EST_HUMAN | wk20h04.x1 NCL_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2412918 3' |
| 5417 | 18520 | 31397 | 1.71 | 2.0E-07 | AW898066.1 | EST_HUMAN | RC3-NN0066-260400-021-g11 NN0066 Homo sapiens cDNA |
| 6702 | 25665 | 33037 | 0.9 | 2.0E-07 | AW449968.1 | EST_HUMAN | UI-H-B13-ake-b-01-0-UI.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734008 3' |
| 6820 | 19874 | 33163 | 1.63 | 2.0E-07 | AI208715.1 | EST_HUMAN | qg56405.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839177 3' |
| 6832 | 19885 | 33178 | 0.81 | 2.0E-07 | AA572953.1 | EST_HUMAN | nm33a06.s1 NCL_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:1081838 similar to contains Alu repetitive element; |
| 8813 | 21780 | | 4.23 | 2.0E-07 | AV729390.1 | EST_HUMAN | AV729390 HTC Homo sapiens cDNA clone HTCAE002 5' |
| 9043 | 22009 | 35430 | 0.99 | 2.0E-07 | AA035198.1 | EST_HUMAN | zk27g09.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471808 3' |
| 10119 | 23045 | | 1.8 | 2.0E-07 | AL163303.2 | NT | Homo sapiens chromosome 21 segment HS21C103 |
| 10630 | 23552 | 37052 | 6.11 | 2.0E-07 | AW892507.1 | EST_HUMAN | CM4-NN0003-280300-124-e06 NN0003 Homo sapiens cDNA |
| 10855 | 23775 | 37272 | 0.92 | 2.0E-07 | P00751 | SWISSPROT | COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PROPERDIN FACTOR B) (GLYCINE-RICH BETA GLYCOPROTEIN) (GBG) (PBF2) |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 10855 | 23775 | 37273 | 0.92 | 2.0E-07 | P00751 | SWISSPROT | COMPLEMENT FACTOR B PRECURSOR (C3/05 CONVERTASE) (PROPERDIN FACTOR B) |
| 12138 | 25503 | | 2.86 | 2.0E-07 | BE153717.1 | EST_HUMAN | (GLYCINE-RICH BETA GLYCOPROTEIN) (GBG) (PBF2) |
| 12224 | 25781 | | 1.86 | 2.0E-07 | AI732462.1 | EST_HUMAN | PMO-HT0339-280100-006-H07 HT0339 Homo sapiens cDNA |
| 1104 | 14148 | | 1.46 | 1.0E-07 | AL163282.2 | NT | zn85h11 x5 Stralagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565029 3' similar to contains THR.b2 THR repetitive element; |
| 2838 | 14558 | 27529 | 2.95 | 1.0E-07 | P09256 | SWISSPROT | Homo sapiens chromosome 21 segment HS21C082 |
| 3757 | 14148 | | 1.25 | 1.0E-07 | AL163282.2 | NT | GLYCOPROTEIN GPV |
| 4321 | 17350 | 30234 | 3.01 | 1.0E-07 | AV718662.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C082 |
| 4321 | 17350 | 30235 | 3.01 | 1.0E-07 | AV718662.1 | EST_HUMAN | AV718662 GLC Homo sapiens cDNA clone GLCFNF04 5' |
| 6652 | 19709 | 32986 | 0.82 | 1.0E-07 | U82671.2 | NT | AV718662 GLC Homo sapiens cDNA clone GLCFNF04 5' |
| 7050 | 20072 | 33378 | 4.44 | 1.0E-07 | BE047871.1 | EST_HUMAN | Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI> |
| 7050 | 20072 | 33379 | 4.44 | 1.0E-07 | BE047871.1 | EST_HUMAN | tz43d06.y1 NCI CGAP_Brm52 Homo sapiens cDNA clone IMAGE:2291339 5' |
| 7735 | 20690 | 34054 | 9.42 | 1.0E-07 | N55081.1 | EST_HUMAN | tz43d06.y1 NCI CGAP_Brm52 Homo sapiens cDNA clone IMAGE:2291339 5' |
| 7910 | 20853 | 34240 | 0.69 | 1.0E-07 | BF375909.1 | EST_HUMAN | y43c07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:245484 3' |
| 7910 | 20853 | 34241 | 0.69 | 1.0E-07 | BF375909.1 | EST_HUMAN | PM4-TN0024-030800-002-b05 TN0024 Homo sapiens cDNA |
| 7940 | 20882 | 34272 | 1.27 | 1.0E-07 | AL163281.2 | NT | PM4-TN0024-030800-002-b05 TN0024 Homo sapiens cDNA |
| 8558 | 21526 | 34944 | 2.28 | 1.0E-07 | P97435 | SWISSPROT | Homo sapiens chromosome 21 segment HS21C081 |
| 8558 | 21526 | 34945 | 2.28 | 1.0E-07 | P97435 | SWISSPROT | ENTEROPEPTIDASE (ENTEROKINASE) |
| 9306 | 22271 | 35702 | 2.83 | 1.0E-07 | AA693576.1 | EST_HUMAN | ENTEROPEPTIDASE (ENTEROKINASE) |
| 9625 | 22569 | 36018 | 0.96 | 1.0E-07 | P57110 | SWISSPROT | z15te10.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:434346 3' |
| 9975 | 22902 | 36368 | 0.53 | 1.0E-07 | BE327843.1 | EST_HUMAN | ADAM-TS 8 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 8) (ADAMTS-8) (ADAM-TS8) (METH-2) |
| 10296 | 23221 | 36705 | 2.5 | 1.0E-07 | BF674524.1 | EST_HUMAN | hu28h06.x1 NCI CGAP_Met15 Homo sapiens cDNA clone IMAGE:3171419 3' similar to contains MER18.13 |
| 10304 | 23229 | 36712 | 1.26 | 1.0E-07 | AA386311.1 | EST_HUMAN | MER18 repetitive element; |
| 10831 | 23782 | | 2.53 | 1.0E-07 | AL163282.2 | NT | 602137714FT NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274426 5' |
| 12500 | 25756 | 31517 | 4.03 | 1.0E-07 | BE048770.1 | EST_HUMAN | EST185054 Brain IV Homo sapiens cDNA |
| 12634 | 25320 | | 1.59 | 1.0E-07 | XG4467.1 | NT | Homo sapiens chromosome 21 segment HS21C082 |
| 12793 | 25423 | | 1.89 | 1.0E-07 | X51755.1 | NT | hr53c11.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132212 3' similar to TR:O95722 O95722 |
| 7498 | 20463 | 33823 | 0.84 | 9.0E-08 | AI539362.1 | EST_HUMAN | DJ1163J1.1; |
| | | | | | | | H.sapiens ALAD gene for porphobilinogen synthase |
| | | | | | | | Human lamblambda-immunoglobulin constant region complex (germline) |
| | | | | | | | tes1b06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090195 3' |

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Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|-----------------------------|-------------------------------|---|
| 10247 | 23172 | 36661 | 2.18 | 9.0E-08 | AV734819.1 | EST_HUMAN | AV734819 cDNA Homo sapiens cDNA clone cdABFB06 5' |
| 11515 | 24456 | 38006 | 1.46 | 9.0E-08 | AI891052.1 | EST_HUMAN | wn30a07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2446932 3' similar to contains OFR.12 |
| 11977 | 24854 | 38452 | 2.32 | 9.0E-08 | AL163301.2 | NT | OFR repetitive element; |
| 12453 | 25212 | | 3.51 | 9.0E-08 | AJ251973.1 | NT | Homo sapiens chromosome 21 segment HS21C101 |
| 609 | 15845 | | 2.97 | 8.0E-08 | AI911352.1 | EST_HUMAN | Homo sapiens partial stein-1 gene |
| 1052 | 14098 | | 0.77 | 8.0E-08 | BE795469.1 | EST_HUMAN | wd16b05.x1 Soares, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2328273 3' |
| 3555 | 16601 | | 2.07 | 8.0E-08 | BE795469.1 | EST_HUMAN | 601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5' |
| | | | | | | | 601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5' |
| 9091 | 22057 | 35482 | 3.38 | 8.0E-08 | AI752387.1 | EST_HUMAN | cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random |
| 9091 | 22057 | 35483 | 3.38 | 8.0E-08 | AI752387.1 | EST_HUMAN | cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random |
| 9985 | 22912 | 36377 | 2.8 | 8.0E-08 | AW970693.1 | EST_HUMAN | EST382776 MAGE resequences, MAGK Homo sapiens cDNA |
| 10928 | 23848 | 37363 | 0.46 | 8.0E-08 | AF111167.2 | NT | Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene |
| 11576 | 24513 | | 2.53 | 8.0E-08 | AF253417.1 | NT | Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds |
| 81 | 13197 | 26121 | 4.07 | 7.0E-08 | Q02357 | SWISSPROT | ANKYRIN 1 (ERYTHROCYTE ANKYRIN) |
| 1363 | 14397 | 27368 | 17.17 | 7.0E-08 | X04809.1 | NT | Rat mRNA for ribosomal protein L31 |
| 3569 | 16634 | 29553 | 0.7 | 7.0E-08 | P15305 | SWISSPROT | DYNEIN HEAVY CHAIN (DYHC) |
| 3569 | 16634 | 29554 | 0.7 | 7.0E-08 | P15305 | SWISSPROT | DYNEIN HEAVY CHAIN (DYHC) |
| 3949 | 16989 | 29904 | 0.9 | 7.0E-08 | P01606 | SWISSPROT | IG KAPPA CHAIN V-J REGION OU |
| 3949 | 16989 | 29905 | 0.9 | 7.0E-08 | P01606 | SWISSPROT | IG KAPPA CHAIN V-J REGION OU |
| 11165 | 24123 | | 2.33 | 7.0E-08 | AI53743.1 | EST_HUMAN | cong3.P11.A5 contig Homo sapiens cDNA 3' |
| 11982 | 24859 | 38454 | 4.32 | 7.0E-08 | U24070.1 | NT | Rattus norvegicus Munc13-1 mRNA, complete cds |
| 12899 | 16634 | 29553 | 1.55 | 7.0E-08 | P15305 | SWISSPROT | DYNEIN HEAVY CHAIN (DYHC) |
| 12899 | 16634 | 29554 | 1.55 | 7.0E-08 | P15305 | SWISSPROT | DYNEIN HEAVY CHAIN (DYHC) |
| 12976 | 25541 | | 1.9 | 7.0E-08 | AJ131016.1 | NT | Homo sapiens SCL gene locus |
| 818 | 13876 | 26824 | 4.23 | 6.0E-08 | AL163248.2 | NT | Homo sapiens chromosome 21 segment HS21C048 |
| 818 | 13876 | 26825 | 4.23 | 6.0E-08 | AL163248.2 | NT | Homo sapiens chromosome 21 segment HS21C048 |
| 2371 | 15379 | 28403 | 2.72 | 6.0E-08 | BE144398.1 | EST_HUMAN | MR0-H70166-191199-004-g09 HT0166 Homo sapiens cDNA |
| 4276 | 17305 | 30184 | 1.28 | 6.0E-08 | AL163248.2 | NT | Homo sapiens chromosome 21 segment HS21C048 |
| | | | | | | | Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds's |
| 8162 | 21100 | 34499 | 0.49 | 6.0E-08 | L44140.1 | NT | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| 8283 | -21252 | | 0.74 | 6.0E-08 | P06547 | SWISSPROT | |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 9683 | 22636 | | 0.54 | 6.0E-08 | AA827075.1 | EST_HUMAN | ab56c05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1335368 3' similar to contains MER12.b3 MER12 repetitive element; |
| 11744 | 24629 | 38208 | 1.91 | 6.0E-08 | P11369 | SWISSPROT | RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE] |
| 85 | 13201 | 26125 | 3.22 | 5.0E-08 | AL163303.2 | NT | Homo sapiens chromosome 21 segment HS21C103 |
| 2245 | 15259 | 28286 | 1.95 | 5.0E-08 | AA493851.1 | EST_HUMAN | nt03b09.s1 NCI_CGAP_Thyl Homo sapiens cDNA clone IMAGE:943193 similar to contains Alu repetitive element; |
| 12185 | 25032 | | 10.16 | 5.0E-08 | P06681 | SWISSPROT | COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE) |
| 12382 | 25162 | 31814 | 1.63 | 5.0E-08 | AW851878.1 | EST_HUMAN | QV0-CT0225-13:099-034-a12 CT0225 Homo sapiens cDNA |
| 1776 | 14804 | 27789 | 1.07 | 4.0E-08 | P25723 | SWISSPROT | DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR |
| 1775 | 14804 | 27790 | 1.07 | 4.0E-08 | P25723 | SWISSPROT | DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR |
| 3077 | 16134 | | 0.95 | 4.0E-08 | AJ078417.1 | EST_HUMAN | aa05e02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1674458 3' similar to contains Alu repetitive element; |
| 3834 | 16974 | 29888 | 0.76 | 4.0E-08 | U82668.1 | NT | Homo sapiens shox gene, alternatively spliced products, complete cds |
| 6545 | 19606 | 32868 | 0.91 | 4.0E-08 | P52624 | SWISSPROT | URIDINE PHOSPHORYLASE (UDRPASE) |
| 9150 | 22116 | 35542 | 0.6 | 4.0E-08 | O15393 | SWISSPROT | TRANSMEMBRANE PROTEASE, SERINE 2 |
| 9494 | 22458 | 35898 | 1.32 | 4.0E-08 | L42571.1 | NT | Cicetulus griseus ribosomal transcription factor (UBF2) mRNA, complete cds |
| 10003 | 22830 | | 0.82 | 4.0E-08 | P08547 | SWISSPROT | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| 10693 | 23615 | | 0.65 | 4.0E-08 | AJ016342.1 | EST_HUMAN | at78d12.s1 Soares_fetal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1622903 3' |
| 10752 | 23674 | 37171 | 3.67 | 4.0E-08 | AJ050027.1 | EST_HUMAN | an22d10.x1 Geesler Wilms tumor Homo sapiens cDNA clone IMAGE:1699411 3' similar to contains Alu repetitive element; contains element MER22 repetitive element ; |
| 11411 | 24355 | 37889 | 1.51 | 4.0E-08 | AA393627.1 | EST_HUMAN | zt76b08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728247 5' similar to TR:G505579 |
| 11411 | 24355 | 37890 | 1.51 | 4.0E-08 | AA393627.1 | EST_HUMAN | zt76b08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728247 5' similar to TR:G505579 |
| 11426 | 24370 | 37807 | 3.11 | 4.0E-08 | BF692493.1 | EST_HUMAN | G505579 NA/CA,K-EXCHANGER. ; |
| 11426 | 24370 | 37908 | 3.11 | 4.0E-08 | BF692493.1 | EST_HUMAN | G02248024F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333300 5' |
| 12190 | 25907 | | 4.96 | 4.0E-08 | W76159.1 | EST_HUMAN | G02248024F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333300 5' |
| 12830 | 25448 | | 1.84 | 4.0E-08 | AJ343353.1 | EST_HUMAN | z06g03.r1 Soares_fetal_heart_NbH19W Homo sapiens cDNA clone IMAGE:345596 5' similar to contains L1.t1 L1 repetitive element ; |
| 3438 | 16485 | 29404 | 0.94 | 3.0E-08 | M83242.1 | NT | ib95a11.x1 NCI_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:2062076 3' similar to contains MER18.b3 MER18 repetitive element ; |
| 5692 | 18787 | 31958 | 3.06 | 3.0E-08 | BE018348.1 | EST_HUMAN | Macaca fascicularis apolipoprotein A-1 gene, complete cds |
| | | | | | | | bb79a10.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR:Q9Z158 Q9Z158 SYNTAXIN 17. ; |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 7168 | 18399 | 31245 | 4.23 | 3.0E-08 | AI792737.1 | EST_HUMAN | qs76f1.1.y6 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:1944045 5' |
| 7787 | 20740 | 34113 | 1.41 | 3.0E-08 | AL163246.2 | NT | Homo sapiens chromosome 21 segment HS21C046 |
| 8025 | 20962 | | 3.85 | 3.0E-08 | AI436352.1 | EST_HUMAN | th93h09.x1 Soares_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126273 3' similar to TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ; |
| 10258 | 23183 | | 0.57 | 3.0E-08 | AF065066.1 | NT | Homo sapiens MHC class 1 region |
| 12157 | 25013 | | 2.76 | 3.0E-08 | R18420.1 | EST_HUMAN | y902f04.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:30948 5' similar to contains Alu repetitive element |
| 207 | 13308 | | 10.54 | 2.0E-08 | AW302996.1 | EST_HUMAN | xs8706.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2767139 3' |
| 230 | 13330 | | 8.83 | 2.0E-08 | AA425598.1 | EST_HUMAN | zw48f07.r1 Soares total_fetus_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:773317 5' similar to contains Alu repetitive element; contains element MER15 repetitive element ; |
| 497 | 13569 | 26492 | 1.3 | 2.0E-08 | AF198349.1 | NT | Gallus gallus Dach2 protein (Dach2) mRNA, complete cds |
| 661 | 13727 | 26651 | 9.73 | 2.0E-08 | AW886438.1 | EST_HUMAN | MR0-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA |
| 661 | 13727 | 26652 | 9.73 | 2.0E-08 | AW886438.1 | EST_HUMAN | MR0-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA |
| 992 | 14044 | | 17 | 2.0E-08 | BE280477.1 | EST_HUMAN | 601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5' |
| 1346 | 14381 | 27350 | 1.93 | 2.0E-08 | AL163247.2 | NT | Homo sapiens chromosome 21 segment HS21C047 |
| 1755 | 14784 | | 1.87 | 2.0E-08 | BE734871.1 | EST_HUMAN | 601570463F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845199 5' |
| 1872 | 14897 | | 3.57 | 2.0E-08 | AW270271.1 | EST_HUMAN | xp43f1.1.x1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743149 3' |
| 2550 | 15552 | | 1.7 | 2.0E-08 | K00216.1 | NT | Sheep His-IRNA-GUG |
| 3221 | 16276 | 29200 | 8.15 | 2.0E-08 | O42280 | SWISSPROT | WNT-14 PROTEIN PRECURSOR |
| 3221 | 16276 | 29201 | 8.15 | 2.0E-08 | O42280 | SWISSPROT | WNT-14 PROTEIN PRECURSOR |
| 3873 | 16912 | | 1.82 | 2.0E-08 | AW813620.1 | EST_HUMAN | RC3-ST0197-161099-012-b03 ST0197 Homo sapiens cDNA |
| 4104 | 17138 | 30033 | 0.68 | 2.0E-08 | U82668.1 | NT | Homo sapiens shox gene, alternatively spliced products, complete cds |
| 4434 | 17461 | | 1.2 | 2.0E-08 | AA459040.1 | EST_HUMAN | aa26c07.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814380 5' similar to contains L1.12 L1 repetitive element ; |
| 4994 | 18009 | | 2.97 | 2.0E-08 | AW572881.1 | EST_HUMAN | he17h08.x2 NCI_CGAP_CW11 Homo sapiens cDNA clone IMAGE:2818327 3' similar to contains Alu repetitive element ; |
| 5719 | 18813 | 31992 | 1.25 | 2.0E-08 | AA813204.1 | EST_HUMAN | ai80h1.1.s1 Soares_testis_NHT Homo sapiens cDNA clone 1377185 3' |
| 5932 | 19018 | 32213 | 0.99 | 2.0E-08 | AW088924.1 | EST_HUMAN | xd32c04.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2595462 3' similar to contains MER18.b3 MER18 MER18 repetitive element ; |
| 8337 | 21306 | 34721 | 1.89 | 2.0E-08 | P10272 | SWISSPROT | POL POLYPROTEIN [CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE] |
| 8447 | 21416 | 34829 | 1.47 | 2.0E-08 | AA490121.1 | EST_HUMAN | ab02g06.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839674 3' |
| 9440 | 22404 | | 0.77 | 2.0E-08 | AU139978.1 | EST_HUMAN | AU139978 PLACE1 Homo sapiens cDNA clone PLACE1011719 5' |

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Table 4
Single Exon Probes Expressed In Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 10886 | 23806 | 37310 | 0.8 | 2.0E-08 | N76097.1 | EST_HUMAN | yw2f02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248283 5' similar to contains LTR1.B3 LTR1 repetitive element ; |
| 10886 | 23806 | 37311 | 0.8 | 2.0E-08 | N76097.1 | EST_HUMAN | yw2f02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248283 5' similar to contains LTR1.B3 LTR1 repetitive element ; |
| 12472 | 25221 | | 1.88 | 2.0E-08 | AL163284.2 | NT | Homo sapiens chromosome 21 segment HS21C084 |
| 12982 | 25953 | | 1.4 | 2.0E-08 | 11431676 | NT | Homo sapiens hypothetical protein FLJ11342 (FLJ11342), mRNA |
| 1510 | 15930 | 27513 | 1.42 | 1.0E-08 | P31792 | SWISSPROT | POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE] |
| 1790 | 14819 | 27804 | 2.12 | 1.0E-08 | AF125348.1 | NT | Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds |
| 2067 | 15084 | | 2.49 | 1.0E-08 | BE141959.1 | EST_HUMAN | PM2-HT0130-150999-001-f12 HT0130 Homo sapiens cDNA |
| 3206 | 16261 | 29181 | 1.19 | 1.0E-08 | BE246844.1 | EST_HUMAN | TCBAP1D5232 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP5232 |
| 3206 | 16261 | 29182 | 1.19 | 1.0E-08 | BE246844.1 | EST_HUMAN | TCBAP1D5232 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP5232 |
| 5680 | 18775 | 31947 | 4.5 | 1.0E-08 | AJ010770.1 | NT | Homo sapiens hyperion gene, exons 1-50 |
| 8046 | 20983 | 34380 | 0.98 | 1.0E-08 | P19474 | SWISSPROT | 52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) |
| 8369 | 21338 | 34749 | 0.47 | 1.0E-08 | AL163302.2 | NT | Homo sapiens chromosome 21 segment HS21C102 |
| 8468 | 21435 | 34852 | 0.56 | 1.0E-08 | AF224569.1 | NT | Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds |
| 8468 | 21435 | 34853 | 0.56 | 1.0E-08 | AF224689.1 | NT | Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds |
| 8892 | 21858 | 35280 | 1.89 | 1.0E-08 | AJ015304.1 | EST_HUMAN | alpha5a05.s1 Soares Testis_NHT Homo sapiens cDNA clone IMAGE:1618736 3' |
| 9559 | 22521 | | 0.46 | 1.0E-08 | P09593 | SWISSPROT | S-ANTIGEN PROTEIN PRECURSOR |
| 9560 | 22522 | 35970 | 0.68 | 1.0E-08 | BE072572.1 | EST_HUMAN | PM2-BT0546-210100-004-302 BT0546 Homo sapiens cDNA |
| 10325 | 23249 | 36728 | 0.81 | 1.0E-08 | P79110 | SWISSPROT | TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRANSPORT PROTEIN) (CTP) |
| 10921 | 23841 | 37357 | 0.67 | 1.0E-08 | P98053 | SWISSPROT | (TRICARBOXYLATE CARRIER PROTEIN) |
| 11644 | 24581 | 38149 | 3.4 | 1.0E-08 | AF044083.1 | NT | Homo sapiens major histocompatibility locus class III region |
| 12129 | 24998 | 38602 | 1.5 | 1.0E-08 | P29315 | SWISSPROT | RIBONUCLEASE INHIBITOR |
| 12129 | 24998 | 38603 | 1.5 | 1.0E-08 | P29315 | SWISSPROT | RIBONUCLEASE INHIBITOR |
| 12569 | 25281 | | 3.12 | 1.0E-08 | X51755.1 | NT | Human lambda-immunoglobulin constant region complex (germline) |
| 12940 | 25520 | | 1.68 | 1.0E-08 | X51755.1 | NT | Human lambda-immunoglobulin constant region complex (germline) |
| 4271 | 17300 | 30179 | 4.15 | 9.0E-09 | AL163279.2 | NT | Homo sapiens chromosome 21 segment HS21C079 |
| 4271 | 17300 | 30180 | 4.15 | 9.0E-09 | AL163279.2 | NT | Homo sapiens chromosome 21 segment HS21C079 |
| 10422 | 23344 | | 0.53 | 9.0E-08 | T97950.1 | EST_HUMAN | ys58a12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121918 3' |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 6628 | 19886 | | 1.59 | 8.0E-09 | AI270815.1 | EST_HUMAN | qu86c11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:1978964 3' similar to contains L1.13 L1 repetitive element ; |
| 7479 | 20445 | 33801 | 7.91 | 8.0E-09 | AI183500.1 | EST_HUMAN | qd42e07.x1 Soares fetal heart NbrHH19W Homo sapiens cDNA clone IMAGE:1732164 3' similar to contains MSR1.11 MSR1 repetitive element ; |
| 8333 | 21302 | 34719 | 3.04 | 8.0E-09 | AW900159.1 | EST_HUMAN | CMD-NN1004-100300-273-e08 NN1004 Homo sapiens cDNA |
| 9340 | 22305 | | 2.64 | 8.0E-09 | AA938892.1 | EST_HUMAN | qp74d08.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1582575 3' |
| 3621 | 16664 | | 1.91 | 7.0E-09 | D88842.1 | NT | Homo sapiens DNA for 3-ketacyl-CoA thiolase beta-subunit of mitochondrial trifunctional protein, exon 2, 3 |
| 4034 | 17072 | | 1.22 | 7.0E-09 | U50871.1 | NT | Human familial Alzheimer's disease (STM2) gene, complete cds |
| 8234 | 21203 | | 0.56 | 7.0E-09 | BF108755.1 | EST_HUMAN | 745e10.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29.b2 MER29 repetitive element ; |
| 8382 | 21351 | | 0.91 | 7.0E-09 | AA256200.1 | EST_HUMAN | z60c05.r1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:681992 5' similar to contains L1.12 L1 repetitive element ; |
| 9615 | 22559 | 36008 | 3.06 | 7.0E-09 | LO9709.1 | NT | Human lysosomal membrane glycoprotein-2 (LAMP2) gene, 5' end and flanking region |
| 10543 | 23465 | 36960 | 1.17 | 7.0E-09 | BE254850.1 | EST_HUMAN | 60111173F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351834 5' |
| 10711 | 23633 | | 0.59 | 7.0E-09 | AA058826.1 | EST_HUMAN | z58e07.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381156 3' similar to contains L1.12 L1 repetitive element ; |
| 11032 | 23996 | | 3.65 | 7.0E-09 | T97650.1 | EST_HUMAN | ye58a12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121918 3' |
| 2162 | 15178 | | 0.98 | 6.0E-09 | AL040439.1 | EST_HUMAN | DKFZp434C0514_t1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434C0514 5' |
| 4059 | 17095 | 29990 | 0.96 | 6.0E-09 | AA557940.1 | EST_HUMAN | nl17a11.s1 NCI_CGAP_HSC1 Homo sapiens cDNA clone IMAGE:1040924 similar to contains L1.12 L1 repetitive element ; |
| 5017 | 18031 | 30917 | 5.44 | 6.0E-09 | BE169421.1 | EST_HUMAN | PM1-H70527-160200-001-h05 HT0527 Homo sapiens cDNA |
| 5454 | 18558 | 31487 | 9.55 | 6.0E-09 | AW195784.1 | EST_HUMAN | xn85h08.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701311 3' |
| 8922 | 21988 | 35315 | 0.88 | 6.0E-09 | BE161653.1 | EST_HUMAN | MR3-HT0448-260300-201-h12 HT0448 Homo sapiens cDNA |
| 9531 | 22494 | 35942 | 2.12 | 6.0E-09 | 4503710 | NT | Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA |
| 10639 | 23561 | | 4.42 | 6.0E-09 | AF200923.2 | NT | Homo sapiens testis-specific kinase substrate (TSKS) gene, complete cds |
| 1413 | 14448 | 27418 | 4.43 | 5.0E-09 | BE149264.1 | EST_HUMAN | RC2-HT0252-120200-014-h10 HT0252 Homo sapiens cDNA |
| 1870 | 14895 | 27894 | 1.02 | 5.0E-09 | AL163284.2 | NT | Homo sapiens chromosome 21 segment HS21C084 |
| 6550 | 19611 | 32872 | 2.31 | 5.0E-09 | AA359454.1 | EST_HUMAN | EST168748 Fetal lung II Homo sapiens cDNA 5' end |
| | | | | | | | Human gemline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S> |
| 7025 | 18357 | 31277 | 0.59 | 5.0E-09 | U66059.1 | NT | |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|--|--------------------------|-------------------------------|---|
| 8932 | 21898 | 35326 | 0.5 | 5.0E-09 | P37071 | SWISSPROT | OLFACTORY RECEPTOR-LIKE PROTEIN COR5 |
| 10455 | 23377 | 36870 | 2.53 | 5.0E-09 | AW799667.1 | EST_HUMAN | PM2-JM0053-240300-005-c09 UM0053 Homo sapiens cDNA |
| 522 | 13593 | | 1.81 | 4.0E-09 | AL163282.2 | NT | Homo sapiens chromosome 21 segment HS21C082 |
| 966 | 14018 | | 2.79 | 4.0E-09 | AL163285.2 | NT | Homo sapiens chromosome 21 segment HS21C085 |
| 1465 | 14498 | 27472 | 2.79 | 4.0E-09 | 9558718 | NT | Homo sapiens hypothetical protein (AF038169), mRNA |
| 2038 | 15057 | 28075 | 1.63 | 4.0E-09 | AF175325.1 | NT | Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds |
| 2038 | 15057 | 28076 | 1.63 | 4.0E-09 | AF175325.1 | NT | Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds |
| 2436 | 15443 | 28461 | 2.87 | 4.0E-09 | AA350878.1 | EST_HUMAN | EST58385 Infant brain Homo sapiens cDNA 5' end similar to similar to heat shock protein, 90 kDa |
| 8179 | 21149 | 34556 | 0.66 | 4.0E-09 | AA495747.1 | EST_HUMAN | zwo4c08.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:768298 5' |
| 8867 | 21834 | 35255 | 0.66 | 4.0E-09 | T64942.1 | EST_HUMAN | yd11a07.s1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:66804 3' |
| | | | | | | | hu09e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13 |
| 2359 | 15367 | 28389 | 4.28 | 3.0E-09 | BE222239.1 | EST_HUMAN | MER18 repetitive element ; |
| 2560 | 15561 | 28579 | 1.39 | 3.0E-09 | BE222239.1 | EST_HUMAN | hu09e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13 |
| 2569 | 15556 | 28674 | 1.03 | 3.0E-09 | P23249 | SWISSPROT | MER18 repetitive element ; PROTEIN MOV-10 |
| 3340 | 16391 | 29312 | 1.15 | 3.0E-09 | BE222239.1 | EST_HUMAN | hu09e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13 |
| 3388 | 16437 | | 0.79 | 3.0E-09 | AA442272.1 | EST_HUMAN | MER18 repetitive element ; |
| 4124 | 17157 | | 0.69 | 3.0E-09 | X16674.1 | NT | zvo4a04.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757422 5' |
| 4457 | 17483 | 30371 | 3.77 | 3.0E-09 | AF175325.1 | NT | H.sapiens PADPRP-I gene for NAD(+) ADP-ribosyltransferase |
| 4540 | 17563 | 30450 | 3.44 | 3.0E-09 | Q9Y3R5 | SWISSPROT | Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds |
| | | | | | | | 258.1 KDA PROTEIN C21ORF5 (K1AA0933) |
| 5225 | 18233 | | 0.99 | 3.0E-09 | D86842.1 | NT | Homo sapiens DNA for 3-ketoacyl-CoA thiolase beta-subunit of mitochondrial trifunctional protein, exon 2, 3 |
| 8232 | 21201 | 34607 | 1.08 | 3.0E-09 | BE465780.1 | EST_HUMAN | hy80a02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3194090 3' similar to TR:O55091 |
| 10609 | 23531 | 37026 | 1.84 | 3.0E-09 | AL163247.2 | NT | O55091 IMPACT PROTEIN ; |
| 11361 | 24310 | 37836 | 3.06 | 3.0E-09 | BF109843.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C047 |
| 11361 | 24310 | 37837 | 3.06 | 3.0E-09 | BF109843.1 | EST_HUMAN | 7172c08.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3' |
| 813 | 13871 | | 10.64 | 2.0E-09 | X16674.1 | NT | 7172c08.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3' |
| 1263 | 14298 | 27267 | 5.84 | 2.0E-09 | AL163284.2 | NT | H.sapiens PADPRP-I gene for NAD(+) ADP-ribosyltransferase |
| 1667 | 14699 | | 9.53 | 2.0E-09 | AL118573.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C084 |
| 2334 | 15345 | 28366 | 2.58 | 2.0E-09 | Q9Y3R5 | SWISSPROT | DKFZp761B1710.1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761B1710 5' |
| 3058 | 16968 | 29913 | 3.67 | 2.0E-09 | O60241 | SWISSPROT | 258.1 KDA PROTEIN C21ORF5 (K1AA0933) |
| 4039 | 17077 | 29977 | 1.65 | 2.0E-09 | AI263479.1 | EST_HUMAN | BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 2 PRECURSOR |
| | | | | | | | q107d09.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1855793 3' |

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Table 4
Single Exon Probes Expressed In Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 5198 | 18207 | 31081 | 0.88 | 2.0E-09 | M23161.1 | NT | Human transposon-like element mRNA |
| 5808 | 18898 | 32081 | 0.69 | 2.0E-09 | A1004082.1 | EST_HUMAN | ol47b09.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1618897 3' |
| 6273 | 18946 | | 0.65 | 2.0E-09 | AL163249.2 | NT | Homo sapiens chromosome 21 segment HS21C049 |
| 6947 | 20171 | | 0.8 | 2.0E-09 | AA357407.1 | EST_HUMAN | EST68142 Kidney/IX Homo sapiens cDNA 5' end similar to EST containing L1 repeat |
| | | | | | | | z63h06.r1 Soares_total_fetus_Nb2-IF8_9w Homo sapiens cDNA clone IMAGE:786187 5' similar to contains |
| 7884 | 20842 | 34006 | 7.6 | 2.0E-09 | AA461430.1 | EST_HUMAN | Alu repetitive element; |
| 7768 | 20719 | 34092 | 0.63 | 2.0E-09 | W28834.1 | EST_HUMAN | 52d11 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA |
| 8126 | 21063 | 34461 | 0.82 | 2.0E-09 | AW862126.1 | EST_HUMAN | MR1-CT0352-240200-105-b06 CT0352 Homo sapiens cDNA |
| 9062 | 22028 | 35452 | 2.25 | 2.0E-09 | AJ271735.1 | NT | Homo sapiens Xq pseudautosomal region; segment 1/2 |
| 12705 | 13871 | | 22.38 | 2.0E-09 | X16674.1 | NT | H. sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase |
| 12772 | 25875 | | 1.67 | 2.0E-09 | AA226070.1 | EST_HUMAN | nc11602.r1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:1007810 similar to contains Alu repetitive |
| 12778 | 25829 | | 1.47 | 2.0E-09 | AW301637.1 | EST_HUMAN | element; |
| 12913 | 25492 | | 1.98 | 2.0E-09 | U82688.1 | NT | xt99a02.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2768234 3' |
| 1111 | 14155 | 27105 | 1.1 | 1.0E-09 | 5031624 | NT | Homo sapiens shox gene, alternatively spliced products, complete cds |
| 1111 | 14155 | 27106 | 1.1 | 1.0E-09 | 5031624 | NT | Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA |
| 1638 | 14870 | | 0.91 | 1.0E-09 | AJ228041.1 | NT | Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA |
| | | | | | | | Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3 |
| 2510 | 15513 | | 1.16 | 1.0E-09 | A1356086.1 | EST_HUMAN | qy64e11.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2016812 3' similar to contains MER12.12 |
| | | | | | | | MER12 repetitive element; |
| 2900 | 15959 | 28878 | 1.83 | 1.0E-09 | U80017.1 | NT | Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory |
| 2937 | 15995 | 28915 | 4.07 | 1.0E-09 | M28689.1 | NT | protein (nrip) and survival motor neuron protein (smn) genes, complete cds |
| 2937 | 15995 | 28916 | 4.07 | 1.0E-09 | M28689.1 | NT | Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds |
| 3051 | 18108 | 28022 | 0.89 | 1.0E-09 | BE535440.1 | EST_HUMAN | Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds |
| | | | | | | | 601058602F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3445177 5' |
| | | | | | | | zh35b03.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:414028 3' similar to contains |
| 4836 | 17853 | | 5.63 | 1.0E-09 | AA719287.1 | EST_HUMAN | Alu repetitive element/contains element MER22 repetitive element; |
| | | | | | | | yc22c09.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:81424 5' similar to contains Alu |
| 5162 | 18171 | 31050 | 0.84 | 1.0E-09 | T60216.1 | EST_HUMAN | repetitive element/contains MER28 repetitive element; |
| 5581 | 18677 | 31640 | 0.82 | 1.0E-09 | AL163283.2 | NT | Homo sapiens chromosome 21 segment HS21C083 |
| 5930 | 19016 | 32211 | 1.35 | 1.0E-09 | U07000.1 | NT | Human breakpoint cluster region (BCR) gene, complete cds |
| 6267 | 19340 | 32572 | 3.11 | 1.0E-09 | P28694 | SWISSPROT | HUMAN BREAKPOINT CLUSTER REGION (BCR) GENE, COMPLETE CDS |
| 8113 | 21050 | 34449 | 0.63 | 1.0E-09 | AV728645.1 | EST_HUMAN | CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS) |
| | | | | | | | AV728645 HTC Homo sapiens cDNA clone HTCBIG07 5' |
| | | | | | | | wd39b05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330481 3' similar to contains |
| 8733 | 21701 | 35127 | 0.87 | 1.0E-09 | A1688474.1 | EST_HUMAN | MER25.11 MER25 repetitive element; |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 10877 | 23599 | | 2.87 | 1.0E-09 | AL163283.2 | NT | Homo sapiens chromosome 21 segment HS21C083 |
| 12081 | 24963 | | 1.53 | 1.0E-09 | AL163283.2 | NT | Homo sapiens chromosome 21 segment HS21C083 |
| 12618 | 25916 | 31425 | 2.01 | 1.0E-09 | 11418127 | NT | Homo sapiens GTP binding protein 1 (GTPBP-1), mRNA |
| 12781 | 25416 | | 1.6 | 1.0E-09 | T93178.1 | EST_HUMAN | ye24e05.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:118688 5' |
| 1312 | 14348 | 27314 | 2.49 | 9.0E-10 | AW867740.1 | EST_HUMAN | MRO-SN0040-050500-002-c07 SN0040 Homo sapiens cDNA |
| 2845 | 15905 | 28930 | 6.64 | 9.0E-10 | A1870071.1 | EST_HUMAN | we78h03.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2347253 3' similar to SW:RL29_HUMAN P47914 60S RIBOSOMAL PROTEIN L29 ; contains element PTR5 repetitive element ; |
| 7008 | 20134 | 33449 | 4.22 | 9.0E-10 | A1452982.1 | EST_HUMAN | ij46b09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144537 3' similar to TR:O00372 O00372 PUTATIVE P150. ; |
| 148 | 13251 | 26180 | 12.13 | 8.0E-10 | U69630.2 | NT | Homo sapiens MCM4 (MCM4) and DNA-PKcs (PRKDC) genes, partial cds |
| 3353 | 18404 | 29325 | 0.78 | 8.0E-10 | BE080748.1 | EST_HUMAN | QV1-BT0831-150200-071-f01 BT0831 Homo sapiens cDNA |
| 4229 | 17258 | 30142 | 3.69 | 8.0E-10 | AA376832.1 | EST_HUMAN | EST89584 Small intestine I Homo sapiens cDNA 5' end |
| 10324 | 23248 | | 2.46 | 8.0E-10 | U39308.2 | NT | Homo sapiens lens major intrinsic protein (MIP) gene, complete cds |
| 702 | 13764 | 26698 | 32.88 | 7.0E-10 | 7706225 | NT | Homo sapiens TPA inducible protein (LOC51586), mRNA |
| 702 | 13764 | 26699 | 32.88 | 7.0E-10 | 7706225 | NT | Homo sapiens TPA inducible protein (LOC51586), mRNA |
| 1829 | 14659 | 27636 | 2.48 | 7.0E-10 | Q13342 | SWISSPROT | LYSP100 PROTEIN (LYMPHOID-RESTRICTED HOMOLOG OF SP100) |
| 2566 | 15667 | | 21.64 | 7.0E-10 | P08547 | SWISSPROT | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| 3104 | 16161 | 28072 | 2.86 | 7.0E-10 | X00856.1 | NT | H sapiens DHFR gene, exon 3 |
| 6309 | 19380 | 32619 | 3.72 | 7.0E-10 | AA345220.1 | EST_HUMAN | EST51247 Gall Bladder II Homo sapiens cDNA 5' end |
| 7647 | 20607 | 33973 | 1.2 | 7.0E-10 | BF352883.1 | EST_HUMAN | IL3-HT0619-110700-209-D12 HT0619 Homo sapiens cDNA |
| 7918 | 20861 | | 1.46 | 7.0E-10 | P35084 | SWISSPROT | DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT |
| 8308 | 21277 | 34688 | 1.29 | 7.0E-10 | AF028701.2 | NT | Homo sapiens presentin-1 gene, exons 1 and 2 |
| 8308 | 21277 | 34689 | 1.29 | 7.0E-10 | AF028701.2 | NT | Homo sapiens presentin-1 gene, exons 1 and 2 |
| 10673 | 23595 | 37092 | 0.68 | 7.0E-10 | L08805.1 | NT | Homo sapiens MAD5MEF2-family transcription factor (MEF2C) mRNA, complete cds |
| 914 | 13969 | 28922 | 2.97 | 6.0E-10 | AJ400877.1 | NT | Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene |
| 2686 | 15682 | 28700 | 1.37 | 6.0E-10 | A1424405.1 | EST_HUMAN | if02d07.x1 NC1 CGAP_P128 Homo sapiens cDNA clone IMAGE:2095021 3' |
| 4768 | 17788 | | 2.72 | 6.0E-10 | AW853719.1 | EST_HUMAN | RC3-C10254-031099-012-g12 C10254 Homo sapiens cDNA |
| 9135 | 22101 | 35527 | 0.89 | 6.0E-10 | P33730 | SWISSPROT | E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1) |
| 9135 | 22101 | 35528 | 0.89 | 6.0E-10 | P33730 | SWISSPROT | (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E) |
| 9992 | 22919 | 36386 | 0.43 | 6.0E-10 | P98073 | SWISSPROT | E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1) |
| | | | | | | | (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E) |
| | | | | | | | ENTEROPEPTIDASE PRECURSOR (ENTEROKINASE) |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 12221 | 25058 | | 1.64 | 6.0E-10 | AW971923.1 | EST_HUMAN | EST384012 MAGE resequences, MAGL Homo sapiens cDNA |
| 761 | 13821 | | 5.01 | 5.0E-10 | AL046804.1 | EST_HUMAN | DKFZp434N219_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N219 5' |
| 3489 | 16535 | 29480 | 1.53 | 5.0E-10 | Q07033 | SWISSPROT | HYPOPHOSPHATASE 48 PROTEIN |
| 5028 | 18040 | 30923 | 1.1 | 5.0E-10 | AF181897.1 | NT | Homo sapiens WRN (WRN) gene, complete cds |
| 7544 | 20507 | | 1.74 | 5.0E-10 | BF105159.1 | EST_HUMAN | 601822184F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4042413 5' |
| 9894 | 22847 | 36303 | 1.95 | 5.0E-10 | P34678 | SWISSPROT | HYPOPHOSPHATASE 67.9 KD PROTEIN ZK888.8 IN CHROMOSOME III |
| 9894 | 22847 | 36304 | 1.95 | 5.0E-10 | P34678 | SWISSPROT | HYPOPHOSPHATASE 67.9 KD PROTEIN ZK888.8 IN CHROMOSOME III |
| 111 | 13222 | | 1.27 | 4.0E-10 | A1221083.1 | EST_HUMAN | qq09f09.x1 Soares, placenta, 8to9weeks_2NbhP8to9W Homo sapiens cDNA clone IMAGE:1758049 3' |
| 583 | 13651 | 26565 | 0.75 | 4.0E-10 | AA515260.1 | EST_HUMAN | nf64a01.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:924648 3' |
| 2012 | 15033 | 28043 | 1.4 | 4.0E-10 | AW594709.1 | EST_HUMAN | hg58g03.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2948844 3' similar to contains Alu repetitive element; |
| 2580 | 15581 | 28600 | 5.49 | 4.0E-10 | AL163303.2 | NT | Homo sapiens chromosome 21 segment HS21C103 |
| 7382 | 20562 | 33703 | 17.71 | 4.0E-10 | AF224669.1 | NT | Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds |
| 10555 | 23477 | 36971 | 0.53 | 4.0E-10 | AW293243.1 | EST_HUMAN | UI-P-B12-ah1-a-07-Q-UJ.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727081 3' |
| 10812 | 23733 | 37235 | 0.87 | 4.0E-10 | A1287342.1 | EST_HUMAN | aq63h11.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2035653 |
| 10933 | 23853 | 37368 | 0.45 | 4.0E-10 | BE169208.1 | EST_HUMAN | PM1-HT0521-120200-001-008 HT0521 Homo sapiens cDNA |
| 10933 | 23853 | 37369 | 0.45 | 4.0E-10 | BE169208.1 | EST_HUMAN | PM1-HT0521-120200-001-008 HT0521 Homo sapiens cDNA |
| 916 | 13970 | 26924 | 1.8 | 3.0E-10 | N36113.1 | EST_HUMAN | yy32f06.s1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:272963 3' similar to contains L1.11 L1 repetitive element; |
| 1353 | 14388 | | 4.8 | 3.0E-10 | AY005150.1 | NT | Homo sapiens extracellular glycoprotein lactin precursor, gene, complete cds |
| 4566 | 17589 | 30480 | 1.04 | 3.0E-10 | AL163203.2 | NT | Homo sapiens chromosome 21 segment HS21C003 |
| 4566 | 17589 | 30481 | 1.04 | 3.0E-10 | AL163203.2 | NT | Homo sapiens chromosome 21 segment HS21C003 |
| 5530 | 18828 | 31564 | 1.06 | 3.0E-10 | N50109.1 | EST_HUMAN | y211g08.s1 Soares, multiple sclerosis_2NbhMSP Homo sapiens cDNA clone IMAGE:282782 3' |
| 6327 | 19397 | 32639 | 4.03 | 3.0E-10 | P20350 | SWISSPROT | RHOMBOD PROTEIN (VEINLET PROTEIN) |
| 8486 | 19851 | 32801 | 3.08 | 3.0E-10 | BE302970.1 | EST_HUMAN | ba76d08.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2906319 5' |
| 8036 | 20973 | 34387 | 1.42 | 3.0E-10 | AV743302.1 | EST_HUMAN | AV743302 CB Homo sapiens cDNA clone CBFBGD08 5' |
| 8036 | 20973 | 34388 | 1.42 | 3.0E-10 | AV743302.1 | EST_HUMAN | AV743302 CB Homo sapiens cDNA clone CBFBGD08 5' |
| 9082 | 22048 | 35471 | 1.04 | 3.0E-10 | H87208.1 | EST_HUMAN | ys74b12.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:220511 3' similar to contains MER28 repetitive element; |
| 9404 | 22369 | 35803 | 1.8 | 3.0E-10 | AW850731.1 | EST_HUMAN | IL3-CT0219-160200-064-B06 C70219 Homo sapiens cDNA |
| 9404 | 22369 | 35804 | 1.8 | 3.0E-10 | AW850731.1 | EST_HUMAN | IL3-CT0219-160200-064-B06 C70219 Homo sapiens cDNA |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|--|--------------------------|-------------------------------|---|
| 9896 | 22649 | | 0.73 | 3.0E-10 | AF20503.1 | NT | Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5 |
| 10828 | 23749 | | 2.05 | 3.0E-10 | T65891.1 | EST_HUMAN | yc11e12.1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:80398 5' |
| 10957 | 23877 | | 1.76 | 3.0E-10 | AA769294.1 | EST_HUMAN | nz36g03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1289908 3' |
| 12865 | 25468 | 31728 | 1.95 | 3.0E-10 | BE179517.1 | EST_HUMAN | IL3-HT0618-110500-138-E07 HT0618 Homo sapiens cDNA |
| 37 | 13157 | 26058 | 1.55 | 2.0E-10 | P48988 | SWISSPROT | MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B) |
| 37 | 13157 | 26059 | 1.55 | 2.0E-10 | P48988 | SWISSPROT | MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B) |
| 1913 | 14937 | | 1.88 | 2.0E-10 | U80017.1 | NT | Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds |
| 2999 | 16057 | | 0.68 | 2.0E-10 | BF675047.1 | EST_HUMAN | 602136840F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273377 5' |
| 5901 | 18988 | | 3.12 | 2.0E-10 | Q28640 | SWISSPROT | (HPRG) |
| 6379 | 19447 | 32688 | 1.55 | 2.0E-10 | AF280107.1 | NT | Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds |
| 7605 | 20568 | 33926 | 6.24 | 2.0E-10 | BE791082.1 | EST_HUMAN | 601586208F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3940824 5' |
| 8347 | 21316 | 34730 | 0.54 | 2.0E-10 | P26809 | SWISSPROT | POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H] |
| 8347 | 21316 | 34731 | 0.54 | 2.0E-10 | P26809 | SWISSPROT | POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H] |
| 9657 | 22600 | | 0.85 | 2.0E-10 | BF434565.1 | EST_HUMAN | 7c79d08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3642303 3' similar to contains L1.13 L1 repetitive element; |
| 1509 | 14542 | | 2.94 | 1.0E-10 | AW867767.1 | EST_HUMAN | MRO-SN0038-290300-001-f01 SN0038 Homo sapiens cDNA |
| 1611 | 14643 | 27619 | 3.27 | 1.0E-10 | AV652123.1 | EST_HUMAN | AV852123 GLC Homo sapiens cDNA clone GLCXA11 3' |
| 2586 | 15587 | | 1.92 | 1.0E-10 | AW852001.1 | EST_HUMAN | QV0-CT0225-191199-058-e08 CT0225 Homo sapiens cDNA |
| 3511 | 16557 | 29481 | 0.64 | 1.0E-10 | AW832912.1 | EST_HUMAN | QV2-TT0003-161199-013-g10 TT0003 Homo sapiens cDNA |
| 3550 | 16596 | | 0.81 | 1.0E-10 | AL041685.1 | EST_HUMAN | DKFZp434N1317_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N1317 5' |
| 3658 | 16596 | | 0.94 | 1.0E-10 | AL041685.1 | EST_HUMAN | DKFZp434N1317_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N1317 5' |
| 4043 | 17081 | | 6.46 | 1.0E-10 | AF213884.1 | NT | Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds |
| 4154 | 17185 | 30072 | 5.55 | 1.0E-10 | U52111.2 | NT | Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein > |
| 4154 | 17185 | 30073 | 5.55 | 1.0E-10 | U52111.2 | NT | Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein > |
| 4190 | 17191 | 30080 | 2.48 | 1.0E-10 | AB031069.1 | NT | Homo sapiens PCCX1 mRNA for protein containing CXXC domain 1, complete cds |

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Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 4199 | 17230 | | 2.63 | 1.0E-10 | M30629.1 | NT | Human pregnancy-specific glycoprotein beta-1 (SP1) mRNA, last exon |
| 5212 | 18221 | | 0.92 | 1.0E-10 | A1797745.1 | EST_HUMAN | w82f04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347615 3' similar to contains MER31.11 MER31 repetitive element; |
| 6875 | 19928 | 33225 | 0.61 | 1.0E-10 | AA631233.1 | EST_HUMAN | nc81a05.s1 NCI_CGAP_C09 Homo sapiens cDNA clone IMAGE:1158704 3' |
| 6991 | 20214 | 33543 | 0.49 | 1.0E-10 | AF003528.1 | NT | Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions |
| 7716 | 20673 | | 0.56 | 1.0E-10 | P08548 | SWISSPROT | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| 7947 | 20888 | 34279 | 0.63 | 1.0E-10 | AU128594.1 | EST_HUMAN | AU128594 NT2RP2 Homo sapiens cDNA clone NT2RP2003751 5' |
| 8582 | 21550 | 34968 | 1.11 | 1.0E-10 | AW408960.1 | EST_HUMAN | FB_6A4 Fetal brain library Homo sapiens cDNA |
| 9002 | 21968 | | 1.1 | 1.0E-10 | A1268340.1 | EST_HUMAN | qm04e10.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1880874 3' similar to contains L1.11 L1 repetitive element; |
| 10562 | 23484 | | 3.95 | 1.0E-10 | AA081968.1 | EST_HUMAN | zn23g06.r1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548314 5' |
| 11259 | 24211 | 37734 | 3.25 | 1.0E-10 | A103280.1 | EST_HUMAN | oy8fh03.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1672661 3' |
| 12166 | 18354 | | 2.46 | 1.0E-10 | X87344.1 | NT | H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes |
| 261 | 13357 | 26282 | 0.98 | 9.0E-11 | BE145600.1 | EST_HUMAN | IL2-HT0203-291099-018-c08 HT0203 Homo sapiens cDNA |
| 2114 | 15131 | 28151 | 6.21 | 9.0E-11 | AL134395.1 | EST_HUMAN | DKFZp547D225_r1 547 (synonym: hfbt1) Homo sapiens cDNA clone DKFZp547D225 5' |
| 2114 | 15131 | 28152 | 6.21 | 9.0E-11 | AL134395.1 | EST_HUMAN | DKFZp547D225_r1 547 (synonym: hfbt1) Homo sapiens cDNA clone DKFZp547D225 5' |
| 3394 | 16443 | 29370 | 2.6 | 9.0E-11 | AL134395.1 | EST_HUMAN | DKFZp547D225_r1 547 (synonym: hfbt1) Homo sapiens cDNA clone DKFZp547D225 5' |
| 3394 | 16443 | 29371 | 2.6 | 9.0E-11 | AL134395.1 | EST_HUMAN | DKFZp547D225_r1 547 (synonym: hfbt1) Homo sapiens cDNA clone DKFZp547D225 5' |
| 4528 | 17552 | 30440 | 0.72 | 9.0E-11 | AA775985.1 | EST_HUMAN | ae78f01.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:970297 3' |
| 5654 | 18750 | | 3.89 | 9.0E-11 | BE079780.1 | EST_HUMAN | RC6-BT0627-140200-011-E06 BT0627 Homo sapiens cDNA |
| 10514 | 23436 | 36934 | 1.22 | 9.0E-11 | AA324960.1 | EST_HUMAN | EST127872 Cerebellum II Homo sapiens cDNA 5' end |
| 10514 | 23436 | 36935 | 1.22 | 9.0E-11 | AA324960.1 | EST_HUMAN | EST127872 Cerebellum II Homo sapiens cDNA 5' end |
| 12546 | 25269 | 31809 | 4.59 | 9.0E-11 | C16635.1 | EST_HUMAN | C16635 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-508B08 5' |
| 3133 | 16190 | | 8.85 | 8.0E-11 | H19971.1 | EST_HUMAN | yn53f11.s1 Soares adult brain N255HB55Y Homo sapiens cDNA clone IMAGE:172173 3' similar to contains L1 repetitive element; |
| 4073 | 17109 | 30003 | 4.35 | 8.0E-11 | N23712.1 | EST_HUMAN | yw48a06.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:255288 3' |
| 5890 | 18978 | 32170 | 0.65 | 8.0E-11 | AW674316.1 | EST_HUMAN | ba60g04.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2800982 3' |
| 6829 | 19883 | | 0.65 | 8.0E-11 | AW168158.1 | EST_HUMAN | xf45h11.x1 NCI_CGAP_Brn50 Homo sapiens cDNA clone IMAGE:2621061 3' similar to contains MER10.11 MER10 repetitive element; |
| 1442 | 14475 | 27452 | 1.87 | 7.0E-11 | AA330942.1 | EST_HUMAN | EST34392 Embryo, 6 week Homo sapiens cDNA 5' end |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 3885 | 16925 | 29834 | 1.11 | 7.0E-11 | AJ277546.2 | NT | Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor |
| 8943 | 21810 | 35228 | 2.79 | 7.0E-11 | AF163864.1 | NT | Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced |
| 10590 | 23512 | | 1.19 | 7.0E-11 | P11369 | SWISSPROT | RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE] |
| 412 | 13485 | 26421 | 6.97 | 6.0E-11 | M55270.1 | NT | Human matrix Gla protein (MGP) gene, complete cds |
| 412 | 13485 | 26422 | 6.97 | 6.0E-11 | M55270.1 | NT | Human matrix Gla protein (MGP) gene, complete cds |
| 6884 | 19936 | 33232 | 0.88 | 6.0E-11 | L44140.1 | NT | Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds |
| 7957 | 20898 | 34291 | 3.22 | 6.0E-11 | P08547 | SWISSPROT | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| 8707 | 21675 | 35100 | 7.37 | 6.0E-11 | AV727859.1 | EST_HUMAN | AV727859 HTC Homo sapiens cDNA clone HTcASC08 5' |
| 9668 | 22621 | 36072 | 0.42 | 6.0E-11 | BE063509.1 | EST_HUMAN | CMO-BT0281-031199-087-403 B10281 Homo sapiens cDNA |
| 12 | 13132 | 26030 | 0.75 | 5.0E-11 | AL163283.2 | NT | Homo sapiens chromosome 21 segment HS21C083 |
| 3377 | 13132 | 26030 | 1.31 | 5.0E-11 | AL163283.2 | NT | Homo sapiens chromosome 21 segment HS21C083 |
| 4256 | 17285 | 30167 | 1.51 | 5.0E-11 | P48034 | SWISSPROT | ALDEHYDE OXIDASE |
| 6665 | 19722 | 32987 | 1.91 | 5.0E-11 | AL163213.2 | NT | Homo sapiens chromosome 21 segment HS21C013 |
| 7774 | 20727 | 34099 | 11.91 | 5.0E-11 | 11416799 | NT | Homo sapiens protocadherin beta 3 (PCDH3), mRNA |
| 1401 | 14434 | | 1.68 | 4.0E-11 | AA436042.1 | EST_HUMAN | zu01b12.r1 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:730559 5' |
| 2802 | 15794 | 28812 | 7.63 | 4.0E-11 | BE885900.1 | EST_HUMAN | 601507531F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909295 5' |
| 2981 | 16039 | 28962 | 0.92 | 4.0E-11 | AL163247.2 | NT | Homo sapiens chromosome 21 segment HS21C047 |
| 4649 | 17670 | 30557 | 1.24 | 4.0E-11 | D44666.1 | EST_HUMAN | HUMSUPY069 Human brain cDNA Homo sapiens cDNA clone 069 |
| 5621 | 19679 | 32957 | 3.27 | 4.0E-11 | P20095 | SWISSPROT | PRE-MRNA SPLICING FACTOR RNA HELICASE PRP2 |
| 7197 | 20221 | 33552 | 0.54 | 4.0E-11 | AA442630.1 | EST_HUMAN | zv69f10.r1 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:757983 5' similar to TR:G1055250 |
| 7600 | 20561 | | 3.97 | 4.0E-11 | AF224669.1 | NT | G1055250 PHEROMONE RECEPTOR VN4. ; |
| 9750 | 22691 | | 1.68 | 4.0E-11 | BE149425.1 | EST_HUMAN | Homo sapiens mamosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds |
| 10020 | 22947 | 36415 | 0.86 | 4.0E-11 | AI609753.1 | EST_HUMAN | RC1-HT0256-210100-013-008 HT0256 Homo sapiens cDNA |
| 12736 | 25388 | 31752 | 1.56 | 4.0E-11 | 11545732 | NT | tf82g12.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2103830 3' similar to WP.ZK353.1 |
| 1488 | 14521 | 27494 | 2.55 | 3.0E-11 | 6878077 | NT | CE00385 ; |
| 4305 | 17334 | | 1.37 | 3.0E-11 | AA309248.1 | EST_HUMAN | Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA |
| 961 | 14014 | 26967 | 1.48 | 2.0E-11 | AI150502.1 | EST_HUMAN | Mus musculus expressed in non-metastatic cells 2, protein (NM23B) (Nme2), mRNA EST180120 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end q36c04.x1 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:1752102 3' similar to contains MER10.13 MER10 repetitive element ; |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 1189 | 14229 | 27186 | 4.46 | 2.0E-11 | R24807.1 | EST_HUMAN | y943e12.1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35144 5' |
| 1189 | 14229 | 27187 | 4.46 | 2.0E-11 | R24807.1 | EST_HUMAN | y943e12.1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35144 5' |
| 1617 | 14849 | 27624 | 5.86 | 2.0E-11 | L17432.1 | NT | Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein |
| 1617 | 14849 | 27625 | 5.86 | 2.0E-11 | L17432.1 | NT | COR3beta (COR3beta) genes, complete cds Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein |
| 1620 | 14853 | 27629 | 1.25 | 2.0E-11 | A1128371.1 | EST_HUMAN | qs51c10.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1713138 3' similar to gb:L02832 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN); contains L1.t1 |
| 2775 | 15787 | 28787 | 1.04 | 2.0E-11 | AF087913.1 | NT | L1 repetitive element ; |
| 3211 | 16286 | 28189 | 8.7 | 2.0E-11 | P10263 | SWISSPROT | Human endogenous retrovirus HERV-P-147D |
| 3337 | 16388 | 28309 | 1 | 2.0E-11 | AK78617.1 | EST_HUMAN | RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1) |
| 3375 | 16425 | 28350 | 0.71 | 2.0E-11 | Q10473 | SWISSPROT | hm54c09.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161938 3' POLYPEPTIDE N-ACETYL GALACTOSAMINYL TRANSFERASE (PROTEIN-JDP ACETYL GALACTOSAMINYL TRANSFERASE) (UDP-GALNAc:POLYPEPTIDE, N- ACETYL GALACTOSAMINYL TRANSFERASE) (GALNAc-T1) |
| 3508 | 16554 | | 1.09 | 2.0E-11 | AF020503.1 | NT | Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5 |
| 4472 | 17498 | | 1.24 | 2.0E-11 | BE065537.1 | EST_HUMAN | RC3-BT0316-170200-014-e05 BT0316 Homo sapiens cDNA |
| 4636 | 17657 | | 0.98 | 2.0E-11 | AL183227.2 | NT | Homo sapiens chromosome 21 segment HS21C027 |
| 4973 | 17988 | | 2.36 | 2.0E-11 | BE062558.1 | EST_HUMAN | QV2-BT0258-261099-014-e01 BT0258 Homo sapiens cDNA |
| 6258 | 19331 | 32562 | 1 | 2.0E-11 | AW877806.1 | EST_HUMAN | QV2-P10073-280300-109-h08 PT0073 Homo sapiens cDNA |
| 6443 | 19508 | 32758 | 1.71 | 2.0E-11 | AA581028.1 | EST_HUMAN | nc83h05.r1 NCL_CGAP_GC1 Homo sapiens cDNA clone IMAGE:797433 5' similar to SW.PR16_YEAST |
| 7401 | 20369 | 33722 | 0.82 | 2.0E-11 | BF592945.1 | EST_HUMAN | P15938 PRE-MRNA SPLICING FACTOR RNA HELICASE PRP18 ; |
| 8214 | 21183 | | 0.51 | 2.0E-11 | P37072 | SWISSPROT | 797c03.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3442565 3' OLFACTORY RECEPTOR-LIKE PROTEIN COR6 |
| 9578 | 22540 | | 1.31 | 2.0E-11 | AF028308.1 | NT | Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families |
| 10647 | 23599 | 37065 | 4.42 | 2.0E-11 | Q13606 | SWISSPROT | OLFACTORY RECEPTOR 511 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1) |
| 10882 | 23802 | 37305 | 0.85 | 2.0E-11 | AW885874.1 | EST_HUMAN | RC4-OT0072-170400-013-e11 OT0072 Homo sapiens cDNA |
| 10882 | 23802 | 37306 | 0.85 | 2.0E-11 | AW885874.1 | EST_HUMAN | RC4-OT0072-170400-013-e11 OT0072 Homo sapiens cDNA |
| 11448 | 24391 | 37935 | 1.54 | 2.0E-11 | AA035369.1 | EST_HUMAN | zk27g02.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471794 3' |
| 11448 | 24391 | 37936 | 1.54 | 2.0E-11 | AA035369.1 | EST_HUMAN | zk27g02.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471794 3' |
| 11477 | 24420 | 37969 | 2.14 | 2.0E-11 | AA261956.1 | EST_HUMAN | zs18b04.r1 NCL_CGAP_GC81 Homo sapiens cDNA clone IMAGE:685519 5' |
| 12336 | 25128 | | 4.12 | 2.0E-11 | AW842143.1 | EST_HUMAN | RC0-CN0027-210100-011-c01 CN0027 Homo sapiens cDNA |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 12354 | 25148 | 31854 | 2.14 | 2.0E-11 | BF377859.1 | EST_HUMAN | CM2-TN0140-070900-372-g01 TN0140 Homo sapiens cDNA |
| 12617 | 25313 | | 1.49 | 2.0E-11 | D25217.2 | NT | Homo sapiens mRNA for KIAA0027 protein, partial cds |
| 12754 | 25399 | | 1.68 | 2.0E-11 | P08547 | SWISSPROT | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| 13070 | 25804 | | 3.68 | 2.0E-11 | 11417966 | NT | Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA |
| 677 | 13740 | 26687 | 0.83 | 1.0E-11 | AJ131016.1 | NT | Homo sapiens SCL gene locus |
| 784 | 13844 | 26789 | 1.89 | 1.0E-11 | AL163209.2 | NT | Homo sapiens chromosome 21 segment HS21C009 |
| 1221 | 14259 | 27216 | 4.66 | 1.0E-11 | AL163279.2 | NT | Homo sapiens chromosome 21 segment HS21C079 |
| 1498 | 14531 | | 2.95 | 1.0E-11 | AF119814.1 | NT | Homo sapiens PRO3078 mRNA, complete cds |
| 2053 | 15072 | 28091 | 1.41 | 1.0E-11 | P16258 | SWISSPROT | OXYSTEROL-BINDING PROTEIN |
| 2138 | 15153 | 28168 | 3.18 | 1.0E-11 | AF000573.1 | NT | Homo sapiens homogenisate 1,2-dioxygenase gene, complete cds |
| 2170 | 15186 | 28207 | 1.15 | 1.0E-11 | AA309318.1 | EST_HUMAN | EST180188 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end similar to EST containing Alu repeat |
| 3510 | 16556 | 29480 | 0.8 | 1.0E-11 | BE004315.1 | EST_HUMAN | CM0-BN0105-170300-292-412 BN0105 Homo sapiens cDNA |
| 4960 | 17975 | 30866 | 1.01 | 1.0E-11 | AI168625.1 | EST_HUMAN | α65H06.s1 Soares NIH-MPc S1 Homo sapiens cDNA clone IMAGE:1681243 3' |
| 5405 | 18508 | 31385 | 14.43 | 1.0E-11 | AL163247.2 | NT | Homo sapiens chromosome 21 segment HS21C047 |
| 5931 | 19017 | 32212 | 0.77 | 1.0E-11 | BF222646.1 | EST_HUMAN | 7a57d01.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:3649845 3' similar to contains MER10.b3 |
| 8112 | 21049 | | 0.51 | 1.0E-11 | AB042297.1 | NT | MER10 repetitive element ; |
| 8543 | 21511 | 34928 | 3.36 | 1.0E-11 | 4885546 | NT | Homo sapiens P1S gene for 6-pyruvoyltetrahydropterin synthase, complete cds |
| 8928 | 21894 | 35322 | 4.18 | 1.0E-11 | R13174.1 | EST_HUMAN | Homo sapiens PHD finger protein 2 (PHF2) mRNA |
| 9403 | 22368 | 35801 | 1.18 | 1.0E-11 | BF365119.1 | EST_HUMAN | yf73d08.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:28166 5' |
| 9403 | 22368 | 35802 | 1.18 | 1.0E-11 | BF365119.1 | EST_HUMAN | QV4-NN1149-250900-423-a03 NN1149 Homo sapiens cDNA |
| 11619 | 24557 | 38120 | 1.48 | 1.0E-11 | BF680078.1 | EST_HUMAN | QV4-NN1149-250900-423-a03 NN1149 Homo sapiens cDNA |
| 2963 | 16021 | 28946 | 0.82 | 9.0E-12 | P20742 | SWISSPROT | 602154807F1 NIH_MGC_B3 Homo sapiens cDNA clone IMAGE:4286977 5' |
| 10157 | 23082 | 36558 | 1.02 | 9.0E-12 | AL163300.2 | NT | PREGNANCY ZONE PROTEIN PRECURSOR |
| 10157 | 23082 | 36559 | 1.02 | 9.0E-12 | AL163300.2 | NT | Homo sapiens chromosome 21 segment HS21C100 |
| 12075 | 24947 | 38542 | 2.85 | 9.0E-12 | AL046939.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C100 |
| 9893 | 22846 | | 0.92 | 8.0E-12 | BE074720.1 | EST_HUMAN | DKFZp586i0417_r1 586 (synonym: hute1) Homo sapiens cDNA clone DKFZp586i0417 5' |
| 12407 | 25180 | | 3.22 | 8.0E-12 | AJ271736.1 | NT | IL5-B10578-130300-038-G12 B10578 Homo sapiens cDNA |
| 4890 | 17711 | 30605 | 1.46 | 7.0E-12 | Q08904 | SWISSPROT | Homo sapiens Xq pseudautosomal region, segment 2/2 |
| 11677 | 24643 | 38220 | 7.41 | 7.0E-12 | AA704735.1 | EST_HUMAN | 34 KD SPICULE MATRIX PROTEIN PRECURSOR (LSM34) |
| 3558 | 16904 | | 0.95 | 6.0E-12 | AV730554.1 | EST_HUMAN | z23g01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451152 3' |
| 4375 | 17403 | 30283 | 9.29 | 6.0E-12 | AA732516.1 | EST_HUMAN | AV730554 HTF Homo sapiens cDNA clone HTFAW F06 5' |
| | | | | | | | nz288f11.s1 NCL_CGAP_G081 Homo sapiens cDNA clone IMAGE:1302573 3' similar to contains Alu repetitive element; |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 6528 | 19591 | 32851 | 0.65 | 6.0E-12 | AF020503.1 | NT | Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5 |
| 9347 | 22312 | 35736 | 0.98 | 6.0E-12 | AF003249.1 | NT | Marone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds |
| 9829 | 22678 | | 1.66 | 6.0E-12 | AA847898.1 | EST_HUMAN | cd10g11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1387588 similar to contains MER29.12 |
| 1044 | 14090 | 27043 | 3.57 | 5.0E-12 | T06573.1 | EST_HUMAN | MER29 repetitive element; |
| 3401 | 16450 | 29376 | 1.17 | 5.0E-12 | BE047779.1 | EST_HUMAN | EST04462 Fetal brain, Stratagene (cat#836206) Homo sapiens cDNA clone HFB0V33 |
| 3740 | 16782 | 29694 | 8.8 | 5.0E-12 | AJ271736.1 | NT | tz42b05.y1 NCI_CGAP_Bim52 Homo sapiens cDNA clone IMAGE:2291217 5' |
| 6137 | 19214 | 32441 | 4.99 | 5.0E-12 | AL163278.2 | NT | Homo sapiens Xq pseudautosomal region; segment 2/2 |
| 6137 | 19214 | 32442 | 4.99 | 5.0E-12 | AL163278.2 | NT | Homo sapiens chromosome 21 segment HS21C078 |
| 6039 | 19697 | 32973 | 9.52 | 5.0E-12 | AW974760.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C078 |
| 7232 | 19977 | 33274 | 1 | 5.0E-12 | AL040739.1 | EST_HUMAN | EST366850 MAGE resequences, MAGN Homo sapiens cDNA |
| 7242 | 19977 | 33274 | 1.03 | 5.0E-12 | AL040739.1 | EST_HUMAN | DKFZp434B1615_s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B1615 3' |
| 8571 | 21539 | 34960 | 1.14 | 5.0E-12 | AA033745.1 | EST_HUMAN | DKFZp434B1615_s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B1615 3' |
| 9015 | 21981 | | 0.7 | 5.0E-12 | AW887037.1 | EST_HUMAN | z01g12.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:375718 3' similar to contains |
| 9346 | 22311 | | 0.54 | 5.0E-12 | AL079581.1 | EST_HUMAN | L1.13 L1 repetitive element; |
| 9464 | 22428 | 35867 | 2.78 | 5.0E-12 | AJ271735.1 | NT | RC1-OT0086-220300-011-b07 OT0086 Homo sapiens cDNA |
| 9778 | 22719 | 36173 | 1.38 | 5.0E-12 | P34982 | SWISSPROT | DKFZp434J0426_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434J0426 5' |
| 10638 | 23560 | | 4.14 | 5.0E-12 | AL163303.2 | NT | Homo sapiens Xq pseudautosomal region; segment 1/2 |
| 10729 | 23851 | 37144 | 0.81 | 5.0E-12 | AL163302.2 | NT | OLFACTORY RECEPTOR 1D2 (OLFACTORY RECEPTOR-LIKE PROTEIN HGMPO7E) (OLFACTORY RECEPTOR 17-4) (OR17-4) |
| 244 | 13342 | 26287 | 4.17 | 4.0E-12 | AA700326.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C103 |
| 245 | 13342 | 26287 | 5.51 | 4.0E-12 | AA700326.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C102 |
| 4650 | 17671 | 30558 | 0.74 | 4.0E-12 | AI689984.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C102 |
| 7881 | 20825 | | 0.72 | 4.0E-12 | BF445140.1 | EST_HUMAN | zj74g11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460676 3' |
| 8585 | 21553 | | 2.92 | 4.0E-12 | AF109907.1 | NT | zj74g11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460676 3' |
| 9035 | 22001 | 35422 | 0.75 | 4.0E-12 | AB042815.1 | NT | zj74g11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460676 3' |
| 11410 | 24363 | 37898 | 3.26 | 4.0E-12 | AJ229043.1 | NT | b26h05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13539 Q13539 |
| 12688 | 25338 | | 2.82 | 4.0E-12 | U78027.1 | NT | MARINER TRANSPOSASE. ; |
| | | | | | | | mad21b03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3366077 3' similar to contains MER7.b2 |
| | | | | | | | MER7 repetitive element; |
| | | | | | | | Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds, and S171 gene, partial cds |
| | | | | | | | Bos taurus M1ch2 mRNA for mitochondrial carrier homolog 2, complete cds |
| | | | | | | | Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3 |
| | | | | | | | Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 618 | 13683 | 26600 | 3.06 | 3.0E-12 | AW341883.1 | EST_HUMAN | hd13d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909377 3' similar to TR:O14517 O14517 SMRP.; |
| 618 | 13683 | 26601 | 3.06 | 3.0E-12 | AW341883.1 | EST_HUMAN | hd13d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909377 3' similar to TR:O14517 O14517 SMRP.; |
| 5211 | 18220 | 31096 | 0.73 | 3.0E-12 | AL163268.2 | NT | Homo sapiens chromosome 21 segment HS21C068 |
| 5527 | 18628 | 31562 | 0.96 | 3.0E-12 | AF111168.2 | NT | Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes |
| 7659 | 20619 | | 0.54 | 3.0E-12 | AB042297.1 | NT | Homo sapiens P TS gene for 6-pyruvoyl-tetrahydropterin synthase, complete cds |
| 8030 | 20967 | | 0.55 | 3.0E-12 | AW854328.1 | EST_HUMAN | RC3-CT0255-031099-011-h02 C10255 Homo sapiens cDNA |
| 8718 | 21886 | 35114 | 0.48 | 3.0E-12 | O35453 | SWISSPROT | SERINE PROTEINASE HEP SIN |
| 9462 | 22426 | 35864 | 0.54 | 3.0E-12 | O35453 | SWISSPROT | SERINE PROTEINASE HEP SIN |
| 11016 | 23981 | 37507 | 2.71 | 3.0E-12 | U37672.1 | NT | Human prostate specific antigen gene, 5' flanking region |
| 11016 | 23981 | 37508 | 2.71 | 3.0E-12 | U37672.1 | NT | Human prostate specific antigen gene, 5' flanking region |
| 1661 | 14953 | 27698 | 2.41 | 2.0E-12 | AW802131.1 | EST_HUMAN | IL5-UM0071-120400-065-a05 UM0071 Homo sapiens cDNA |
| 3480 | 16528 | 28451 | 0.85 | 2.0E-12 | 6754495 | NT | Mus musculus keratin-associated protein 6.2 (Krtap6-2), mRNA |
| 4141 | 17172 | 30060 | 1.09 | 2.0E-12 | J01884.1 | NT | Rat U3A small nuclear RNA |
| 4141 | 17172 | 30061 | 1.09 | 2.0E-12 | J01884.1 | NT | Rat U3A small nuclear RNA |
| 4451 | 17477 | | 1.97 | 2.0E-12 | BE063609.1 | EST_HUMAN | GM0-BT0281-031199-087-a03 BT0281 Homo sapiens cDNA |
| 5321 | 18427 | 31177 | 0.71 | 2.0E-12 | P11369 | SWISSPROT | RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE] |
| 6622 | 19680 | | 1.83 | 2.0E-12 | AW971857.1 | EST_HUMAN | EST383946 MAGE resequences, MAGL Homo sapiens cDNA |
| 7381 | 20351 | 33702 | 3.22 | 2.0E-12 | T08169.1 | EST_HUMAN | EST06080 Infant Brain, Berto Soares Homo sapiens cDNA clone HIBBA13 5' end |
| 7667 | 20630 | 33889 | 1.18 | 2.0E-12 | BE173035.1 | EST_HUMAN | MR0-HT0559-200400-015-a08 HT0559 Homo sapiens cDNA |
| 7778 | 20731 | | 0.57 | 2.0E-12 | AW842798.1 | EST_HUMAN | MR2-CN0037-210200-101-b02 CN0037 Homo sapiens cDNA |
| 7922 | 20866 | 34253 | 2.1 | 2.0E-12 | 11422229 | NT | Homo sapiens Ac-like transposable element (ALTE), mRNA |
| 9077 | 22043 | 35466 | 0.43 | 2.0E-12 | Q10473 | SWISSPROT | POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (PROTEIN-UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYL GALACTOSAMINYLTRANSFERASE) (GALNAC-T1) |
| 9663 | 22820 | | 1.65 | 2.0E-12 | AF196964.1 | NT | Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds |
| 10345 | 23269 | | 14.41 | 2.0E-12 | BE165980.1 | EST_HUMAN | MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA |
| 10881 | 23801 | 37304 | 0.8 | 2.0E-12 | AI334130.1 | EST_HUMAN | qq0702.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1931835 3' similar to TR:Q13538 Q13538 ORF2: FUNCTION UNKNOWN ; |
| 12308 | 25116 | | 3.11 | 2.0E-12 | AL163283.2 | NT | Homo sapiens chromosome 21 segment HS21C083 |
| 12511 | 25245 | | 1.69 | 2.0E-12 | 11418248 | NT | Homo sapiens sulfotransferase-related protein (SULTX3), mRNA |

Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 123 | 13231 | 26159 | 2.83 | 1.0E-12 | AW627874.1 | EST_HUMAN | h180a09.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2870040 3' similar to contains MER18.t1 MER18 repetitive element; |
| 2004 | 15025 | | 1.46 | 1.0E-12 | A1871726.1 | EST_HUMAN | wm51f07.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2439493 3' similar to contains L1.b3 L1 repetitive element; |
| 3085 | 16142 | 29053 | 0.78 | 1.0E-12 | AF000991.1 | NT | Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds |
| 3085 | 16142 | 28054 | 0.78 | 1.0E-12 | AF000991.1 | NT | Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds |
| 3888 | 16928 | 28836 | 31.6 | 1.0E-12 | AU132248.1 | EST_HUMAN | AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5' |
| 3888 | 16928 | 28837 | 31.6 | 1.0E-12 | AU132248.1 | EST_HUMAN | AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5' |
| 6078 | 19158 | | 2.05 | 1.0E-12 | U82828.1 | NT | Homo sapiens ataxia telangiectasia (ATM) gene, complete cds |
| 6159 | 19234 | | 1.65 | 1.0E-12 | Q9Y2G7 | SWISSPROT | HYPOPHOSPHATASE 1 (HPP1) gene, complete cds |
| 6277 | 19349 | 32582 | 0.57 | 1.0E-12 | BF642800.1 | EST_HUMAN | EST000008 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1847869 5' |
| 6277 | 19349 | 32583 | 0.57 | 1.0E-12 | BF642800.1 | EST_HUMAN | EST000008 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1847869 5' |
| 6882 | 19739 | 33014 | 0.78 | 1.0E-12 | AF228943.1 | NT | Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene |
| 7323 | 20284 | 33637 | 1.9 | 1.0E-12 | AF186864.1 | NT | Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds |
| 7357 | 20327 | 33675 | 11.35 | 1.0E-12 | A1248533.1 | EST_HUMAN | qh66a04.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849614 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN); contains MER10.t1 MER10 repetitive element; |
| 7357 | 20327 | 33676 | 11.35 | 1.0E-12 | A1248533.1 | EST_HUMAN | qh66a04.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849614 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN); contains MER10.t1 MER10 repetitive element; |
| 8834 | 21801 | 35220 | 0.48 | 1.0E-12 | U66059.1 | NT | Human germ-line T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3 TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV8S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S> |
| 9053 | 22019 | 35444 | 1.16 | 1.0E-12 | AA782323.1 | EST_HUMAN | ac26a05.x1 Strabagene ovary (#837217) Homo sapiens cDNA clone IMAGE:857577 3' |
| 12213 | 25052 | 38626 | 2.82 | 1.0E-12 | AW962164.1 | EST_HUMAN | EST374237 MAGE resequences, MAGG Homo sapiens cDNA |
| 12434 | 25200 | | 2.54 | 1.0E-12 | A1738592.1 | EST_HUMAN | w13h08.x1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:2392085 3' |
| 12582 | 25881 | | 2.51 | 1.0E-12 | AL163268.2 | NT | Homo sapiens chromosome 21 segment HS21C088 |
| 1054 | 14100 | 27050 | 0.7 | 9.0E-13 | AW082714.1 | EST_HUMAN | xb61f07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2580805 3' similar to contains MER28.t3 MER28 repetitive element; |
| 3643 | 16886 | | 1.01 | 9.0E-13 | AJ271735.1 | NT | Homo sapiens Xq pseudautosomal region; segment 1/2 |
| 3967 | 17007 | 28923 | 0.98 | 9.0E-13 | AB028900.1 | NT | Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5 |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 9660 | 22887 | | 2.59 | 9.0E-13 | N69693.1 | EST_HUMAN | z226b06.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:293651 3' |
| 718 | 13780 | 26714 | 6.78 | 8.0E-13 | U29185.1 | NT | Homo sapiens prion protein (PrP) gene, complete cds |
| 718 | 13780 | 26715 | 6.78 | 8.0E-13 | U29185.1 | NT | Homo sapiens prion protein (PrP) gene, complete cds |
| 1855 | 14881 | 27877 | 3.1 | 8.0E-13 | U80017.1 | NT | Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nailp) and survival motor neuron protein (smn) genes, complete cds |
| 8449 | 21418 | 34831 | 0.75 | 8.0E-13 | A1884398.1 | EST_HUMAN | wm31h09.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437601 3' |
| 8449 | 21418 | 34832 | 0.75 | 8.0E-13 | A1884398.1 | EST_HUMAN | wm31h09.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437601 3' |
| 10505 | 23427 | | 4 | 8.0E-13 | U78027.1 | NT | Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds |
| 8127 | 21064 | 34462 | 0.58 | 7.0E-13 | A1884398.1 | EST_HUMAN | wm31h09.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437601 3' |
| 8127 | 21064 | 34463 | 0.58 | 7.0E-13 | A1884398.1 | EST_HUMAN | wm31h09.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437601 3' |
| 8576 | 21544 | | 0.49 | 7.0E-13 | Q98155 | SWISSPROT | OLFACTORY RECEPTOR-LIKE PROTEIN OLF2 |
| 12682 | 26350 | | 5.56 | 7.0E-13 | BE778223.1 | EST_HUMAN | 601463285F1 NIH_MGC 67 Homo sapiens cDNA clone IMAGE:3866613 5' |
| 2111 | 15128 | 28148 | 3.56 | 6.0E-13 | AL163207.2 | NT | Homo sapiens chromosome 21 segment HS21C007 |
| 3333 | 16384 | | 0.74 | 5.0E-13 | R78338.1 | EST_HUMAN | y182f04.r1 Soares placenta Nb2f1P Homo sapiens cDNA clone IMAGE:145759 5' |
| 3408 | 18457 | | 1.35 | 5.0E-13 | AA435773.1 | EST_HUMAN | z177a12.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728350 3' similar to contains Alu repetitive element; contains element MER22 repetitive element ; |
| 7060 | 20082 | 33390 | 0.7 | 5.0E-13 | P08983 | SWISSPROT | GAP JUNCTION BETA-1 PROTEIN (CONNEXIN 30) (CX30) |
| 11209 | 24163 | 37693 | 2.07 | 5.0E-13 | P07313 | SWISSPROT | MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK) |
| 1883 | 14908 | | 6.02 | 4.0E-13 | AW378614.1 | EST_HUMAN | PM2-HT0224-221099-001-e11 HT0224 Homo sapiens cDNA |
| 2467 | 15471 | | 2.44 | 4.0E-13 | AF003529.1 | NT | Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions |
| 4778 | 17798 | | 0.99 | 4.0E-13 | AA454054.1 | EST_HUMAN | z48d07.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:795469 5' |
| 5667 | 18762 | 31831 | 4.36 | 4.0E-13 | BE169131.1 | EST_HUMAN | PM2-HT0520-230200-002-c08 HT0520 Homo sapiens cDNA |
| 7413 | 20380 | 33731 | 1.05 | 4.0E-13 | AB037750.1 | NT | Homo sapiens mRNA for KIAA1329 protein, partial cds |
| 7970 | 20314 | 34192 | 0.88 | 4.0E-13 | AA431529.1 | EST_HUMAN | z178g12.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:782182 5' similar to TR:G452763 G452763 COR1 MRNA ; |
| 7989 | 20928 | | 1.47 | 4.0E-13 | N44291.1 | EST_HUMAN | y93g05.r1 Soares melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:273080 5' similar to PIR:A32995 A32995 t complex sterility protein - mouse ; |
| 9193 | 22159 | 35537 | 1.2 | 4.0E-13 | AL049310.1 | EST_HUMAN | DKFZp434A0128_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434A0128 5' |
| 9660 | 22798 | 36249 | 0.59 | 4.0E-13 | AA076907.1 | EST_HUMAN | 7B04H11 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B04H11 |
| 10380 | 23303 | 36779 | 5.26 | 4.0E-13 | A1289831.1 | EST_HUMAN | q132d05.x1 NCI_CGAP_K145 Homo sapiens cDNA clone IMAGE:1899945 3' similar to contains Alu repetitive element; |
| 11502 | 24444 | 37895 | 1.9 | 4.0E-13 | AA435819.1 | EST_HUMAN | z178g10.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728514 3' |
| 11502 | 24444 | 37896 | 1.9 | 4.0E-13 | AA435819.1 | EST_HUMAN | z178g10.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728514 3' |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|-----------------------------|-------------------------------|---|
| 181 | 13281 | | 5.91 | 3.0E-13 | AF003528.1 | NT | Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions |
| 868 | 13922 | | 3.35 | 3.0E-13 | AA430310.1 | EST_HUMAN | z68908.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781408 5' |
| 2378 | 15386 | 28410 | 1.65 | 3.0E-13 | AJ271736.1 | NT | Homo sapiens Xq pseudobscosomal region; segment 2/2 |
| 2487 | 15491 | | 2.11 | 3.0E-13 | AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C010 |
| 2673 | 15670 | 28888 | 2.5 | 3.0E-13 | BF37262.1 | EST_HUMAN | CM3-FT0100-140700-242-h08 FT0100 Homo sapiens cDNA |
| 3201 | 16256 | | 2.19 | 3.0E-13 | AA745844.1 | EST_HUMAN | ob18d02.s1 NCI_QGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324035 3' |
| 3514 | 16560 | 29484 | 0.9 | 3.0E-13 | P18616 | SWISSPROT | DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (VERSION 1) |
| 3514 | 16560 | 29485 | 0.9 | 3.0E-13 | P18616 | SWISSPROT | DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (VERSION 1) |
| 5618 | 18714 | 31872 | 0.64 | 3.0E-13 | AA134017.1 | EST_HUMAN | zn88h10.r1 Stragene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565315 5' similar to contains THR.12 THR repetitive element ; |
| 5618 | 18714 | 31873 | 0.64 | 3.0E-13 | AA134017.1 | EST_HUMAN | zn88h10.r1 Stragene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565315 5' similar to contains THR.12 THR repetitive element ; |
| 6106 | 19185 | 32404 | 0.71 | 3.0E-13 | AW005639.1 | EST_HUMAN | wz88c02.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2565890 3' similar to TR:O75139 O75139 KIAA0644 PROTEIN ; |
| 8215 | 21184 | 34594 | 8.24 | 3.0E-13 | U52111.2 | NT | Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenergic dystrophy protein > |
| 8412 | 21381 | 34787 | 0.51 | 3.0E-13 | AA352487.1 | EST_HUMAN | EST80487 Activated T-cells XX Homo sapiens cDNA 5' end similar to similar to serine protease P100, Ra-reactive factor |
| 8412 | 21381 | 34788 | 0.51 | 3.0E-13 | AA352487.1 | EST_HUMAN | EST80487 Activated T-cells XX Homo sapiens cDNA 5' end similar to similar to serine protease P100, Ra-reactive factor |
| 10558 | 23480 | 36975 | 0.46 | 3.0E-13 | AW935497.1 | EST_HUMAN | RC2-DT0007-110100-014-g10 DT0007 Homo sapiens cDNA |
| 11038 | 24000 | | 2.68 | 3.0E-13 | AJ064768.1 | EST_HUMAN | HA05308 Human fetal liver cDNA library Homo sapiens cDNA |
| 11385 | 24332 | 37861 | 3.32 | 3.0E-13 | BE063509.1 | EST_HUMAN | CMO-BT0281-031199-087-a03 BT0281 Homo sapiens cDNA |
| 11924 | 24805 | 38398 | 1.54 | 3.0E-13 | AL163248.2 | NT | Homo sapiens chromosome 21 segment HS21C048 |
| 151 | 13254 | 26183 | 3.93 | 2.0E-13 | U52111.2 | NT | Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenergic dystrophy protein > |
| 1275 | 14310 | 27271 | 7.14 | 2.0E-13 | AF239710.1 | NT | Homo sapiens DNA polymerase delta small subunit (POLD2) gene, exons 1 through 11 and complete cds |
| 3294 | 16347 | 29267 | 1.08 | 2.0E-13 | BF431699.1 | EST_HUMAN | hab16005.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE: 3' |
| 3518 | 16564 | 29489 | 1.25 | 2.0E-13 | AF109907.1 | NT | Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 4135 | 17167 | | 1.61 | 2.0E-13 | AL163278.2 | NT | Homo sapiens chromosome 21 segment HS21C078 |
| 6245 | 19318 | 32548 | 4.71 | 2.0E-13 | Q08852 | SWISSPROT | CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER PROTEIN 1) |
| 6987 | 20210 | 33538 | 6.49 | 2.0E-13 | X16912.1 | NT | Human PFKL gene for liver-type 6-phosphofructokinase (EC 2.7.1.11) exon 2 |
| 7255 | 19990 | 33287 | 0.59 | 2.0E-13 | 10835072 | NT | Homo sapiens N-myristoyltransferase 1 (NMT1), mRNA |
| 7255 | 19990 | 33288 | 0.59 | 2.0E-13 | 10835072 | NT | Homo sapiens N-myristoyltransferase 1 (NMT1), mRNA |
| 10824 | 23745 | 37246 | 4.53 | 2.0E-13 | 5031896 | NT | Homo sapiens mab-21 (C. elegans)-like 1 (MAB21L1), mRNA |
| 12387 | 25165 | | 5.43 | 2.0E-13 | AW892155.1 | EST_HUMAN | CMD-NN0001-100300-274-511 NN0001 Homo sapiens cDNA |
| 291 | 13385 | 26312 | 1.49 | 1.0E-13 | S74129.1 | NT | FGF-1=fibroblast growth factor 1 [human, kidney, Genomic, 342 nt, segment 2 of 2] |
| 889 | 13944 | 26902 | 4.85 | 1.0E-13 | AJ007973.1 | NT | Homo sapiens LGMD2B gene |
| 1339 | 14373 | 27343 | 1.39 | 1.0E-13 | X87344.1 | NT | H. sapiens DMA, DMB, HLA-Z1, IPP2, LIMP2, TAP1, LIMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes |
| 2037 | 15058 | 28074 | 2.43 | 1.0E-13 | AA720574.1 | EST_HUMAN | nm21g02.s1 NCJ_CGAP_GC80 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.13 |
| 4623 | 17644 | 30532 | 2.2 | 1.0E-13 | BF340987.1 | EST_HUMAN | THR repetitive element; |
| 6586 | 19646 | 32815 | 0.61 | 1.0E-13 | AA090732.1 | EST_HUMAN | 602038009F1 NCJ_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4185986 5' |
| 8242 | 21211 | 34616 | 0.78 | 1.0E-13 | AA577812.1 | EST_HUMAN | y1535 seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5' |
| 8242 | 21211 | 34617 | 0.78 | 1.0E-13 | AA577812.1 | EST_HUMAN | nm24d01.s1 NCJ_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084801 3' similar to contains Alu |
| 10450 | 23372 | | 0.82 | 1.0E-13 | O15481 | SWISSPROT | repetitive element; contains element MER24 repetitive element; |
| 10664 | 23586 | 37084 | 0.49 | 1.0E-13 | AF300701.1 | NT | repetitive element; contains element MER24 repetitive element; |
| 11707 | 24872 | 38249 | 10.13 | 1.0E-13 | BF108755.1 | EST_HUMAN | nm24d01.s1 NCJ_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084801 3' similar to contains Alu |
| 12206 | 25048 | | 2.34 | 1.0E-13 | AV716377.1 | EST_HUMAN | repetitive element; contains element MER24 repetitive element; |
| 12844 | 25454 | | 3.21 | 1.0E-13 | AJ271735.1 | NT | MELANOMA-ASSOCIATED ANTIGEN B4 (MAGE-B4 ANTIGEN) |
| 333 | 13422 | 26345 | 3.14 | 9.0E-14 | AA781159.1 | EST_HUMAN | MELANOMA-ASSOCIATED ANTIGEN B4 (MAGE-B4 ANTIGEN) |
| 334 | 13423 | 26346 | 2.37 | 9.0E-14 | AA781159.1 | EST_HUMAN | Mus musculus osteoclast protein tyrosine phosphatase mRNA, complete cds |
| 2508 | 15511 | | 4.8 | 9.0E-14 | AW861577.1 | EST_HUMAN | 7145e10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29 b2 MER29 repetitive element; |
| 2597 | 15598 | 28617 | 1.03 | 9.0E-14 | AJ133127.1 | NT | contains MER29 b2 MER29 repetitive element; |
| 2597 | 15598 | 28618 | 1.03 | 9.0E-14 | AJ133127.1 | NT | AV715377 DOB Homo sapiens cDNA clone DCBAIE03 5' |
| 2764 | 15756 | 28777 | 6.94 | 9.0E-14 | AB038162.1 | NT | Homo sapiens Xq pseudautosomal region, segment 1/2 |
| | | | | | | | Homo sapiens Xq pseudautosomal region, segment 1/2 |
| | | | | | | | aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19 repetitive element; |
| | | | | | | | aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19 repetitive element; |
| | | | | | | | RC4-CT0322-080100-013-009 CT0322 Homo sapiens cDNA |
| | | | | | | | Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene) |
| | | | | | | | Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene) |
| | | | | | | | Homo sapiens TFF gene cluster for trefoil factor, complete cds |

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Table 4
Single Exon Probes Expressed In Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 3128 | 16185 | 28094 | 5.43 | 9.0E-14 | AW513296.1 | EST_HUMAN | xc64h05.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2707833 3' |
| 3252 | 13422 | 26345 | 0.67 | 9.0E-14 | AA781159.1 | EST_HUMAN | aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19 |
| 3811 | 16851 | 29759 | 7.16 | 9.0E-14 | D14547.1 | NT | repetitive element ; |
| 4789 | 17807 | 30699 | 1.68 | 9.0E-14 | AJ002153.1 | NT | Human DNA, SINE repetitive element |
| 3509 | 16555 | | 1.44 | 8.0E-14 | BE468283.1 | EST_HUMAN | Seguinus oedipus gene for seminal vesicle secreted protein semenogelin I |
| 3978 | 17018 | | 3.46 | 8.0E-14 | R76269.1 | EST_HUMAN | hz71c09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3213424 3' |
| 9803 | 21126 | 34530 | 21.45 | 8.0E-14 | X89211.1 | NT | y72e03.r1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:144796 3' |
| 9918 | 22739 | 36192 | 3.1 | 8.0E-14 | AA216916.1 | EST_HUMAN | H. sapiens DNA for endogenous retroviral like element |
| 11762 | 24690 | | 1.52 | 8.0E-14 | BE062558.1 | EST_HUMAN | zq17c10.s1 Striatogene fetal retina 937202 Homo sapiens cDNA clone IMAGE:629970 3' |
| 12590 | 25284 | 31783 | 2.99 | 8.0E-14 | AI888118.1 | EST_HUMAN | QV2-BT0258-261099-014-a01 BT0258 Homo sapiens cDNA |
| 1633 | 15873 | | 3.99 | 7.0E-14 | AW151673.1 | EST_HUMAN | wc92h08.x1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:2326143 3' |
| 9272 | 22238 | | 0.51 | 7.0E-14 | AL163285.2 | NT | x167e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12 |
| 367 | 13453 | 26381 | 16.94 | 6.0E-14 | AF020503.1 | NT | MER10 repetitive element ; |
| 10181 | 23106 | 36587 | 2.54 | 6.0E-14 | AF020503.1 | NT | Homo sapiens chromosome 21 segment HS21C085 |
| 10181 | 23106 | 36588 | 2.54 | 6.0E-14 | AF020503.1 | NT | Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5 |
| 620 | 13685 | 26603 | 5.23 | 5.0E-14 | Q63120 | SWISSPROT | Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5 |
| 3683 | 16726 | | 0.95 | 5.0E-14 | AL163247.2 | NT | Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5 |
| 5093 | 18103 | 30979 | 1.39 | 5.0E-14 | AW073791.1 | EST_HUMAN | Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5 |
| 5811 | 18707 | 31864 | 4.84 | 5.0E-14 | P08547 | SWISSPROT | CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER 1 (MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN) |
| 1125 | 15859 | | 1.95 | 4.0E-14 | P04928 | SWISSPROT | Homo sapiens chromosome 21 segment HS21C047 |
| 1895 | 14920 | 27916 | 7 | 4.0E-14 | AJ007973.1 | NT | xb03b05.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575186 3' similar to contains L1.12 L1 |
| 3785 | 16807 | | 1 | 4.0E-14 | AA046502.1 | EST_HUMAN | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| 4320 | 17349 | 30233 | 0.98 | 4.0E-14 | N46328.1 | EST_HUMAN | S-ANTIGEN PROTEIN PRECURSOR |
| 8291 | 21260 | | 0.6 | 4.0E-14 | X87344.1 | NT | Homo sapiens LGMD2B gene |
| | | | | | | | z67a06.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487858 5' |
| | | | | | | | y73c12.s1 Soares_multiple_sclerosis_2NbHMSF Homo sapiens cDNA clone IMAGE:279180 3' similar to contains L1.13 L1 repetitive element ; |
| | | | | | | | H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 12905 | 25988 | | 6.38 | 4.0E-14 | A186224.1 | EST_HUMAN | wmb0303.x1 NCL_CGAP_U14 Homo sapiens cDNA clone IMAGE:2435332 3' similar to contains Alu repetitive element; |
| 950 | 14003 | 26955 | 4.69 | 3.0E-14 | X65466.1 | NT | R. norvegicus mRNA for GPG2 protein |
| 4963 | 17978 | 30868 | 1.16 | 3.0E-14 | 7656864 | NT | Homo sapiens a disintegrin and metalloproteinase domain 29 (ADAM29), mRNA |
| 6898 | 19950 | 33246 | 0.96 | 3.0E-14 | A1420786.1 | EST_HUMAN | ta91c12.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:O00519 O00519 FATTY ACID AMIDE HYDROLASE.; |
| 6898 | 19950 | 33247 | 0.96 | 3.0E-14 | A1420786.1 | EST_HUMAN | ta91c12.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:O00519 O00519 FATTY ACID AMIDE HYDROLASE.; |
| 7021 | 25675 | | 0.51 | 3.0E-14 | AL163248.2 | NT | Homo sapiens chromosome 21 segment HS21C048 |
| 7229 | 20251 | 33585 | 0.57 | 3.0E-14 | AA386311.1 | EST_HUMAN | EST185054 Brain IV Homo sapiens cDNA |
| 8139 | 22105 | 35531 | 0.83 | 3.0E-14 | N42165.1 | EST_HUMAN | y07b10.1 Soares melanocyte 2Nbr-IM Homo sapiens cDNA clone IMAGE:270523 5' |
| 11337 | 24287 | 37811 | 2.83 | 3.0E-14 | BE888016.1 | EST_HUMAN | 601511330F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5' |
| 11568 | 18347 | 31293 | 6.06 | 3.0E-14 | AW265354.1 | EST_HUMAN | xp45f12.x1 NCL_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains Alu repetitive element; contains element MERB repetitive element; |
| 12824 | 25854 | | 1.68 | 3.0E-14 | AL163285.2 | NT | Homo sapiens chromosome 21 segment HS21C085 |
| 390 | 13465 | 26395 | 2.76 | 2.0E-14 | AJ271736.1 | NT | Homo sapiens Xq pseudautosomal region; segment 2/2 |
| 390 | 13465 | 26396 | 2.76 | 2.0E-14 | AJ271736.1 | NT | Homo sapiens Xq pseudautosomal region; segment 2/2 |
| 691 | 15847 | 26682 | 9.98 | 2.0E-14 | AL163303.2 | NT | Homo sapiens chromosome 21 segment HS21C103 |
| 2397 | 15404 | | 1.89 | 2.0E-14 | AW372868.1 | EST_HUMAN | RC3-BT0377-091299-031-D12 BT0377 Homo sapiens cDNA |
| 2472 | 15476 | | 1.4 | 2.0E-14 | 7657529 | NT | Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA |
| 2531 | 15534 | 28554 | 2.2 | 2.0E-14 | AL163209.2 | NT | Homo sapiens chromosome 21 segment HS21C009 |
| 2547 | 15548 | | 1.03 | 2.0E-14 | BE222432.1 | EST_HUMAN | hy80g10.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3180738 3' similar to contains Alu repetitive element; contains OFR.t1 OFR repetitive element; |
| 2683 | 15678 | | 1.48 | 2.0E-14 | P08548 | SWISSPROT | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| 5602 | 18698 | 31669 | 0.91 | 2.0E-14 | BF380661.1 | EST_HUMAN | IL2-UT0072-240800-142-D07 UT0072 Homo sapiens cDNA |
| 5702 | 18797 | 31972 | 0.81 | 2.0E-14 | A1312351.1 | EST_HUMAN | ta78h01.x2 NCL_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050225 3' similar to contains L1 L1 repetitive element; |
| 5809 | 18899 | 32082 | 3.16 | 2.0E-14 | U01317.1 | NT | Human beta globin region on chromosome 11 |
| 7067 | 20089 | | 0.92 | 2.0E-14 | BE000550.1 | EST_HUMAN | RC3-BN0072-240200-011-606 BN0072 Homo sapiens cDNA |
| 7290 | 20262 | 33596 | 0.57 | 2.0E-14 | 4585709 | NT | Homo sapiens a disintegrin and metalloproteinase domain 11 (ADAM11), mRNA |
| 7502 | 20467 | 33828 | 0.87 | 2.0E-14 | P56163 | SWISSPROT | ZINC-FINGER PROTEIN NEURO-D4 |
| 7751 | 20704 | 34072 | 21.51 | 2.0E-14 | BE158761.1 | EST_HUMAN | IL2-HT0397-071299-024-D04 HT0397 Homo sapiens cDNA |
| 7751 | 20704 | 34073 | 21.51 | 2.0E-14 | BE158761.1 | EST_HUMAN | IL2-HT0397-071299-024-D04 HT0397 Homo sapiens cDNA |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 10277 | 23202 | 36687 | 0.52 | 2.0E-14 | A1978795.1 | EST_HUMAN | vr59g10.x1 NCL_CGAP_U1 Homo sapiens cDNA clone IMAGE:2492034 3' similar to contains Alu repetitive element |
| 10783 | 23704 | 37203 | 0.53 | 2.0E-14 | AV741648.1 | EST_HUMAN | AV741648 CB Homo sapiens cDNA clone CBFBBF04 5' |
| 11133 | 24093 | 37622 | 3.94 | 2.0E-14 | AW139800.1 | EST_HUMAN | UI-H-B1-adv-a-10-0-UI.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718234 3' |
| 12822 | 25857 | | 1.71 | 2.0E-14 | AF008191.1 | NT | Homo sapiens putative G6 protein (GR6) gene, complete cds |
| 1068 | 14113 | 27063 | 2.09 | 1.0E-14 | AL163246.2 | NT | Homo sapiens chromosome 21 segment HS21C046 |
| 1405 | 14438 | 27408 | 8.16 | 1.0E-14 | AL163268.2 | NT | Homo sapiens chromosome 21 segment HS21C068 |
| 1405 | 14438 | 27407 | 8.16 | 1.0E-14 | AL163268.2 | NT | Homo sapiens chromosome 21 segment HS21C068 |
| 2017 | 15038 | 28049 | 15.42 | 1.0E-14 | L44140.1 | NT | Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphata dehydrogenase (G6PD) gene, complete cds's |
| 2195 | 15210 | 28228 | 5.77 | 1.0E-14 | AL163303.2 | NT | Homo sapiens chromosome 21 segment HS21C103 |
| 2419 | 15426 | 28449 | 5.29 | 1.0E-14 | AF001689.1 | NT | Homo sapiens ribosomal protein L23A (RPL23A) gene, complete cds |
| 2955 | 16013 | 28940 | 1.05 | 1.0E-14 | P05227 | SWISSPROT | HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-II) |
| 3182 | 16237 | 29154 | 6.2 | 1.0E-14 | BF335227.1 | EST_HUMAN | RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA |
| 3182 | 16237 | 29155 | 6.2 | 1.0E-14 | BF335227.1 | EST_HUMAN | RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA |
| 3901 | 16941 | 29852 | 1.75 | 1.0E-14 | AA682694.1 | EST_HUMAN | ae69c12.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:2753059 3' |
| 4500 | 17525 | 30410 | 2.07 | 1.0E-14 | AW275852.1 | EST_HUMAN | xq39h10.x1 NCL_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2753059 3' |
| 5907 | 18993 | 32184 | 2.1 | 1.0E-14 | AF126145.1 | NT | Bos taurus xenobiotic/medium-chain fatty acid:CoA ligase form XL-III mRNA, nuclear mRNA encoding mitochondrial protein, complete cds |
| 6831 | 25669 | 33176 | 11.02 | 1.0E-14 | 11437150 | NT | Homo sapiens prominin (mouse)-like 1 (PROML1), mRNA |
| 6831 | 25669 | 33177 | 11.02 | 1.0E-14 | 11437150 | NT | Homo sapiens prominin (mouse)-like 1 (PROML1), mRNA |
| 1579 | 14612 | 27584 | 1.78 | 9.0E-15 | 7427522 | NT | Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA |
| 2183 | 15108 | | | | | | Homo sapiens transcription factor GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T64 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin gene, complete cds; and L-type calcium channel a2 |
| 7738 | 20693 | 34056 | 1.37 | 9.0E-15 | AF106779.1 | NT | GAG POLYPROTEIN [CONTAINS: CORE PROTEINS P15, P12, P30, P10] |
| 8350 | 21319 | 34733 | 1.17 | 9.0E-15 | BE003559.1 | EST_HUMAN | 601677750F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960156 5' |
| 2822 | 13553 | | 1.42 | 8.0E-15 | BE261482.1 | EST_HUMAN | 601148632F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3164023 5' |
| 7987 | 20356 | 33708 | 1.55 | 7.0E-15 | BF035327.1 | EST_HUMAN | 601458531F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3662086 5' |
| 10801 | 23722 | | 2.45 | 7.0E-15 | AW241958.1 | EST_HUMAN | xn77d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2700483 3' similar to contains THR12 THR repetitive element |
| 996 | 14047 | 27001 | 6.55 | 6.0E-15 | AJ271736.1 | NT | Homo sapiens Xq pseudautosomal region; segment 2/2 |
| 6027 | 19110 | 32311 | 1.11 | 6.0E-15 | X73462.1 | NT | O aries mRNA for hair keratin cytochrome-rich protein |
| 6027 | 19110 | 32312 | 1.11 | 6.0E-15 | X73462.1 | NT | O aries mRNA for hair keratin cytochrome-rich protein |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 410 | 13483 | 26418 | 5.24 | 5.0E-15 | AL163208.2 | NT | Homo sapiens chromosome 21 segment HS21C008 |
| 2771 | 15763 | 28784 | 2.05 | 5.0E-15 | U91328.1 | NT | Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds |
| 3482 | 16528 | | 1.08 | 5.0E-15 | AW298817.1 | EST_HUMAN | UHLBWQ-epb-g-10-0.U1 s1 NCL_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2731219 3' |
| 11035 | 23999 | | 2.27 | 5.0E-15 | AV730056.1 | EST_HUMAN | AV730056 HTF Homo sapiens cDNA clone HTFAVE06 5' |
| 427 | 13122 | 26020 | 3.54 | 4.0E-15 | AL163303.2 | NT | Homo sapiens chromosome 21 segment HS21C103 |
| 6822 | 19876 | 33165 | 0.98 | 4.0E-15 | AB007970.1 | NT | Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501 |
| 11401 | 21088 | 34487 | 1.79 | 4.0E-15 | AJ130894.1 | NT | Homo sapiens mRNA for transcription factor |
| 11401 | 21088 | 34488 | 1.79 | 4.0E-15 | AJ130894.1 | NT | Homo sapiens mRNA for transcription factor |
| 4245 | 17274 | | 6.54 | 3.0E-15 | N89452.1 | EST_HUMAN | LY1142F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone LY1142 5' similar to ANF(CARDIODILATIN) |
| 5067 | 18077 | 30958 | 0.67 | 3.0E-15 | AA078097.1 | EST_HUMAN | 7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03 |
| 5067 | 18077 | 30959 | 0.67 | 3.0E-15 | AA078097.1 | EST_HUMAN | 7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03 |
| 6986 | 20209 | | 1.27 | 3.0E-15 | Q64825 | SWISSPROT | GLUTATHIONE PEROXIDASE RY2D1 PRECURSOR (ODORANT-METABOLIZING PROTEIN RY2D1) |
| 7495 | 20460 | 33819 | 3.86 | 3.0E-15 | M27685.1 | NT | Mus musculus ultra high sulfur keratin gene, complete cds |
| 7495 | 20460 | 33820 | 3.86 | 3.0E-15 | M27685.1 | NT | Mus musculus ultra high sulfur keratin gene, complete cds |
| 10285 | 23210 | | 2.66 | 3.0E-15 | AA807128.1 | EST_HUMAN | oc36a07 s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1351764 3' similar to contains MER19.11 |
| 11146 | 24106 | 37633 | 3.42 | 3.0E-15 | AB026898.1 | NT | MER19 repetitive element; |
| 250 | 13347 | 26273 | 4.45 | 2.0E-15 | AF223391.1 | NT | Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds) |
| 368 | 13454 | 26382 | 4.01 | 2.0E-15 | AF223391.1 | NT | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced |
| 368 | 13454 | 26383 | 4.01 | 2.0E-15 | AF223391.1 | NT | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced |
| 2381 | 15389 | 28413 | 1.02 | 2.0E-15 | BE350127.1 | EST_HUMAN | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced |
| 2381 | 15389 | 28414 | 1.02 | 2.0E-15 | BE350127.1 | EST_HUMAN | h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 |
| 4095 | 17129 | 30023 | 1.21 | 2.0E-15 | AW238499.1 | EST_HUMAN | MER29 repetitive element; |
| | | | | | | | h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 |
| | | | | | | | MER29 repetitive element; |
| | | | | | | | h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 |
| | | | | | | | MER29 repetitive element; |
| | | | | | | | h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 |
| | | | | | | | MER29 repetitive element; |
| | | | | | | | h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 |
| | | | | | | | MER29 repetitive element; |
| | | | | | | | h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 |
| | | | | | | | MER29 repetitive element; |
| | | | | | | | h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 |
| | | | | | | | MER29 repetitive element; |
| | | | | | | | h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 |
| | | | | | | | MER29 repetitive element; |
| | | | | | | | h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 |
| | | | | | | | MER29 repetitive element; |
| | | | | | | | h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 |
| | | | | | | | MER29 repetitive element; |
| | | | | | | | h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 |
| | | | | | | | MER29 repetitive element; |
| | | | | | | | h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 |
| | | | | | | | MER29 repetitive element; |
| | | | | | | | h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 |
| | | | | | | | MER29 repetitive element; |
| | | | | | | | h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 |
| | | | | | | | MER29 repetitive element; |
| | | | | | | | h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 |
| | | | | | | | MER29 repetitive element; |
| | | | | | | | h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 |
| | | | | | | | MER29 repetitive element; |
| | | | | | | | h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 |
| | | | | | | | MER29 repetitive element; |
| | | | | | | | h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 |
| | | | | | | | MER29 repetitive element; |
| | | | | | | | h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 |
| | | | | | | | MER29 repetitive element; |
| | | | | | | | h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 |
| | | | | | | | MER29 repetitive element; |
| | | | | | | | h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 |
| | | | | | | | MER29 repetitive element; |
| | | | | | | | h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 |
| | | | | | | | MER29 repetitive element; |
| | | | | | | | h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 |
| | | | | | | | MER29 repetitive element; |
| | | | | | | | h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 |
| | | | | | | | MER29 repetitive element; |
| | | | | | | | h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 |
| | | | | | | | MER29 repetitive element; |
| | | | | | | | h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 |
| | | | | | | | MER29 repetitive element; |
| | | | | | | | h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 |
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| | | | | | | | h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 |
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| | | | | | | | MER29 repetitive element; |
| | | | | | | | h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 4653 | 17674 | | 2.73 | 2.0E-15 | AI806335.1 | EST_HUMAN | wf0706.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2349923 3' similar to TR:Q61043 Q61043 NINEIN. ; |
| 6306 | 19377 | 32616 | 1.02 | 2.0E-15 | BE562352.1 | EST_HUMAN | 601344253F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677268 5' |
| 6306 | 19377 | 32617 | 1.02 | 2.0E-15 | BE662352.1 | EST_HUMAN | 601344253F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677268 5' |
| 7321 | 20292 | | 1.42 | 2.0E-15 | AJ400877.1 | NT | Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene |
| 7486 | 20451 | 33810 | 2.84 | 2.0E-15 | AA704195.1 | EST_HUMAN | zj77e03.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460924 3' |
| 7625 | 20585 | 33948 | 4.75 | 2.0E-15 | W05064.1 | EST_HUMAN | za78d10.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:288675 5' similar to WP:IF44F4.8 CE02227 TRANSPOSASE ; |
| 8117 | 21054 | 34451 | 0.67 | 2.0E-15 | AL163247.2 | NT | Homo sapiens chromosome 21 segment HS21C047 |
| 9257 | 22223 | 35653 | 2.73 | 2.0E-15 | D14547.1 | NT | Human DNA, SINE repetitive element |
| 9427 | 22391 | 35629 | 0.74 | 2.0E-15 | AA397758.1 | EST_HUMAN | zj77g08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728414 5' |
| 9427 | 22391 | 35830 | 0.74 | 2.0E-15 | AA397758.1 | EST_HUMAN | zj77g08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728414 5' |
| 9759 | 22700 | 36157 | 1.19 | 2.0E-15 | AW379465.1 | EST_HUMAN | CM0-HT0244-201099-078-at12 HT0244 Homo sapiens cDNA |
| 9759 | 22700 | 36158 | 1.19 | 2.0E-15 | AW379465.1 | EST_HUMAN | CM0-HT0244-201099-078-at12 HT0244 Homo sapiens cDNA |
| 11187 | 24143 | | 4.15 | 2.0E-15 | AJ271735.1 | NT | Homo sapiens Xq pseudautosomal region; segment 1/2 |
| 12834 | 18339 | 31288 | 3.19 | 2.0E-15 | AF223391.1 | NT | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced |
| 12934 | 18339 | 31289 | 3.19 | 2.0E-15 | AF223391.1 | NT | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced |
| 2785 | 15777 | | 2.95 | 1.0E-15 | AI689984.1 | EST_HUMAN | b26h05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13539 Q13539 MARINER TRANSPOSASE. ; |
| 3025 | 18082 | 29005 | 1.53 | 1.0E-15 | BE043584.1 | EST_HUMAN | hk40e02.y1 NCI_CGAP_Ov34 Homo sapiens cDNA clone IMAGE:2999162 5' |
| 3158 | 18214 | 29129 | 1.2 | 1.0E-15 | P08547 | SWISSPROT | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| 5189 | 18198 | 31071 | 1.11 | 1.0E-15 | AI984928.1 | EST_HUMAN | wf86e04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494590 3' |
| 6508 | 19572 | 32825 | 1.63 | 1.0E-15 | T95763.1 | EST_HUMAN | ye40e10.s1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:120234 3' similar to contains MER6 repetitive element ; |
| 7205 | 20229 | | 1.93 | 1.0E-15 | BE074217.1 | EST_HUMAN | QV3-BT0569-270100-074-g05 BT0569 Homo sapiens cDNA |
| 7239 | 19974 | 33272 | 0.76 | 1.0E-15 | P39057 | SWISSPROT | DYNEN BETA CHAIN, CILIARY |
| 8574 | 21542 | 34962 | 1.04 | 1.0E-15 | AL163280.2 | NT | Homo sapiens chromosome 21 segment HS21C080 |
| 8763 | 21730 | 35152 | 4.51 | 1.0E-15 | AJ200976.1 | EST_HUMAN | qf68h06.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3' |
| 8763 | 21730 | 35153 | 4.51 | 1.0E-15 | AJ200976.1 | EST_HUMAN | qf68h06.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3' |
| 9394 | 22359 | 35789 | 0.49 | 1.0E-15 | AL163207.2 | NT | Homo sapiens chromosome 21 segment HS21C007 |
| 9397 | 22362 | 35793 | 1.5 | 1.0E-15 | 4507208 | NT | Homo sapiens spermidine synthase (SRM) mRNA |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 9602 | 22806 | 36055 | 0.79 | 1.0E-15 | Q39575 | SWISSPROT | DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM |
| 9990 | 22917 | 36383 | 0.95 | 1.0E-15 | AA864653.1 | EST_HUMAN | oh37c03.s1 NCL_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1459972 3' similar to contains L1.13 L1 repetitive element: |
| 11169 | 24127 | 37657 | 4.18 | 1.0E-15 | AF044083.1 | NT | Homo sapiens major histocompatibility locus class III region |
| 13008 | 25720 | 31612 | 9.25 | 1.0E-15 | A1783944.1 | EST_HUMAN | tr31c05.x1 NCL_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219912 3' similar to contains Alu repetitive element: |
| 4532 | 17555 | 30443 | 1.15 | 9.0E-16 | 4503168 | NT | Homo sapiens cut (Drosophila)-like 1 (CCAAT displacement protein) (CUTL1) mRNA |
| 11338 | 24288 | 37812 | 1.94 | 9.0E-16 | F08688.1 | EST_HUMAN | HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05 |
| 5786 | 18878 | 32060 | 0.79 | 7.0E-16 | 4885120 | NT | Homo sapiens chemokine (C-C motif) receptor 8 (CCR8) mRNA |
| 7564 | 20527 | 33885 | 1.45 | 7.0E-16 | O88807 | SWISSPROT | PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4) |
| 7564 | 20527 | 33886 | 1.45 | 7.0E-16 | O88807 | SWISSPROT | PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4) |
| 12957 | 25809 | | 1.88 | 7.0E-16 | T94149.1 | EST_HUMAN | (PEPTIDYLARGININE DEIMINASE TYPE ALPHA) |
| 2151 | 15167 | | 7.77 | 6.0E-16 | AW972611.1 | EST_HUMAN | ye28c12.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:119062 5' |
| 1489 | 14522 | 27495 | 1.28 | 5.0E-16 | AJ251154.1 | NT | EST1384702 IMAGE resequences, MAGL Homo sapiens cDNA |
| 2889 | 15885 | 28702 | 2.52 | 5.0E-16 | AA992176.1 | EST_HUMAN | Mus musculus olfactory receptor cluster, OR37A, OR37B, OR37C, OR37E genes and OR37D pseudogene |
| 10414 | 23336 | 36821 | 0.48 | 5.0E-16 | AL163246.2 | NT | o180c04.s1 Scores_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1623078 3' similar to contains element L1 repetitive element: |
| 11849 | 24732 | 38319 | 2.54 | 5.0E-16 | BF217368.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C046 |
| 13044 | 25585 | | 10.68 | 5.0E-16 | 11418127 | NT | 601885734F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4104129 5' |
| 2249 | 15263 | | 1.64 | 4.0E-16 | AB001523.1 | NT | Homo sapiens GTP binding protein 1 (GTPBP1), mRNA |
| 2388 | 15396 | 28421 | 2.21 | 4.0E-16 | AW797168.1 | EST_HUMAN | Homo sapiens gene for TMEM1 and PWP2, complete and partial cds |
| 2388 | 15396 | 28422 | 2.21 | 4.0E-16 | AW797168.1 | EST_HUMAN | QV1-UM0036-200300-115-g02 UM0036 Homo sapiens cDNA |
| 3471 | 16517 | 28438 | 3.94 | 4.0E-16 | Q16653 | SWISSPROT | MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR |
| 4168 | 17197 | 30083 | 4.74 | 4.0E-16 | BE083875.1 | EST_HUMAN | PM4-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA |
| 4166 | 17197 | 30084 | 4.74 | 4.0E-16 | BE083875.1 | EST_HUMAN | PM4-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA |
| 7980 | 20919 | 34310 | 37.37 | 4.0E-16 | AL163284.2 | NT | Homo sapiens chromosome 21 segment HS21C084 |
| 9650 | 22594 | 36042 | 0.97 | 4.0E-16 | 11423191 | NT | Homo sapiens hypothetical protein FLJ10024 (FLJ10024), mRNA |
| 12290 | 25106 | | 2.41 | 4.0E-16 | P08548 | SWISSPROT | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| 12392 | 25169 | 31816 | 2.11 | 4.0E-16 | 6912459 | NT | Homo sapiens Gb2-associated binder 2 (KIA00571), mRNA |
| 12656 | 25336 | | 1.36 | 4.0E-16 | R18591.1 | EST_HUMAN | yf96b11.1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:30489 5' |
| 133 | 13238 | 26169 | 1.24 | 3.0E-16 | AW022862.1 | EST_HUMAN | dl45c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5' |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 133 | 13238 | 26170 | 1.24 | 3.0E-16 | AW022662.1 | EST_HUMAN | df45c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5' |
| 466 | 13539 | | 1.91 | 3.0E-16 | AL046445.1 | EST_HUMAN | DKFZp434P037_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434P037 5' |
| 476 | 13548 | | 3.08 | 3.0E-16 | AF135446.1 | NT | Homo sapiens TSX (TSX) pseudogene, exon 5 |
| 1446 | 14479 | 27455 | 1.53 | 3.0E-16 | Q28983 | SW/ISSPROT | ZONADHESIN PRECURSOR |
| 2988 | 16046 | 28966 | 3.94 | 3.0E-16 | P03200 | SW/ISSPROT | ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (MA) [CONTAINS: GLYCOPROTEIN GP220] |
| 3953 | 16993 | 29909 | 0.96 | 3.0E-16 | T08169.1 | EST_HUMAN | EST060600 Infant Brain, Bento Soares Homo sapiens cDNA clone HIBBA13 5' end |
| 3980 | 17020 | | 0.77 | 3.0E-16 | AF020503.1 | NT | Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5 |
| 3981 | 17021 | | 1.06 | 3.0E-16 | U03887.1 | NT | Human BXP20 gene |
| 5350 | 18455 | | 1.11 | 3.0E-16 | AA077225.1 | EST_HUMAN | 7B10F02 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B10F02 |
| 5698 | 18793 | 31866 | 1.2 | 3.0E-16 | AF003528.1 | NT | Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions |
| 9005 | 21971 | 35392 | 4.92 | 3.0E-16 | AI002836.1 | EST_HUMAN | am98h05.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684185 3' similar to contains THR.b2 THR repetitive element; |
| 10250 | 23175 | | 0.9 | 3.0E-16 | BF690617.1 | EST_HUMAN | 602246538F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332032 5' |
| 10478 | 23400 | 36897 | 5.77 | 3.0E-16 | L78810.1 | NT | Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds |
| 13079 | 25961 | 31317 | 1.4 | 3.0E-16 | AL043288.2 | EST_HUMAN | DKFZp434L1623_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L1623 5' |
| 873 | 14025 | | 1.04 | 2.0E-16 | AL163279.2 | NT | Homo sapiens chromosome 21 segment HS21C079 |
| 2395 | 15402 | | 1.32 | 2.0E-16 | AA621761.1 | EST_HUMAN | af06d04.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1030855 3' |
| 2899 | 15695 | | 1.25 | 2.0E-16 | J03061.1 | NT | Human SSAV-related endogenous retroviral LTR-like element |
| 4207 | 17236 | 30123 | 1.14 | 2.0E-16 | X89211.1 | NT | H.sapiens DNA for endogenous retroviral like element |
| 6905 | 19957 | 33254 | 0.83 | 2.0E-16 | Q31125 | SW/ISSPROT | HISTIDINE-RICH PROTEIN KE4 |
| 7984 | 20923 | 34316 | 1.4 | 2.0E-16 | AI470723.1 | EST_HUMAN | ff16e11.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141708 3' similar to contains element MER33 repetitive element; |
| 8300 | 21269 | 34681 | 1.88 | 2.0E-16 | AI732837.1 | EST_HUMAN | n24-7706.x5 NCL_CGAP_P112 Homo sapiens cDNA clone IMAGE:1290947 similar to TR:O54849 O54849 HYPOTHETICAL 42.9 KD PROTEIN. [2] TR:O08905 contains MER7 t1 MER7 repetitive element; |
| 8498 | 21466 | 34882 | 0.73 | 2.0E-16 | BE858026.1 | EST_HUMAN | 782h09.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:3303521 3' |
| 8498 | 21466 | 34883 | 0.73 | 2.0E-16 | BE858026.1 | EST_HUMAN | 782h09.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:3303521 3' |
| 8872 | 21839 | 35261 | 0.75 | 2.0E-16 | AW877214.1 | EST_HUMAN | CM4-PT0034-180200-508-a01 PT0034 Homo sapiens cDNA |
| 8872 | 21839 | 35262 | 0.75 | 2.0E-16 | AW877214.1 | EST_HUMAN | CM4-PT0034-180200-508-a01 PT0034 Homo sapiens cDNA |
| 11274 | 24226 | 37752 | 1.59 | 2.0E-16 | 5902145 | NT | Homo sapiens ubiquitin carrier protein E2-C (UBCH10), mRNA |
| 186 | 13286 | 26210 | 2.57 | 1.0E-16 | AF200719.1 | NT | Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 382 | 13495 | | 37.96 | 1.0E-16 | AA628592.1 | EST_HUMAN | cd39g11.s1 Soares_tetral_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1034084 3' similar to contains OFR12 OFR repetitive element ; |
| 1988 | 15009 | 28014 | 2.22 | 1.0E-16 | BF327942.1 | EST_HUMAN | QV0-BN0148-070700-293-a10 BN0148 Homo sapiens cDNA |
| 5810 | 18900 | 32083 | 0.68 | 1.0E-16 | AF163864.1 | NT | Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced |
| 6574 | 19634 | | 25.8 | 1.0E-16 | U45983.1 | NT | Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds |
| 6726 | 19782 | 33061 | 3.06 | 1.0E-16 | Q02779 | SWISSPROT | MITOGEN-ACTIVATED PROTEIN KINASE KINASE 10 (MIXED LINEAGE KINASE 2) (PROTEIN KINASE MST) |
| 7802 | 19634 | | 6.75 | 1.0E-16 | U45983.1 | NT | Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds |
| 8638 | 22582 | 36031 | 1.06 | 1.0E-16 | AW875651.1 | EST_HUMAN | QV2-PT0012-040400-124-e03 PT0012 Homo sapiens cDNA |
| 3751 | 16793 | 29704 | 2.77 | 9.0E-17 | AW900048.1 | EST_HUMAN | CM1-NN1003-200300-153-a01 NN1003 Homo sapiens cDNA |
| 6886 | 19638 | | 2.35 | 9.0E-17 | AI392964.1 | EST_HUMAN | tg22c11.x1 NCI_CGAP CLL1 Homo sapiens cDNA clone IMAGE:2109524 3' similar to contains MER28 12 MER28 repetitive element ; |
| 8445 | 21414 | | 5.47 | 9.0E-17 | AW150257.1 | EST_HUMAN | kg48g12.x1 NCI_CGAP_U1f1 Homo sapiens cDNA clone IMAGE:2630950 3' similar to contains OFR12 OFR repetitive element ; |
| 10584 | 23506 | | 2.3 | 9.0E-17 | AF200719.1 | NT | Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds |
| 1020 | 14066 | | 2.01 | 8.0E-17 | AW890701.1 | EST_HUMAN | QV0-OT0032-080300-165-d01 OT0032 Homo sapiens cDNA |
| 3907 | 16947 | | 0.88 | 8.0E-17 | AL163280.2 | NT | Homo sapiens chromosome 21 segment HS21C080 |
| 5863 | 25842 | 31927 | 3.24 | 8.0E-17 | BE172081.1 | EST_HUMAN | MR0-HT0559-060300-003-e04 HT0559 Homo sapiens cDNA |
| 7490 | 20455 | | 1.82 | 8.0E-17 | AV730759.1 | EST_HUMAN | AV730759 HTF Homo sapiens cDNA clone HTFAQB07 5' |
| 8019 | 20956 | 34349 | 0.54 | 8.0E-17 | 6753651 | NT | Mus musculus dynein, axon, heavy chain 11 (Dnahc11), mRNA |
| 1452 | 14485 | | 2.63 | 7.0E-17 | 6753097 | NT | Mus musculus apolipoprotein B editing complex 2 (ApoBec2), mRNA |
| 5396 | 18499 | | 3.14 | 7.0E-17 | AF216650.1 | NT | Homo sapiens putative MTAP (MTAP) mRNA, partial cds, alternatively spliced |
| 6945 | 19998 | 33193 | 7.34 | 7.0E-17 | AF229843.1 | NT | Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene |
| 204 | 13305 | 26234 | 6.62 | 6.0E-17 | AW983880.1 | EST_HUMAN | RC1-HN0003-220300-021-b04 HN0003 Homo sapiens cDNA |
| 6446 | 19511 | 32761 | 1.8 | 6.0E-17 | AW662772.1 | EST_HUMAN | hi81d04.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2978695 3' similar to contains L1.12 L1 repetitive element ; |
| 10655 | 23577 | 37074 | 0.54 | 6.0E-17 | P20138 | SWISSPROT | MYELOID CELL SURFACE ANTIGEN CD33 PRECURSOR (GP87) |
| 10926 | 23846 | | 0.46 | 6.0E-17 | W92331.1 | EST_HUMAN | ze15f03.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:359093 3' |
| 421 | 13116 | 26014 | 3.22 | 5.0E-17 | T84110.1 | EST_HUMAN | yc05h08.r1 Stralagene lung (#937210) Homo sapiens cDNA clone IMAGE:79839 5' |
| 7840 | 20787 | 34162 | 1.76 | 5.0E-17 | T81043.1 | EST_HUMAN | yc26f04.r1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:109327 5' |
| 9717 | 22745 | 36196 | 1.24 | 4.0E-17 | AW129185.1 | EST_HUMAN | xf20e04.x1 NCI_CGAP Kid8 Homo sapiens cDNA clone IMAGE:2818622 3' similar to contains Alu repetitive element; contains MER19.b1 MER19 repetitive element ; |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 11821 | 24704 | 38286 | 1.96 | 4.0E-17 | AL163247.2 | NT | Homo sapiens chromosome 21 segment HS21C047 |
| 12303 | 25114 | | 2.02 | 4.0E-17 | A1073546.1 | EST_HUMAN | ov45604.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1640286 3' similar to TR:Q16530 |
| 1490 | 14523 | | 1.72 | 3.0E-17 | D14547.1 | NT | Q16530 PMS3 MRNA ;contains MER10.12 MER10 repetitive element ; |
| 2108 | 15125 | 28144 | 1.22 | 3.0E-17 | AW119123.1 | EST_HUMAN | Human DNA, SINE repetitive element |
| 3208 | 16263 | | 1.66 | 3.0E-17 | P35410 | SWISSPROT | xd89c09.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2604784 3' |
| 3656 | 16699 | 29614 | 1.33 | 3.0E-17 | BE328522.1 | EST_HUMAN | MAS-RELATED G PROTEIN-COUPLED RECEPTOR MRG |
| 3656 | 16699 | 29615 | 1.33 | 3.0E-17 | BE328522.1 | EST_HUMAN | hw05b04.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181999 3' |
| 5068 | 18078 | | 1.17 | 3.0E-17 | BF511266.1 | EST_HUMAN | hw05b04.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181999 3' |
| | | | | | | | UI-H-B14-adj-c-08-0-UI.s1 NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085043 3' |
| 8811 | 21579 | 34995 | 1.16 | 3.0E-17 | N68451.1 | EST_HUMAN | zai14b02.s1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:282491 3' similar to contains PTR5.t3 PTR5 repetitive element ; |
| 10060 | 22987 | 36455 | 4.94 | 3.0E-17 | AB028898.1 | NT | Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds) |
| 10746 | 23668 | 37164 | 0.73 | 3.0E-17 | BF327012.1 | EST_HUMAN | QV3-BN0047-270700-283-at12 BN0047 Homo sapiens cDNA |
| 10746 | 23668 | 37165 | 0.73 | 3.0E-17 | BF327012.1 | EST_HUMAN | QV3-BN0047-270700-283-at12 BN0047 Homo sapiens cDNA |
| 12266 | 25089 | | 3.31 | 3.0E-17 | 11417966 | NT | Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA |
| 353 | 13442 | 26367 | 3.4 | 2.0E-17 | A1270080.1 | EST_HUMAN | qt63a08.x1 NCL_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959922 3' similar to contains Alu repetitive element; |
| 354 | 13442 | 26367 | 3.97 | 2.0E-17 | A1270080.1 | EST_HUMAN | qt63a06.x1 NCL_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959922 3' similar to contains Alu repetitive element; |
| 990 | 14042 | | 2.04 | 2.0E-17 | AA722832.1 | EST_HUMAN | zg81d04.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:396751 3' |
| 2453 | 15458 | 28479 | 2.3 | 2.0E-17 | Q28983 | SWISSPROT | ZONADHESIN PRECURSOR |
| 2453 | 15458 | 28480 | 2.3 | 2.0E-17 | Q28983 | SWISSPROT | ZONADHESIN PRECURSOR |
| 2941 | 15989 | 28922 | 6.23 | 2.0E-17 | P12036 | SWISSPROT | NEUROFILAMENT TRIPLET H PROTEIN (200 KDA NEUROFILAMENT PROTEIN) (NEUROFILAMENT HEAVY POLYPEPTIDE) (NF-H) |
| 5440 | 18542 | 31452 | 1.8 | 2.0E-17 | M27685.1 | NT | Mus musculus ultra high sulfur keratin gene, complete cds |
| 5440 | 18542 | 31453 | 1.8 | 2.0E-17 | M27685.1 | NT | Mus musculus ultra high sulfur keratin gene, complete cds |
| 6395 | 19463 | | 1.99 | 2.0E-17 | AF055068.1 | NT | Homo sapiens MHC class 1 region |
| 6638 | 19696 | | 1.66 | 2.0E-17 | AF134881.1 | EST_HUMAN | DKFZp762J0610_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762J0610 5' |
| 8133 | 21070 | 34469 | 0.85 | 2.0E-17 | AB037839.1 | NT | Homo sapiens mRNA for KIAA1418 protein, partial cds |
| 8420 | 21389 | 34789 | 1.47 | 2.0E-17 | Q96156 | SWISSPROT | OLFACTORY RECEPTOR-LIKE PROTEIN OLF3 |
| 8900 | 21767 | 35191 | 1.29 | 2.0E-17 | AA300840.1 | EST_HUMAN | EST13504 Testis tumor Homo sapiens cDNA 5' end similar to glycogenin |
| 10228 | 23153 | 36643 | 2.35 | 2.0E-17 | BE299888.1 | EST_HUMAN | 600944890F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2660615 5' |
| 10264 | 23189 | 35673 | 2.83 | 2.0E-17 | AL163247.2 | NT | Homo sapiens chromosome 21 segment HS21C047 |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 10264 | 23189 | 36674 | 2.83 | 2.0E-17 | AL163247.2 | NT | Homo sapiens chromosome 21 segment HS21C047 |
| 10622 | 23544 | 37044 | 5.23 | 2.0E-17 | D13391.1 | NT | Human CYP19 gene for aromatase cytochrome P-450, promoter region (containing two cis-acting transcriptional regulatory elements) |
| 10745 | 23667 | 37162 | 0.66 | 2.0E-17 | P98063 | SWISSPROT | BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1) |
| 10745 | 23667 | 37163 | 0.66 | 2.0E-17 | P98063 | SWISSPROT | BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1) |
| 10772 | 23693 | 37190 | 0.57 | 2.0E-17 | A1798902.1 | EST_HUMAN | we94b04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348719 3' |
| 10772 | 23693 | 37191 | 0.57 | 2.0E-17 | A1798902.1 | EST_HUMAN | we94b04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348719 3' |
| 12366 | 25153 | | 1.31 | 2.0E-17 | AF213884.1 | NT | Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds |
| 751 | 13812 | 26755 | 3.24 | 1.0E-17 | P08183 | SWISSPROT | MUL.TIDRUG RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1) |
| 1721 | 14751 | | 1.35 | 1.0E-17 | AJ271736.1 | NT | Homo sapiens Xq pseudautosomal region; segment 2/2 |
| 1782 | 14811 | 27797 | 4.54 | 1.0E-17 | AL163207.2 | NT | Homo sapiens chromosome 21 segment HS21C007 |
| 2124 | 15141 | 28158 | 1.95 | 1.0E-17 | P02461 | SWISSPROT | COLLAGEN ALPHA 1(III) CHAIN PRECURSOR |
| 2343 | 15353 | 28374 | 2.43 | 1.0E-17 | U79410.1 | NT | Homo sapiens thrombospondin 2 (THBS2) gene, promoter region and exons 1A and 1B |
| 3581 | 16626 | | 1.05 | 1.0E-17 | AF224669.1 | NT | Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds |
| 4162 | 17193 | | 8.5 | 1.0E-17 | R09942.1 | EST_HUMAN | yf30e07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:128388 5' |
| 5600 | 19660 | | 0.68 | 1.0E-17 | AW469468.1 | EST_HUMAN | he38e05.x1 NCI_CGAP_CVL1 Homo sapiens cDNA clone IMAGE:2921312 3' similar to contains Alu repetitive element; contains LTR8.1 LTR8 repetitive element |
| 6809 | 19863 | 33151 | 1.73 | 1.0E-17 | A1185642.1 | EST_HUMAN | q65b05.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743825 3' |
| 6809 | 19863 | 33152 | 1.73 | 1.0E-17 | A1185642.1 | EST_HUMAN | q65b05.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743825 3' |
| 7296 | 20268 | 33603 | 0.96 | 1.0E-17 | Q16831 | SWISSPROT | URIDINE PHOSPHORYLASE (UDRPASE) |
| 8939 | 21905 | 35329 | 1.7 | 1.0E-17 | BE062744.1 | EST_HUMAN | QV0-BT0263-101299-072-407 BT0263 Homo sapiens cDNA |
| 10366 | 23289 | 36766 | 0.87 | 1.0E-17 | AW996538.1 | EST_HUMAN | QV3-BN0046-220300-129-c10 BN0046 Homo sapiens cDNA |
| 11747 | 24632 | 38212 | 1.64 | 1.0E-17 | Q28824 | SWISSPROT | MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE (MLCK) [CONTAINS: TELOKIN] |
| 13104 | 25825 | | 1.63 | 1.0E-17 | BE221470.1 | EST_HUMAN | hu25e05.x1 NCI_CGAP_Met15 Homo sapiens cDNA clone IMAGE:3171104 3' similar to contains MER13.b1 |
| 9856 | 22792 | | 2.96 | 9.0E-18 | AI472167.1 | EST_HUMAN | q66d03.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2148389 3' |
| 3800 | 16840 | 29747 | 1.87 | 8.0E-18 | 4758977 | NT | Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA |
| 3899 | 16939 | 29850 | 3.75 | 8.0E-18 | Q07537 | SWISSPROT | POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (PROTEIN-UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N-ACETYL GALACTOSAMINYLTRANSFERASE) (GALNAC-T1) |
| 349 | 13438 | 26361 | 23.15 | 7.0E-18 | AW316976.1 | EST_HUMAN | xx10b04.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gp.L20868 60S RIBOSOMAL PROTEIN L4 (HUMAN); |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 349 | 13438 | 26362 | 23.15 | 7.0E-18 | AW316976.1 | EST_HUMAN | xx10b04.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S |
| 7677 | 20635 | 33997 | 0.95 | 7.0E-18 | AW887542.1 | EST_HUMAN | RIBOSOMAL PROTEIN L4 (HUMAN); RC3-OT0091-170300-011-403 OT0091 Homo sapiens cDNA |
| 12789 | 13438 | 26361 | 2.67 | 7.0E-18 | AW316976.1 | EST_HUMAN | xx10b04.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S |
| 12789 | 13438 | 26362 | 2.67 | 7.0E-18 | AW316976.1 | EST_HUMAN | RIBOSOMAL PROTEIN L4 (HUMAN); xx10b04.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S |
| 3308 | 18359 | 29278 | 1.29 | 6.0E-18 | X71791.2 | NT | Rattus norvegicus partial GdnfPn-1 gene for glia-derived nedin/protease nexin 1, enhancer region |
| 4777 | 17797 | | 4.3 | 6.0E-18 | P52181 | SWISSPROT | PROTEIN-GLUTAMINE GAMMA-GLUTAMYLTRANSFERASE (TISSUE TRANSGLUTAMINASE) (TGASE C) (TGC) |
| 8593 | 21561 | | 2.64 | 6.0E-18 | 11428155 | NT | Homo sapiens similar to high-mobility group (nonhistone chromosomal) protein 4 (H. sapiens) (LOC83446), mRNA |
| 8691 | 21659 | 35082 | 0.57 | 6.0E-18 | AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C010 |
| 11469 | 24412 | 37861 | 1.54 | 6.0E-18 | AL163246.2 | NT | Homo sapiens chromosome 21 segment HS21C046 |
| 11657 | 24593 | 38166 | 2.06 | 6.0E-18 | X87344.1 | NT | H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes |
| 12527 | 25256 | 31805 | 2.95 | 6.0E-18 | U87929.1 | NT | Human aconitase hydratase (ACO2) gene, exon 4 |
| 1150 | 14192 | 27144 | 17.6 | 5.0E-18 | AI280214.1 | EST_HUMAN | qm66g11.x1 Soares_placenta_86c9weeks_2NbHP8b9W Homo sapiens cDNA clone IMAGE:1893668 3' similar to contains Alu repetitive element; |
| 5345 | 18450 | 31321 | 0.99 | 5.0E-18 | AF087913.1 | NT | Human endogenous retrovirus HERV-P-T47D |
| 9070 | 22036 | 35459 | 5.53 | 5.0E-18 | BE143312.1 | EST_HUMAN | MR0-HT0161-221089-002-c06 HT0161 Homo sapiens cDNA |
| 11323 | 24273 | 37800 | 3.26 | 5.0E-18 | 10242378 | NT | Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA |
| 11323 | 24273 | 37801 | 3.26 | 5.0E-18 | 10242378 | NT | Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA |
| 12649 | 25332 | | 6.29 | 5.0E-18 | AW867182.1 | EST_HUMAN | MR1-SN0035-090400-001-g11 SN0035 Homo sapiens cDNA |
| 12890 | 25544 | | 3.2 | 5.0E-18 | AV650547.1 | EST_HUMAN | AV650547 GLC Homo sapiens cDNA clone GLCGGA02 3' |
| 125 | 13232 | 26160 | 1.04 | 4.0E-18 | BE044076.1 | EST_HUMAN | hc36h04.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3 |
| 125 | 13232 | 26161 | 1.04 | 4.0E-18 | BE044076.1 | EST_HUMAN | WER29 repetitive element; |
| 1729 | 14759 | 27744 | 1.61 | 4.0E-18 | AA621814.1 | EST_HUMAN | hc36h04.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M26326 |
| 1908 | 14930 | | 0.95 | 4.0E-18 | AI738592.1 | EST_HUMAN | KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN); w33h08.x1 NCL_CGAP_C6t18 Homo sapiens cDNA clone IMAGE:2392095 3' |
| 2211 | 15228 | 28247 | 1.1 | 4.0E-18 | Q06430 | SWISSPROT | N-ACETYLACTOSAMINIDE BETA-1,6-N-ACETYLGLUCOSAMINYLTRANSFERASE (N-ACETYLGLUCOSAMINYLTRANSFERASE) (H-BRANCHING ENZYME) (IGNT) |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No.: | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|---------------------------|-------------------------------|---|
| 2211 | 15226 | 28248 | 1.1 | 4.0E-18 | Q06430 | SWISSPROT | N-ACETYLACTOSAMINIDE BETA-1,6-N-ACETYLGLUCOSAMINYL TRANSFERASE (N-ACETYLGLUCOSAMINYLTRANSFERASE) (I-BRANCHING ENZYME) (IGNT) |
| 3806 | 16846 | 29753 | 0.76 | 4.0E-18 | A1581586.1 | EST_HUMAN | ar93b06.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173139 3' similar to contains Alu repetitive element; |
| 5437 | 18539 | 31447 | 2.29 | 4.0E-18 | A1017565.1 | EST_HUMAN | ou23e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3' |
| 5437 | 18539 | 31448 | 2.29 | 4.0E-18 | A1017565.1 | EST_HUMAN | ou23e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3' |
| 8178 | 21148 | | 0.67 | 4.0E-18 | AA746811.1 | EST_HUMAN | nx64e08.s1 NCL_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1266898 similar to contains L1.12 L1 repetitive element; |
| 11348 | 24298 | 37826 | 4.22 | 4.0E-18 | AA371807.1 | EST_HUMAN | EST83633 Pituitary gland, subtracted (prolactin/growth hormone) II Homo sapiens cDNA 5' end similar to EST containing O family repeat |
| 850 | 13906 | 26885 | 24.96 | 3.0E-18 | AA814196.1 | EST_HUMAN | ab23h11.s1 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324581 3' similar to SW:RS5_HUMAN |
| 930 | 13983 | 26936 | 3.54 | 3.0E-18 | BE088634.1 | EST_HUMAN | P46782 40S RIBOSOMAL PROTEIN S5 ; |
| 3972 | 17012 | 29928 | 1.31 | 3.0E-18 | AL163247.2 | NT | CVIC-B10690-210300-298-907 BT0650 Homo sapiens cDNA |
| 7003 | 20129 | 33444 | 6.43 | 3.0E-18 | BE001671.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C047 |
| 11271 | 24223 | 37748 | 1.76 | 3.0E-18 | BF218650.1 | EST_HUMAN | PWC-BN0081-100300-007-b08 BN0081 Homo sapiens cDNA |
| 12774 | 25412 | | 5.15 | 3.0E-18 | AW022015.1 | EST_HUMAN | 601884856F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103652 5' |
| 251 | 13348 | 26274 | 5.97 | 2.0E-18 | AW836820.1 | EST_HUMAN | df31h12.y1 Marfan Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485126 5' |
| 1155 | 14197 | | 67.85 | 2.0E-18 | BE256097.1 | EST_HUMAN | QV1-L1T0036-150200-070-e07 LT0036 Homo sapiens cDNA |
| 3140 | 18197 | 29107 | 1.27 | 2.0E-18 | Q39575 | SWISSPROT | 601114352F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355044 5' |
| 5485 | 18585 | | 3.85 | 2.0E-18 | AA668610.1 | EST_HUMAN | DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM |
| 5584 | 18680 | 31644 | 3.38 | 2.0E-18 | D14547.1 | NT | ak53a07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409652 3' similar to TR:O14577 |
| 5584 | 18680 | 31645 | 3.38 | 2.0E-18 | D14547.1 | NT | O14577 BAC CLONE RG114A06 FROM 7Q31, COMPLETE SEQUENCE. ; |
| 5978 | 19063 | | 1.67 | 2.0E-18 | BF347229.1 | EST_HUMAN | Human DNA, SINE repetitive element |
| 6289 | 19361 | 32598 | 1 | 2.0E-18 | X60459.1 | NT | Human DNA, SINE repetitive element |
| 6289 | 19361 | 32599 | 1 | 2.0E-18 | X60459.1 | NT | Human IFNAR gene for Interferon alpha/beta receptor |
| 6409 | 19477 | 32724 | 0.75 | 2.0E-18 | BF352940.1 | EST_HUMAN | Human IFNAR gene for Interferon alpha/beta receptor |
| 6451 | 19516 | 32787 | 4.42 | 2.0E-18 | AW665853.1 | EST_HUMAN | IL3-HT0619-220700-222-Q12 HT0619 Homo sapiens cDNA |
| 7670 | 20629 | 33993 | 0.72 | 2.0E-18 | AA457619.1 | EST_HUMAN | hi94g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979984 3' similar to contains MER19.12 MER19 repetitive element; |
| 8487 | 21455 | 34872 | 0.52 | 2.0E-18 | BE439524.1 | EST_HUMAN | aa89d11.r1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838485 5' similar to TR:G61634 G61634 POLYPEPTIDE PR77 ; |
| | | | | | | | HTM1-160F1 HTM1 Homo sapiens cDNA |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 10407 | 23329 | 36813 | 1.31 | 2.0E-18 | AW151673.1 | EST_HUMAN | x157e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12 MER10 repetitive element; |
| 10407 | 23329 | 36814 | 1.31 | 2.0E-18 | AW151673.1 | EST_HUMAN | x157e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12 MER10 repetitive element; |
| 11319 | 24269 | 37797 | 3.07 | 2.0E-18 | AW47079.1 | EST_HUMAN | hs33d06.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.b3 THR repetitive element; |
| 12039 | 24914 | 38508 | 2.88 | 2.0E-18 | AW151299.1 | EST_HUMAN | xg47d09.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2630728 3' similar to contains MER8.b2 MER8 repetitive element; |
| 12461 | 14197 | | 3.97 | 2.0E-18 | BE256097.1 | EST_HUMAN | 601114352F1 NIH_JVGC_16 Homo sapiens cDNA clone IMAGE:3355044 5' ye43g05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120536 5' similar to contains L1 repetitive element; |
| 4445 | 17471 | | 0.93 | 1.0E-18 | T95406.1 | EST_HUMAN | AV653405 GLC Homo sapiens cDNA clone GLCDKE11 3' |
| 5429 | 18532 | 31412 | 2.71 | 1.0E-18 | AV653405.1 | EST_HUMAN | Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds |
| 5650 | 18748 | 31914 | 1.87 | 1.0E-18 | D00099.1 | NT | Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds |
| 5650 | 18748 | 31915 | 1.87 | 1.0E-18 | D00099.1 | NT | Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds |
| 6597 | 19657 | 32929 | 1.33 | 1.0E-18 | AL163280.2 | NT | Homo sapiens chromosome 21 segment HS21C080 |
| 8785 | 21752 | 35174 | 1.13 | 1.0E-18 | AL148288.1 | EST_HUMAN | oz69d09.x1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1680693 3' similar to contains L1.1' L1 repetitive element; |
| 10259 | 23184 | 36669 | 4.28 | 1.0E-18 | U91328.1 | NT | Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NP73) gene, complete cds |
| 12412 | 25184 | 31821 | 6.49 | 1.0E-18 | AF003529.1 | NT | Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions |
| 547 | 13618 | 26540 | 5.55 | 9.0E-19 | AA281961.1 | EST_HUMAN | z111d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 MER19 repetitive element; |
| 548 | 13618 | 26540 | 4.1 | 9.0E-19 | AA281961.1 | EST_HUMAN | z111d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 MER19 repetitive element; |
| 8181 | 21151 | | 5.71 | 9.0E-19 | F08888.1 | EST_HUMAN | HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05 |
| 9036 | 22002 | 35423 | 2.64 | 9.0E-19 | AL163203.2 | NT | Homo sapiens chromosome 21 segment HS21C003 |
| 9036 | 22002 | 35424 | 2.64 | 9.0E-19 | AL163203.2 | NT | Homo sapiens chromosome 21 segment HS21C003 |
| 11462 | 24405 | 37863 | 3.37 | 9.0E-19 | AB032669.1 | NT | Homo sapiens mRNA for KIAA1143 protein, partial cds |
| 12172 | 13618 | 26540 | 1.94 | 9.0E-19 | AA281961.1 | EST_HUMAN | z111d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 MER19 repetitive element; |
| 1050 | 14096 | | 1.31 | 8.0E-19 | AW974902.1 | EST_HUMAN | EST387007 MAGE resequences, MAGN Homo sapiens cDNA |
| 4433 | 17460 | | 0.96 | 8.0E-19 | P08548 | SWISSPROT | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| 8488 | 21456 | 34873 | 1.04 | 8.0E-19 | BE158936.1 | EST_HUMAN | MRO-HT0404-210200-001-g06 HT0404 Homo sapiens cDNA |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 2257 | 15271 | 28296 | 1.43 | 7.0E-19 | 4758139 | NT | Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 6 (RNA helicase, 54kD) (DDX6) mRNA |
| 6598 | 19658 | 32930 | 1.95 | 7.0E-19 | AF092090.1 | NT | Rattus norvegicus cp151 mRNA, partial cds |
| 7519 | 20484 | 33845 | 1.02 | 7.0E-19 | P26444 | SWISSPROT | BETA CRYSTALLIN A2 |
| 10372 | 23295 | 36771 | 0.43 | 7.0E-19 | A1344591.1 | EST_HUMAN | t601c08.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2052302 3' |
| 12313 | 25969 | | 3.28 | 7.0E-19 | AA705884.1 | EST_HUMAN | z60b01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:435148 3' |
| 3782 | 16833 | | 1.6 | 6.0E-19 | AW852930.1 | EST_HUMAN | PMD-CT0248-131099-001-g01 CT0248 Homo sapiens cDNA |
| 4490 | 17515 | 30403 | 1.44 | 6.0E-19 | P34986 | SWISSPROT | OLFACTORY RECEPTOR 6 (M50) |
| 4490 | 17515 | 30404 | 1.44 | 6.0E-19 | P34986 | SWISSPROT | OLFACTORY RECEPTOR 6 (M50) |
| 4837 | 17854 | | 1.47 | 6.0E-19 | AJ271735.1 | NT | Homo sapiens Xq pseudautosomal region; segment 1/2 |
| 5064 | 18074 | 30854 | 1.29 | 6.0E-19 | AL120817.1 | EST_HUMAN | DKFZp762F192.1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762F192 5' |
| 5958 | 19043 | 32242 | 4.88 | 5.0E-19 | Q00193 | SWISSPROT | ZONA PELLUCIDA SPERM-BINDING PROTEIN B PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP-X) (RC55) |
| 6342 | 19411 | 32662 | 0.69 | 5.0E-19 | AW663302.1 | EST_HUMAN | h77b06.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968787 5' |
| 10780 | 23711 | 37213 | 0.78 | 5.0E-19 | AJ287699.1 | NT | Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exon 14 |
| 11865 | 24747 | 38329 | 4.78 | 5.0E-19 | AW183725.1 | EST_HUMAN | X87602.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2664171 3' similar to contains element MSR1 repetitive element : |
| 556 | 13626 | 26544 | 0.89 | 4.0E-19 | AB007970.1 | NT | Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501 |
| 2691 | 15887 | 28704 | 1.69 | 4.0E-19 | BF697362.1 | EST_HUMAN | 602130910F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287674 5' |
| 5470 | 18571 | 31481 | 1.05 | 4.0E-19 | AF224669.1 | NT | Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds |
| 3866 | 16905 | 29812 | 1.4 | 3.0E-19 | Q28997 | SWISSPROT | BETA-2 ADRENERGIC RECEPTOR |
| 3866 | 16905 | 29813 | 1.4 | 3.0E-19 | Q28997 | SWISSPROT | BETA-2 ADRENERGIC RECEPTOR |
| 4315 | 17344 | 30227 | 0.69 | 3.0E-19 | O43900 | SWISSPROT | LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6) |
| 4315 | 17344 | 30228 | 0.69 | 3.0E-19 | O43900 | SWISSPROT | LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6) |
| 4475 | 17501 | 30385 | 1.78 | 3.0E-19 | AV708136.1 | EST_HUMAN | AV708136 ADC Homo sapiens cDNA clone ADCAMA11 5' |
| 5352 | 18457 | | 0.63 | 3.0E-19 | AF223467.1 | NT | Homo sapiens NPD008 protein (NPD008) mRNA, complete cds |
| 7612 | 20572 | | 1.81 | 3.0E-19 | 11432214 | NT | Homo sapiens similar to aldo-keto reductase family 1, member B11 (aldose reductase-like) (H. sapiens) (LOC63222), mRNA |
| 9814 | 21137 | 34539 | 1.11 | 3.0E-19 | X89685.1 | NT | M.musculus mRNA for TPO333 protein |
| 12552 | 25275 | | 16.28 | 3.0E-19 | AF165620.1 | NT | Homo sapiens phorbol 1 protein (PBI) mRNA, complete cds |
| 2567 | 15566 | 26588 | 27.04 | 2.0E-19 | AL163201.2 | NT | Homo sapiens chromosome 21 segment HS21C001 |
| 4474 | 17500 | | 1.23 | 2.0E-19 | AJ311783.1 | EST_HUMAN | q961602.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1915898 3' similar to TR:Q69386 Q69386 POL/ENV GENE ; |

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Table 4
Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|-----------------------------|-------------------------------|---|
| 6172 | 19247 | 32480 | 0.61 | 2.0E-19 | AV731382.1 | EST_HUMAN | AV731382 HTF Homo sapiens cDNA clone HTFAZC06 5' |
| 7561 | 20524 | 33882 | 0.72 | 2.0E-19 | 7657286 | NT | Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA |
| 8673 | 21641 | 35066 | 9.35 | 2.0E-19 | AA012854.1 | EST_HUMAN | 2834c09.r1 Soares refina N2b4HR Homo sapiens cDNA clone IMAGE:360880 5' |
| 10269 | 23194 | 36682 | 0.66 | 2.0E-19 | Q95155 | SWISSPROT | OLFACTORY RECEPTOR-LIKE PROTEIN OLF2 |
| 482 | 13555 | | 2.11 | 1.0E-19 | BE408611.1 | EST_HUMAN | 6013040125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5' |
| 2174 | 15190 | 28211 | 1.66 | 1.0E-19 | H30795.1 | EST_HUMAN | y079g07.r1 Soares adult brain N2b4HB5Y Homo sapiens cDNA clone IMAGE:184188 5' similar to contains MER10 repetitive element; |
| 2729 | 15723 | | 2.48 | 1.0E-19 | D38044.1 | NT | Human gene for Ah-receptor, exon 7-9 |
| 2860 | 15920 | | 4.26 | 1.0E-19 | 4758977 | NT | Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA |
| 3412 | 16460 | 29361 | 1.18 | 1.0E-19 | AA834967.1 | EST_HUMAN | aj49b12.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1393631 3' similar to contains MER37.12 |
| 5186 | 18195 | | 0.9 | 1.0E-19 | AW117377.1 | EST_HUMAN | xd88h10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2804739 3' similar to contains L1.b2 L1 L1 repetitive element; |
| 6193 | 18267 | 32502 | 2.73 | 1.0E-19 | U12186.1 | NT | Oryctolagus cuniculus sodium/dicarboxylate cotransporter mRNA, partial cds |
| 6333 | 25995 | | 0.63 | 1.0E-19 | AA595527.1 | EST_HUMAN | ht22d03.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:953093 similar to contains L1.L1 L1 repetitive element; |
| 7690 | 20834 | 34213 | 0.99 | 1.0E-19 | U08813.1 | NT | Oryctolagus cuniculus Na+/glucose cotransporter-related protein mRNA, complete cds |
| 7690 | 20834 | 34214 | 0.99 | 1.0E-19 | U08813.1 | NT | Oryctolagus cuniculus Na+/glucose cotransporter-related protein mRNA, complete cds |
| 8085 | 25694 | | 0.71 | 1.0E-19 | AF200719.1 | NT | Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds |
| 8793 | 21760 | 35182 | 1.72 | 1.0E-19 | M64657.1 | NT | Rabbit phosphorylase kinase beta subunit mRNA, complete cds |
| 9093 | 22059 | | 2.74 | 1.0E-19 | T99920.1 | EST_HUMAN | y072b02.r1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:123243 5' similar to contains OFR repetitive element; |
| 10106 | 23032 | | 0.97 | 1.0E-19 | U60822.1 | NT | Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds |
| 10547 | 23469 | 36954 | 27.33 | 1.0E-19 | AW812259.1 | EST_HUMAN | RC0-ST0174-191099-031-b05 ST0174 Homo sapiens cDNA |
| 10557 | 23478 | 36974 | 2.1 | 1.0E-19 | N44631.1 | EST_HUMAN | y031a09.r1 Soares melanocyte 2Nb4HM Homo sapiens cDNA clone IMAGE:272872 5' |
| 11809 | 24684 | | 3.69 | 1.0E-19 | AW023137.1 | EST_HUMAN | df49h01.y1 Marfan Fetal Cochlea Homo sapiens cDNA clone IMAGE:2487000 5' |
| 6803 | 19857 | 33143 | 2.45 | 8.0E-20 | 7657286 | NT | Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA |
| 6803 | 19857 | 33144 | 2.45 | 8.0E-20 | 7657286 | NT | Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA |
| 7761 | 20714 | 34084 | 1.31 | 8.0E-20 | A1221371.1 | EST_HUMAN | qg86f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842089 3' |
| 7761 | 20714 | 34085 | 1.31 | 8.0E-20 | A1221371.1 | EST_HUMAN | qg86f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842089 3' |
| 3289 | 16342 | 29283 | 0.72 | 7.0E-20 | BF328455.1 | EST_HUMAN | PM4-AN0096-050900-003-a04 AN0096 Homo sapiens cDNA |
| 7188 | 18419 | 31220 | 5.56 | 7.0E-20 | AL138120.1 | EST_HUMAN | DKFZp547D092.r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D092 5' |
| 8841 | 21808 | 35227 | 9.11 | 7.0E-20 | AA557657.1 | EST_HUMAN | nl46c04.s1 NCI_CGAP_P14 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2 MER29 repetitive element; |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 8841 | 21808 | 35228 | 9.11 | 7.0E-20 | AA557657.1 | EST_HUMAN | nl46c04.s1 NCI_CGAP_P14 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2 |
| 12023 | 24899 | | 6.31 | 7.0E-20 | 6912633 | NT | MER29 repetitive element ; |
| 3568 | 16613 | 29535 | 3.93 | 6.0E-20 | P39188 | SWISSPROT | Homo sapiens ribosomal protein L13a (RPL13A), mRNA |
| 4301 | 17330 | 30210 | 2.98 | 6.0E-20 | BE622434.1 | EST_HUMAN | ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY |
| 4826 | 17647 | | 1.05 | 5.0E-20 | AV725123.1 | EST_HUMAN | 601441231F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916231 5' |
| 7322 | 20293 | 33636 | 1.19 | 5.0E-20 | AF075301.1 | EST_HUMAN | AV725123 HTC Homo sapiens cDNA clone HTCBA01 5' |
| 8277 | 21246 | 34657 | 5 | 5.0E-20 | W90525.1 | EST_HUMAN | AF076301 Human fetal liver cDNA library Homo sapiens cDNA clone HA0250 |
| 8277 | 21246 | 34658 | 5 | 5.0E-20 | W90525.1 | EST_HUMAN | zh78d08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to contains MER30.t1 MER30 repetitive element ; |
| 8440 | 21409 | 34822 | 0.79 | 5.0E-20 | BE165980.1 | EST_HUMAN | zh78d08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to contains MER30.t1 MER30 repetitive element ; |
| 9187 | 22153 | 35582 | 1.24 | 5.0E-20 | AB028174.1 | NT | MR3-HT0487-150200-113-q01 HT0487 Homo sapiens cDNA |
| 9187 | 22153 | 35583 | 1.24 | 5.0E-20 | AB028174.1 | NT | Mus musculus MMAN-g mRNA, complete cds |
| 9800 | 21123 | | 0.93 | 5.0E-20 | O60809 | SWISSPROT | Mus musculus MMAN-g mRNA, complete cds |
| 1624 | 14657 | 27635 | 1.73 | 4.0E-20 | AL163247.2 | NT | HYPOTHETICAL PROTEIN DJ845024.1 |
| 5732 | 18826 | | 0.89 | 4.0E-20 | Q99880 | SWISSPROT | Homo sapiens chromosome 21 segment HS21C047 |
| 8258 | 21227 | | 5.27 | 4.0E-20 | AI874352.1 | EST_HUMAN | HISTONE H2B C (H2B/C) |
| 10865 | 23785 | 37286 | 1.9 | 4.0E-20 | AW937468.1 | EST_HUMAN | z64g03.x1 NCI_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2293396 3' |
| 2149 | 15165 | 28181 | 0.91 | 3.0E-20 | U03888.1 | NT | QV3-DT0043-090200-080-c04 DT0043 Homo sapiens cDNA |
| 4237 | 17266 | 30153 | 1.63 | 3.0E-20 | P23273 | SWISSPROT | Human BXP21 gene |
| 4655 | 17876 | 30582 | 1.43 | 3.0E-20 | AA037616.1 | EST_HUMAN | OLFACTORY RECEPTOR-LIKE PROTEIN I14 |
| 9287 | 22253 | | 3.32 | 3.0E-20 | D14547.1 | NT | z636b12.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:484895 3' similar to contains L1.13 L1 repetitive element ; |
| 10694 | 23606 | 37099 | 0.68 | 3.0E-20 | BF185264.1 | EST_HUMAN | Human DNA, SINE repetitive element |
| 11024 | 23989 | | 1.59 | 3.0E-20 | P11369 | SWISSPROT | 601843561F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4064343 5' |
| 11840 | 24723 | 38308 | 8.22 | 3.0E-20 | AI284244.1 | EST_HUMAN | RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE] |
| 11840 | 24723 | 38309 | 8.22 | 3.0E-20 | AI284244.1 | EST_HUMAN | q70d02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1864803 3' similar to contains Alu repetitive element ; |
| 12326 | 25130 | 31849 | 4.15 | 3.0E-20 | BE888422.1 | EST_HUMAN | q70d02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1864803 3' similar to contains Alu repetitive element ; |
| 831 | 13898 | | 33.91 | 2.0E-20 | AW303868.1 | EST_HUMAN | q70d02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1864803 3' similar to contains Alu repetitive element ; |

Table 4

Single Exon Probes Expressed in Bone Marrow

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 1113 | 14157 | 27107 | 3.88 | 2.0E-20 | AA516335.1 | EST_HUMAN | hg69h09.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:940097 similar to TR:G1224066 G1224066 ORF2: FUNCTION UNKNOWN.; |
| 1113 | 14157 | 27108 | 3.88 | 2.0E-20 | AA516335.1 | EST_HUMAN | hg69h09.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:940097 similar to TR:G1224066 G1224066 ORF2: FUNCTION UNKNOWN.; |
| 2828 | 13888 | | 15.67 | 2.0E-20 | AW303888.1 | EST_HUMAN | x24e10.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2781098 3' similar to SW:RS5_MOUSE P87461 40S RIBOSOMAL PROTEIN S5.; |
| 4983 | 17998 | 30886 | 4.76 | 2.0E-20 | Q28983 | SWISSPROT | ZONADHESIN PRECURSOR |
| 4983 | 17998 | 30887 | 4.76 | 2.0E-20 | Q28983 | SWISSPROT | ZONADHESIN PRECURSOR |
| 8455 | 21424 | 34840 | 0.9 | 2.0E-20 | AA309457.1 | EST_HUMAN | EST180326 Liver III Homo sapiens cDNA 5' end |
| 9545 | 22508 | 35957 | 7.56 | 2.0E-20 | D10083.1 | NT | Homo sapiens RGH1 gene, retrovirus-like element |
| 9545 | 22508 | 35958 | 7.56 | 2.0E-20 | D10083.1 | NT | Homo sapiens RGH1 gene, retrovirus-like element |
| 12703 | 25714 | 31611 | 3.98 | 2.0E-20 | H56371.1 | EST_HUMAN | CHR220310 Chromosome 22 exon Homo sapiens cDNA clone C22_391 5' |
| 2029 | 15822 | 28063 | 4.32 | 1.0E-20 | AA281951.1 | EST_HUMAN | z11d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 MER19 repetitive element.; |
| 4467 | 17493 | 30380 | 1.04 | 1.0E-20 | BF115158.1 | EST_HUMAN | hr84b06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3135155 3' similar to contains L1.12 L1 repetitive element.; |
| 7079 | 20100 | 33411 | 1.04 | 1.0E-20 | AF049567.1 | EST_HUMAN | AF049567 Human activated dendritic cell mRNA Homo sapiens cDNA clone GA05 |
| 9518 | 22481 | 35926 | 2.24 | 1.0E-20 | 11418491 | NT | Homo sapiens Autosomal Highly Conserved Protein (AHCP), mRNA |
| 11878 | 24761 | 38346 | 2.11 | 1.0E-20 | AF223391.1 | NT | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced |
| 12458 | 25215 | | 3.09 | 1.0E-20 | AA420453.1 | EST_HUMAN | nc60g08.r1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:745684 similar to contains L1.13 L1 repetitive element.; |
| 2923 | 15981 | | 1 | 9.0E-21 | AJ003514.1 | EST_HUMAN | AJ003514 Selected chromosome 21 cDNA library Homo sapiens cDNA clone MPI12-8J21 |
| 12175 | 25023 | | 3.77 | 9.0E-21 | AW898189.1 | EST_HUMAN | RC3-NN0088-090500-021-b03 NN0068 Homo sapiens cDNA |
| 9163 | 22129 | | 1.13 | 8.0E-21 | AW674891.1 | EST_HUMAN | b630a02.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2884714 5' similar to SW:NIAM_HUMAN O95169 NADH-UBIQUINONE OXIDOREDUCTASE ASH1 SUBUNIT PRECURSOR.; |
| 11866 | 24748 | 38330 | 4.38 | 8.0E-21 | AA809411.1 | EST_HUMAN | cb71f08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336835 3' |
| 12342 | 25140 | | 2.94 | 8.0E-21 | Q21330 | SWISSPROT | ATP SYNTHASE A CHAIN (PROTEIN 6) |
| 2082 | 15096 | 28115 | 1.59 | 7.0E-21 | P15900 | SWISSPROT | LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3) |
| 2082 | 15099 | 28116 | 1.59 | 7.0E-21 | P15900 | SWISSPROT | LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3) |
| 3716 | 16759 | 29671 | 0.63 | 7.0E-21 | AL163300.2 | NT | Homo sapiens chromosome 21 segment HS21C100 |
| 4283 | 17312 | | 5.22 | 7.0E-21 | AA046502.1 | EST_HUMAN | z167a06.r1 Soares_pregnan1 uterus_NbHPU Homo sapiens cDNA clone IMAGE:487858 5' |
| 6573 | 19633 | 32900 | 0.81 | 7.0E-21 | AL163218.2 | NT | Homo sapiens chromosome 21 segment HS21C018 |